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(54) Title: CHLAMYDIA PNEUMONIAE GENOME SEQUENCE

(57) Abstract

C. pneumoniae genome sequence and analysis of the encoded polypeptides and RNAs are provided. The *C. pneumoniae* gene nucleic acid compositions find use in identifying homologous or related proteins and the DNA sequences encoding such proteins; in producing compositions that modulate the expression or function of the protein; and in studying associated physiological pathways. In addition, modulation of the gene activity *in vivo* is used for prophylactic and therapeutic purposes, such as identification of cell type based on expression, and the like.

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CHLAMYDIA PNEUMONIAE GENOME SEQUENCE

CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is related to 60/128,606, filed April 8, 1999 and

5 60/108,279, filed November 12, 1998, which are incorporated herein by reference.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

10 ## FIELD OF THE INVENTION

This invention relates to nucleic acids and polypeptides from *Chlamydia pneumoniae* and to their use in the diagnosis, prevention and treatment of diseases associated with *C. pneumoniae*.

15 ## BACKGROUND OF THE INVENTION

Chlamydiaceae is a family of obligate intracellular parasite with a tropism for epithelial cells lining the mucus membranes. The bacteria have two morphologically distinct forms, "elementary body" and "reticulate body". The elementary body is the infectious form, and has a rigid cell wall, primarily of cross-linked outer membrane

20 proteins. The reticulate body is the intracellular, metabolically active form. A unique developmental cycle between these two forms characterizes *Chlamydia* growth.

C. pneumoniae is a human respiratory pathogen that causes acute respiratory disease, and approximately 10% of community-acquired pneumonia. Antibody prevalence studies have shown that virtually everyone is infected with *C.*

25 *pneumoniae* at some time, and that reinfection is common. In addition to respiratory disease, studies have shown an association of this organism with coronary artery disease. It has been demonstrated in atherosclerotic lesions of the aorta and coronary arteries by immunocytochemistry and by polymerase chain reaction (Kuo *et al.* (1993) J Infect Dis **167**(4):841-849).

30 Recent reports have further demonstrated the presence of *C. pneumoniae* in the walls of abdominal aortic aneurysms (Juvonen *et al.* (1997) J Vasc Surg **25**(3):499-505). Abdominal aortic aneurysms are frequently associated with atherosclerosis, and inflammation may be an important factor in aneurysmal dilatation.

C. pneumoniae may play a role in maintaining an inflammation and triggering the development of aortic aneurysms.

Muhlestein *et al.* (1996) JACC 27:1555-61, reported a differential incidence of *Chlamydia* species within the coronary artery wall of patients with atherosclerosis versus those with other forms of cardiovascular disease. The extremely high rate of possible infection in patients with symptomatic atherosclerotic disease compared to the very low rate in patients with normal coronary arteries or coronary artery disease from chronic transplant rejection provides evidence for a direct link between the atherosclerotic process and *Chlamydia* infection. Because a history of chlamydial infection is so prevalent in the population, the issue of causality remains. On a physiologic and pathologic level, abnormal interactions among endothelial cells, platelets, macrophages and lymphocytes may lead to a cascade of events resulting in acute endothelial damage, thrombosis and repair, chronically leading to the development of atheroma in blood vessels.

C. pneumoniae is related to other *Chlamydia* species, but the level of sequence similarity is relatively low. Very little is known about the biology of this organism, although it appears to be an important human pathogen. Allelic diversity and structural relationships between specific genes of Chlamydial species is described in Kaltenboeck *et al.* (1993) J Bacteriol 175(2):487-502; Gaydos *et al.* (1992) Infect Immun 60(12):5319-5323; Everett *et al.* (1997) Int J Syst Bacteriol 47(2):461-473; and Pudjiatmoko *et al.* (1997) Int J Syst Bacteriol 47(2):425-431.

A number of studies have been published describing methods for detection of *C. pneumoniae*, and for distinguishing between Chlamydial species. Such methods include PCR detection (Rasmussen *et al.* (1992) Mol Cell Probes 6(5):389-394; Holland *et al.* (1990) J Infect Dis 162(4):984-987); a simplified polymerase chain reaction-enzyme immunoassay (Wilson et al. (1996) J Appl Bacteriol 80(4):431-438); sequence determination and restriction endonuclease cleavage (Herrmann *et al.* (1996) J Clin Microbiol 34(8):1897-1902).

Antigenic and molecular analyses of different *C. pneumoniae* strains is described in Jantos *et al.* (1997) J Clin Microbiol 35(3):620-623. Some genes of *C. pneumoniae* have been isolated and sequenced. These include the Gro E operon (Kikuta et al. (1991) Infect Immun 59(12):4665-4669); the major outer membrane protein Perez *et*

al. (1991) Infect Immun 59(6):2195-2199; the DnaK protein homolog (Kornak *et al.*
(1991) Infect Immun 59(2):721-725); as well as a number of ribosomal and other genes.

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SUMMARY OF THE INVENTION

This invention provides the genomic sequence of *Chlamydia pneumoniae.*
The sequence information is useful for a variety of diagnostic and analytical methods.
The genomic sequence may be embodied in a variety of media, including computer
10   readable forms, or as a nucleic acid comprising a selected fragment of the sequence.
Such fragments generally consist of an open reading frame, transcriptional or translational
control elements, or fragments derived therefrom. Proteins encoded by the open reading
frames are useful for diagnostic purposes, as well as for their enzymatic or structural
activity.

15

DEFINITIONS

The term "amino acid" refers to naturally occurring and synthetic amino
acids, as well as amino acid analogs and amino acid mimetics that function in a manner
similar to the naturally occurring amino acids. Naturally occurring amino acids are those
20   encoded by the genetic code, as well as those amino acids that are later modified, e.g.,
hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to
compounds that have the same basic chemical structure as a naturally occurring amino
acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and
an R group., e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl
25   sulfonium Such analogs have modified R groups (e.g., norleucine) or modified peptide
backbones, but retain the same basic chemical structure as a naturally occurring amino
acid. Amino acid mimetics refers to chemical compounds that have a structure that is
different from the general chemical structure of an amino acid, but that functions in a
manner similar to a naturally occurring amino acid.

30   Amino acids may be referred to herein by either their commonly known
three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB
Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by
their commonly accepted single-letter codes.

"Amplification" primers are oligonucleotides comprising either natural or analogue nucleotides that can serve as the basis for the amplification of a select nucleic acid sequence. They include, e.g., polymerase chain reaction primers and ligase chain reaction oligonucleotides.

5   "Antibody" refers to an immunoglobulin molecule able to bind to a specific epitope on an antigen. Antibodies can be a polyclonal mixture or monoclonal. Antibodies can be intact immunoglobulins derived from natural sources or from recombinant sources and can be immunoreactive portions of intact immunoglobulins. Antibodies may exist in a variety of forms including, for example, Fv, F_{ab}, and $F(ab)_2$, as

10   well as in single chains. Single-chain antibodies, in which genes for a heavy chain and a light chain are combined into a single coding sequence, may also be used.

An "antigen" is a molecule that is recognized and bound by an antibody, e.g., peptides, carbohydrates, organic molecules, or more complex molecules such as glycolipids and glycoproteins. The part of the antigen that is the target of antibody

15   binding is an antigenic determinant and a small functional group that corresponds to a single antigenic determinant is called a hapten.

"Biological sample" refers to any sample obtained from a living or dead organism. Examples of biological samples include biological fluids and tissue specimens. Such biological samples can be prepared for analysis of the presence of *C. pneumoniae*

20   nucleic acids, proteins, or antibodies specifically reactive with the proteins.

The term "*C. pneumoniae* gene" shall be intended to mean the open reading frame encoding specific *C. pneumoniae* polypeptides, as well as adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 2 kb beyond the coding region, but possibly further in either direction. The gene may be

25   introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially

30   identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues

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(Batzer *et al.*, *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* 260:2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes* 8:91-98 (1994)). Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all

5   encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the

10   nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

15   As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid.

20   Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

           The following groups each contain amino acids that are conservative substitutions for one another:

25   1)   Alanine (A), Glycine (G);

        2)   Serine (S), Threonine (T);

        3)   Aspartic acid (D), Glutamic acid (E);

        4)   Asparagine (N), Glutamine (Q);

        5)   Cysteine (C), Methionine (M);

30   6)   Arginine (R), Lysine (K), Histidine (H);

        7)   Isoleucine (I), Leucine (L), Valine (V); and

        8)   Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

see, e.g., Creighton, *Proteins* (1984)).

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence over a

5   comparison window, as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. This definition also refers to the complement of a test sequence, which has a designated percent sequence or subsequence complementarity when the test sequence has a designated or substantial identity to a reference sequence. For example, a designated amino acid percent identity

10   of 95% refers to sequences or subsequences that have at least about 95% amino acid identity when aligned for maximum correspondence over a comparison window as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Such sequences would then be said to have substantial identity, or to be substantially identical to each other. Preferably, sequences have at least

15   about 70% identity, more preferably 80% identity, more preferably 90-95% identity and above. Preferably, the percent identity exists over a region of the sequence that is at least about 25 amino acids in length, more preferably over a region that is 50-100 amino acids in length.

When percentage of sequence identity is used in reference to proteins or

20   peptides, it is recognized that residue positions that are not identical often differ by conservative amino acid substitutions, where amino acids residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may

25   be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a

30   conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated according to, e.g., the algorithm of Meyers & Miller, *Computer Applic. Biol. Sci.* 4:11-17 (1988) e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA)..

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For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are

5   designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated or default program parameters.

A comparison window includes reference to a segment of any one of the
10   number of contiguous positions selected from the group consisting of from 25 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison
15   can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics
20   Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g.,* Ausubel *et al., supra*).

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a tree or
25   dendogram showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J. Mol. Evol.* 35:351-360 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment
30   procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The

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final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the

5 percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, e.g, version 7.0 (Devereaux *et al., Nuc. Acids Res.* 12:387-395 (1984).

Another example of algorithm that is suitable for determining percent
10 sequence identity (i.e., substantial similarity or identity) is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query
15 sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al, supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the
20 cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues, always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by
25 the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10,
30 M=5, N=4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as default parameters a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by

5   which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

10   An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ

15   only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below.

       Another indication that polynucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Stringent

20   conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically stringent conditions for a

25   Southern blot protocol involve hybridizing in a buffer comprising 5x SSC, 1% SDS at 65°C or hybridizing in a buffer containing 5x SSC and 1% SDS at 42°C and washing at 65°C with a 0.2x SSC, 0.1% SDS wash.

       A "label" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include

30   ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, dioxigenin, or haptens and proteins for which antisera or monoclonal antibodies are available.

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which

5   have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

Unless otherwise indicated, a particular nucleic acid sequence also

10   implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a

15   nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester

20   bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably

25   directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

A labeled nucleic acid probe or oligonucleotide is one that is bound, either

30   covalently, through a linker, or through ionic, van der Waals or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

"Pharmaceutically acceptable" means a material that is not biologically or otherwise undesirable, i.e., the material can be administered to an individual along with a *Chlamydia* antigen without causing any undesirable biological effects or interacting in a deleterious manner with any of the other components of the pharmaceutical composition.

5   The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an analog or mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

10   The phrase "specifically or selectively hybridizing to," refers to hybridization between a probe and a target sequence in which the probe binds substantially only to the target sequence, forming a hybridization complex, when the target is in a heterogeneous mixture of polynucleotides and other compounds. Such hybridization is determinative of the presence of the target sequence. Although the probe

15   may bind other unrelated sequences, at least 90%, preferably 95% or more of the hybridization complexes formed are with the target sequence.

The term "recombinant" when used with reference to a cell, or nucleic acid, or vector, indicates that the cell, or nucleic acid, or vector, has been modified by the introduction of a heterologous nucleic acid or the alteration of a native nucleic acid, or

20   that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

The phrase "specifically immunoreactive with", when referring to a protein

25   or peptide, refers to a binding reaction between the protein and an antibody which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other compounds. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such

30   conditions may require an antibody that is selected for its specificity for a particular protein. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein and are described in detail below.

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The phrase "substantially pure" or "isolated" when referring to a
Chlamydia peptide or protein, means a chemical composition which is free of other
subcellular components of the *Chlamydia* organism. Typically, a monomeric protein is
substantially pure when at least about 85% or more of a sample exhibits a single
5   polypeptide backbone. Minor variants or chemical modifications may typically share the
same polypeptide sequence. Depending on the purification procedure, purities of 85%,
and preferably over 95% pure are possible. Protein purity or homogeneity may be
indicated by a number of means well known in the art, such as polyacrylamide gel
electrophoresis of a protein sample, followed by visualizing a single polypeptide band on
10   a polyacrylamide gel upon silver staining. For certain purposes high resolution will be
needed and HPLC or a similar means for purification utilized.

DETAILED DESCRIPTION

The present invention provides the nucleotide sequence of the *C.*
15   *pneumoniae* genome SEQ ID NO: 1 or a representative fragment thereof, in a form which
can be readily used, analyzed, and interpreted by a skilled artisan. As used herein, a
"representative fragment" of the nucleotide sequence depicted in SEQ ID NO: 1 refers to
any portion which is not presently represented within a publicly available database.
Preferred representative fragments of the present invention are open reading frames,
20   expression modulating fragments, uptake modulating fragments, and fragments which can
be used to diagnose the presence of *C. pneumoniae* in sample. Using the information
provided in the present application, together with routine cloning and sequencing
methods, one of ordinary skill in the art will be able to clone and sequence all
"representative fragments" of interest including open reading frames (ORFs) encoding a
25   large variety of *C. pneumoniae* proteins. A non-limiting identification of such preferred
representative fragments is provided in Tables 2 and 3.

Diagnostic use of *C. pneumoniae* nucleic acids

Hybridization-based assays

Using the nucleic acids disclosed here, one of skill can design nucleic acid
30   hybridization-based assays for the detection of *C. pneumoniae*. Any of a number of well
known techniques for the specific detection of target nucleic acids can be used.
Exemplary hybridization-based assays include, but are not limited to, traditional "direct

probe" methods such as Southern Blots, dot blots, in situ hybridization (e.g., FISH), PCR, and the like. The methods can be used in a wide variety of formats including, but not limited to substrate- (e.g. membrane or glass) bound methods or array-based approaches as described below. As noted above, this invention also embraces methods for detecting

5   the presence of Chlamydia DNA or RNA in biological samples. These sequences can be used to detect Chlamydia in biological samples from patients suspected of being infected. A variety of methods of specific DNA and RNA measurement using nucleic acid hybridization techniques are known to those of skill in the art (see Sambrook et al., supra).

10   In situ hybridization assays are well known (e.g., Angerer (1987) Meth. Enzymol 152: 649). Generally, in situ hybridization comprises the following major steps: (1) fixation of tissue or biological structure to analyzed; (2) prehybridization treatment of the biological structure to increase accessibility of target DNA, and to reduce nonspecific binding; (3) hybridizaticn of the mixture of nucleic acids to the nucleic acid in the

15   biological structure or tissue; (4) post-hybridization washes to remove nucleic acid fragments not bound in the hybridization and (5) detection of the hybridized nucleic acid fragments. The reagent used in each of these steps and the conditions for use vary depending on the particular application.

In a typical in situ hybridization assay, cells are fixed to a solid support,

20   typically a glass slide. If a nucleic acid is to be probed, the cells are typically denatured with heat or alkali. The cells are then contacted with a hybridization solution at a moderate temperature to permit annealing of labeled probes specific to the nucleic acid sequence encoding the protein. The targets (e.g., cells) are then typically washed at a predetermined stringency or at an increasing stringency until an appropriate signal to

25   noise ratio is obtained.

The nucleic acids of this invention are particularly well suited to array-based hybridization formats. Arrays are a multiplicity of different "probe" or "target" nucleic acids (or other compounds) attached to one or more surfaces (e.g., solid, membrane, or gel). In a preferred embodiment, the multiplicity of nucleic acids (or other

30   moieties) is attached to a single contiguous surface or to a multiplicity of surfaces juxtaposed to each other.

In an array format a large number of different hybridization reactions can be run essentially "in parallel." This provides rapid, essentially simultaneous, evaluation

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of a number of hybridizations in a single "experiment". Methods of performing hybridization reactions in array based formats are well known to those of skill in the art (*see, e.g.,* Pastinen (1997) Genome Res. 7: 606-614; Jackson (1996) *Nature Biotechnology* 14:1685; Chee (1995) *Science* 274: 610; WO 96/17958.

5   Arrays, particularly nucleic acid arrays can be produced according to a wide variety of methods well known to those of skill in the art. For example, in a simple embodiment, "low density" arrays can simply be produced by spotting (*e.g.* by hand using a pipette) different nucleic acids at different locations on a solid support (*e.g.* a glass surface, a membrane, *etc.*).

10   This simple spotting, approach has been automated to produce high density spotted arrays (*see, e.g.,* U.S. Patent No: 5,807,522). This patent describes the use of an automated systems that taps a microcapillary against a surface to deposit a small volume of a biological sample. The process is repeated to generate high density arrays. Arrays can also be produced using oligonucleotide synthesis technology. Thus, for
15   example, U.S. Patent No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092 teach the use of light-directed combinatorial synthesis of high density oligonucleotide arrays.

          Many methods for immobilizing nucleic acids on a variety of solid surfaces are known in the art. A wide variety of organic and inorganic polymers, as well
20   as other materials, both natural and synthetic, can be employed as the material for the solid surface. Illustrative solid surfaces include, e.g., nitrocellulose, nylon, glass, quartz, diazotized membranes (paper or nylon), silicones, polyformaldehyde, cellulose, and cellulose acetate. In addition, plastics such as polyethylene, polypropylene, polystyrene, and the like can be used. Other materials which may be employed include paper,
25   ceramics, metals, metalloids, semiconductive materials, cermets or the like. In addition, substances that form gels can be used. Such materials include, e.g., proteins (e.g., gelatins), lipopolysaccharides, silicates, agarose and polyacrylamides. Where the solid surface is porous, various pore sizes may be employed depending upon the nature of the system.

30   In preparing the surface, a plurality of different materials may be employed, particularly as laminates, to obtain various properties. For example, proteins (*e.g.,* bovine serum albumin) or mixtures of macromolecules (*e.g.,* Denhardt's solution) can be employed to avoid non-specific binding, simplify covalent conjugation, enhance

signal detection or the like. If covalent bonding between a compound and the surface is desired, the surface will usually be polyfunctional or be capable of being polyfunctionalized. Functional groups which may be present on the surface and used for linking can include carboxylic acids, aldehydes, amino groups, cyano groups, ethylenic

5   groups, hydroxyl groups, mercapto groups and the like. The manner of linking a wide variety of compounds to various surfaces is well known and is amply illustrated in the literature.

For example, methods for immobilizing nucleic acids by introduction of various functional groups to the molecules is known (see, e.g., Bischoff (1987) Anal.

10   Biochem., 164: 336-344; Kremsky (1987) Nucl. Acids Res. 15: 2891-2910). Modified nucleotides can be placed on the target using PCR primers containing the modified nucleotide, or by enzymatic end labeling with modified nucleotides. Use of glass or membrane supports (e.g., nitrocellulose, nylon, polypropylene) for the nucleic acid arrays of the invention is advantageous because of well developed technology employing

15   manual and robotic methods of arraying targets at relatively high element densities. Such membranes are generally available and protocols and equipment for hybridization to membranes is well known.

Target elements of various sizes, ranging from 1 mm diameter down to 1 µm can be used. Smaller target elements containing low amounts of concentrated, fixed

20   probe DNA are used for high complexity comparative hybridizations since the total amount of sample available for binding to each target element will be limited. Thus it is advantageous to have small array target elements that contain a small amount of concentrated probe DNA so that the signal that is obtained is highly localized and bright. Such small array target elements are typically used in arrays with densities greater than

25   $10^4/cm^2$. Relatively simple approaches capable of quantitative fluorescent imaging of 1 cm^2 areas have been described that permit acquisition of data from a large number of target elements in a single image (see, e.g., Wittrup (1994) Cytometry 16:206-213).

If fluorescently labeled nucleic acid samples are used, arrays on solid surface substrates with much lower fluorescence than membranes, such as glass, quartz,

30   or small beads, can achieve much better sensitivity. Substrates such as glass or fused silica are advantageous in that they provide a very low fluorescence substrate, and a highly efficient hybridization environment. Covalent attachment of the target nucleic acids to glass or synthetic fused silica can be accomplished according to a number of

known techniques (described above). Nucleic acids can be conveniently coupled to glass using commercially available reagents. For instance, materials for preparation of silanized glass with a number of functional groups are commercially available or can be prepared using standard techniques (see, *e.g.*, Gait (1984) Oligonucleotide Synthesis: A

5   Practical Approach, IRL Press, Wash., D.C.). Quartz cover slips, which have at least 10-fold lower autofluorescence than glass, can also be silanized.

Alternatively, probes can also be immobilized on commercially available coated beads or other surfaces. For instance, biotin end-labeled nucleic acids can be bound to commercially available avidin-coated beads. Streptavidin or anti-digoxigenin

10   antibody can also be attached to silanized glass slides by protein-mediated coupling using e.g., protein A following standard protocols (see, *e.g.*, Smith (1992) *Science* 258: 1122-1126). Biotin or digoxigenin end-labeled nucleic acids can be prepared according to standard techniques. Hybridization to nucleic acids attached to beads is accomplished by suspending them in the hybridization mix, and then depositing them on the glass substrate

15   for analysis after washing. Alternatively, paramagnetic particles, such as ferric oxide particles, with or without avidin coating, can be used.

A variety of other nucleic acid hybridization formats are known to those skilled in the art. For example, common formats include sandwich assays and competition or displacement assays. Hybridization techniques are generally described in

20   Hames and Higgins (1985) *Nucleic Acid Hybridization, A Practical Approach*, IRL Press; Gall and Pardue (1969) *Proc. Natl. Acad. Sci. USA* 63: 378-383; and John *et al.* (1969) *Nature* 223: 582-587.

Sandwich assays are commercially useful hybridization assays for detecting or isolating nucleic acid sequences. Such assays utilize a "capture" nucleic acid

25   covalently immobilized to a solid support and a labeled "signal" nucleic acid in solution. The sample will provide the target nucleic acid. The "capture" nucleic acid and "signal" nucleic acid probe hybridize with the target nucleic acid to form a "sandwich" hybridization complex. To be most effective, the signal nucleic acid should not hybridize with the capture nucleic acid.

30   Detection of a hybridization complex may require the binding of a signal generating complex to a duplex of target and probe polynucleotides or nucleic acids. Typically, such binding occurs through ligand and anti-ligand interactions as between a ligand-conjugated probe and an anti-ligand conjugated with a signal.

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The sensitivity of the hybridization assays may be enhanced through use of a nucleic acid amplification system that multiplies the target nucleic acid being detected. Examples of such systems include the polymerase chain reaction (PCR) system and the ligase chain reaction (LCR) system. Other methods recently described in the art are the

5   nucleic acid sequence based amplification (NASBAO, Cangene, Mississauga, Ontario) and Q Beta Replicase systems.

Nucleic acid hybridization simply involves providing a denatured probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. The nucleic acids

10   that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids, or in the addition of chemical agents, or the raising of the pH. Under low stringency conditions

15   (e.g., low temperature and/or high salt and/or high target concentration) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization requires fewer mismatches.

20   One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency to ensure hybridization and then subsequent washes are performed at higher stringency to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e.g., down to as low as 0.25

25   X SSPE-T at 37°C to 70°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present.

In general, there is a tradeoff between hybridization specificity

30   (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher

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stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular probes of interest.

Methods of optimizing hybridization conditions are well known to those of

5   skill in the art (see, e.g., Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24: Hybridization With Nucleic Acid Probes*, Elsevier, N.Y.).

Labeling and detection of nucleic acids.
In a preferred embodiment, the hybridized nucleic acids are detected by detecting one or more labels attached to the sample or probe nucleic acids. The labels

10   may be incorporated by any of a number of means well known to those of skill in the art. Means of attaching labels to nucleic acids include, for example nick translation or end-labeling (e.g. with a labeled RNA) by kinasing of the nucleic acid and subsequent attachment (ligation) of a nucleic acid linker joining the sample nucleic acid to a label (e.g., a fluorophore). A wide variety of linkers for the attachment of labels to nucleic

15   acids are also known. In addition, intercalating dyes and fluorescent nucleotides can also be used.

Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin

20   for staining with labeled streptavidin conjugate, magnetic beads (e.g., Dynabeads™), fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like, see, e.g., Molecular Probes, Eugene, Oregon, USA), radiolabels (e.g., ^{3}H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold (e.g., gold

25   particles in the 40 -80 nm diameter size range scatter green light with high efficiency) or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Patents teaching the use of such labels include U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241.

A fluorescent label is preferred because it provides a very strong signal

30   with low background. It is also optically detectable at high resolution and sensitivity through a quick scanning procedure. The nucleic acid samples can all be labeled with a single label, e.g., a single fluorescent label. Alternatively, in another embodiment, different nucleic acid samples can be simultaneously hybridized where each nucleic acid

sample has a different label. For instance, one target could have a green fluorescent label and a second target could have a red fluorescent label. The scanning step will distinguish cites of binding of the red label from those binding the green fluorescent label. Each nucleic acid sample (target nucleic acid) can be analyzed independently from one another.

5   Suitable chromogens which can be employed include those molecules and compounds which absorb light in a distinctive range of wavelengths so that a color can be observed or, alternatively, which emit light when irradiated with radiation of a particular wave length or wave length range, e.g., fluorescers.

Desirably, fluorescers should absorb light above about 300 nm, preferably

10   about 350 nm, and more preferably above about 400 nm, usually emitting at wavelengths greater than about 10 nm higher than the wavelength of the light absorbed. It should be noted that the absorption and emission characteristics of the bound dye can differ from the unbound dye. Therefore, when referring to the various wavelength ranges and characteristics of the dyes, it is intended to indicate the dyes as employed and not the dye

15   which is unconjugated and characterized in an arbitrary solvent.

Fluorescers are generally preferred because by irradiating a fluorescer with light, one can obtain a plurality of emissions. Thus, a single label can provide for a plurality of measurable events.

Detectable signal can also be provided by chemiluminescent and

20   bioluminescent sources. Chemiluminescent sources include a compound which becomes electronically excited by a chemical reaction and can then emit light which serves as the detectable signal or donates energy to a fluorescent acceptor. Alternatively, luciferins can be used in conjunction with luciferase or lucigenins to provide bioluminescence. Spin labels are provided by reporter molecules with an unpaired electron spin which can

25   be detected by electron spin resonance (ESR) spectroscopy. Exemplary spin labels include organic free radicals, transitional metal complexes, particularly vanadium, copper, iron, and manganese, and the like. Exemplary spin labels include nitroxide free radicals.

The label may be added to the target (sample) nucleic acid(s) prior to, or

30   after the hybridization. So called "direct labels" are detectable labels that are directly attached to or incorporated into the target (sample) nucleic acid prior to hybridization. In contrast, so called "indirect labels" are joined to the hybrid duplex after hybridization. Often, the indirect label is attached to a binding moiety that has been attached to the

target nucleic acid prior to the hybridization. Thus, for example, the target nucleic acid may be biotinylated before the hybridization. After hybridization, an avidin-conjugated fluorophore will bind the biotin bearing hybrid duplexes providing a label that is easily detected. For a detailed review of methods of labeling nucleic acids and detecting labeled

5   hybridized nucleic acids see *Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24: Hybridization With Nucleic Acid Probes*, P. Tijssen, ed. Elsevier, N.Y., (1993)).

Fluorescent labels are easily added during an *in* vitro transcription reaction. Thus, for example, fluorescein labeled UTP and CTP can be incorporated into

10   the RNA produced in an *in vitro* transcription.

The labels can be attached directly or through a linker moiety. In general, the site of label or linker-label attachment is not limited to any specific position. For example, a label may be attached to a nucleoside, nucleotide, or analogue thereof at any position that does not interfere with detection or hybridization as desired. For example,

15   certain Label-ON Reagents from Clontech (Palo Alto, CA) provide for labeling interspersed throughout the phosphate backbone of an oligonucleotide and for terminal labeling at the 3' and 5' ends. As shown for example herein, labels can be attached at positions on the ribose ring or the ribose can be modified and even eliminated as desired. The base moieties of useful labeling reagents can include those that are naturally

20   occurring or modified in a manner that does not interfere with the purpose to which they are put. Modified bases include but are not limited to 7-deaza A and G, 7-deaza-8-aza A and G, and other heterocyclic moieties.

It will be recognized that fluorescent labels are not to be limited to single species organic molecules, but include inorganic molecules, multi-molecular mixtures of

25   organic and/or inorganic molecules, crystals, heteropolymers, and the like. Thus, for example, CdSe-CdS core-shell nanocrystals enclosed in a silica shell can be easily derivatized for coupling to a biological molecule (Bruchez *et al.* (1998) *Science,* 281: 2013-2016). Similarly, highly fluorescent quantum dots (zinc sulfide-capped cadmium selenide) have been covalently coupled to biomolecules for use in ultrasensitive

30   biological detection (Warren and Nie (1998) *Science*, 281: 2016-2018).

Amplification-based assays.

In another embodiment, amplification-based assays can be used to detect nucleic acids. In such amplification-based assays, the nucleic acid sequences act as a

template in an amplification reaction (*e.g.* Polymerase Chain Reaction (PCR). Detailed protocols for quantitative PCR are provided in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Other suitable amplification methods include, but are not limited to ligase
5   chain reaction (LCR) (*see* Wu and Wallace (1989) *Genomics* 4: 560, Landegren *et al.* (1988) *Science* 241: 1077, and Barringer *et al.* (1990) *Gene* 89: 117, transcription amplification (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86: 1173), and self-sustained sequence replication (Guatelli *et al.* (1990) *Proc. Nat. Acad. Sci. USA* 87: 1874).

10   Detection of *C. pneumoniae* gene expression

The nucleic acids of the invention can also be used to *C. pneumoniae* detect gene transcripts. Methods of detecting and/or quantifying gene transcripts using nucleic acid hybridization techniques are known to those of skill in the art (see Sambrook *et al. supra*). For example , a Northern transfer may be used for the detection of the
15   desired mRNA directly. In brief, the mRNA is isolated from a given cell sample using, for example, an acid guanidinium-phenol-chloroform extraction method. The mRNA is then electrophoresed to separate the mRNA species and the mRNA is transferred from the gel to a nitrocellulose membrane. As with the Southern blots, labeled probes are used to identify and/or quantify the target mRNA.

20   In another preferred embodiment, the gene transcript can be measured using amplification (*e.g.* PCR) based methods as described above for directly assessing copy number of the target sequences.

Expression of *C. pneumoniae* proteins

The nucleic acids disclosed here can be used for recombinant expression
25   of the proteins. In these methods, the nucleic acids encoding the proteins of interest are introduced into suitable host cells, followed by induction of the cells to produce large amounts of the protein. The invention relies on routine techniques in the field of recombinant genetics, well known to those of ordinary skill in the art. A basic text disclosing the general methods of use in this invention is Sambrook *et al., Molecular*
30   *Cloning, A Laboratory Manual* (2nd ed. 1989).

Standard transfection methods are used to produce prokaryotic, mammalian, yeast or insect cell lines which express large quantities of the desired

polypeptide, which is then purified using standard techniques (*see, e.g.*, Colley *et al.*, *J. Biol. Chem.* 264:17619-17622, 1989; *Guide to Protein Purification, supra*).

The nucleotide sequences used to transfect the host cells can be modified to yield *Chlamydia* polypeptides with a variety of desired properties. For example, the

5   polypeptides can vary from the naturally-occurring sequence at the primary structure level by amino acid, insertions, substitutions, deletions, and the like. These modifications can be used in a number of combinations to produce the final modified protein chain.

The amino acid sequence variants can be prepared with various objectives in mind, including facilitating purification and preparation of the recombinant

10   polypeptide. The modified polypeptides are also useful for modifying plasma half life, improving therapeutic efficacy, and lessening the severity or occurrence of side effects during therapeutic use. The amino acid sequence variants are usually predetermined variants not found in nature but exhibit the same immunogenic activity as naturally occurring protein. In general, modifications of the sequences encoding the polypeptides

15   may be readily accomplished by a variety of well-known techniques, such as site-directed mutagenesis (*see* Gillman & Smith, *Gene* 8:81-97 (1979); Roberts *et al.*, *Nature* 328:731-734 (1987)). One of ordinary skill will appreciate that the effect of many mutations is difficult to predict. Thus, most modifications are evaluated by routine screening in a suitable assay for the desired characteristic. For instance, the effect of various

20   modifications on the ability of the polypeptide to elicit a protective immune response can be easily determined using *in vitro* assays. For instance, the polypeptides can be tested for their ability to induce lymphoproliferation, T cell cytotoxicity, or cytokine production using standard techniques.

The particular procedure used to introduce the genetic material into the

25   host cell for expression of the polypeptide is not particularly critical. Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA

30   or other foreign genetic material into a host cell (*see* Sambrook *et al.*, *supra*). It is only necessary that the particular procedure utilized be capable of successfully introducing at least one gene into the host cell which is capable of expressing the gene.

Any of a number of well known cells and cell lines can be used to express the polypeptides of the invention. For instance, prokaryotic cells such as *E. coli* can be used. Eukaryotic cells include, yeast, Chinese hamster ovary (CHO) cells, COS cells, and insect cells.

5   The particular vector used to transport the genetic information into the cell is also not particularly critical. Any of the conventional vectors used for expression of recombinant proteins in prokaryotic and eukaryotic cells may be used. Expression vectors for mammalian cells typically contain regulatory elements from eukaryotic viruses.

10   The expression vector typically contains a transcription unit or expression cassette that contains all the elements required for the expression of the polypeptide DNA in the host cells. A typical expression cassette contains a promoter operably linked to the DNA sequence encoding a polypeptide and signals required for efficient polyadenylation of the transcript. The term "operably linked" as used herein refers to linkage of a

15   promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. The promoter is preferably positioned about the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

20   Following the growth of the recombinant cells and expression of the polypeptide, the culture medium is harvested for purification of the secreted protein. The media are typically clarified by centrifugation or filtration to remove cells and cell debris and the proteins are concentrated by adsorption to any suitable resin or by use of ammonium sulfate fractionation, polyethylene glycol precipitation, or by ultrafiltration.

25   Other routine means known in the art may be equally suitable. Further purification of the polypeptide can be accomplished by standard techniques, for example, affinity chromatography, ion exchange chromatography, sizing chromatography, His$_6$ tagging and Ni-agarose chromatography (as described in Dobeli *et al.*, *Mol. and Biochem. Parasit.* 41:259-268 (1990)), or other protein purification techniques to obtain homogeneity. The

30   purified proteins are then used to produce pharmaceutical compositions, as described below.

An alternative method of preparing recombinant polypeptides useful as vaccines involves the use of recombinant viruses (e.g., vaccinia). Vaccinia virus is grown

in suitable cultured mammalian cells such as the HeLa S3 spinner cells, as described by
Mackett *et al.*, in *DNA cloning Vol. II: A practical approach*, pp. 191-211 (Glover, ed.).

Antibody Production

The proteins of the present invention can be used to produce antibodies
5   specifically reactive with *C pneumoniae* antigens. If isolated proteins are used, they may
be recombinantly produced or isolated from *Chlamydia* cultures. Synthetic peptides
made using the protein sequences may also be used.

Methods of production of polyclonal antibodies are known to those of skill
in the art. In brief, an immunogen, preferably a purified protein, is mixed with an
10   adjuvant and animals are immunized. When appropriately high titers of antibody to the
immunogen are obtained, blood is collected from the animal and antisera is prepared.
Further fractionation of the antisera to enrich for antibodies reactive to *Chlamydia*
proteins can be done if desired (*see* Harlow & Lane, *Antibodies: A Laboratory Manual*
(1988)).

15   Polyclonal antisera are used to identify and characterize *Chlamydia* in the
tissues of patients using, for instance, *in situ* techniques and immunoperoxidase test
procedures described in Anderson *et al. JAVMA* 198:241 (1991) and Barr *et al. Vet.
Pathol.* 28:110-116 (1991).

Monoclonal antibodies may be obtained by various techniques familiar to
20   those skilled in the art. Briefly, spleen cells from an animal immunized with a desired
antigen are immortalized, commonly by fusion with a myeloma cell (*see* Kohler &
Milstein, *Eur. J. Immunol.* 6:511-519 (1976)). Alternative methods of immortalization
include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other
methods well known in the art. Colonies arising from single immortalized cells are
25   screened for production of antibodies of the desired specificity and affinity for the
antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced
by various techniques, including injection into the peritoneal cavity of a vertebrate host.

Monoclonal antibodies produced in such a manner are used, for instance,
in ELISA diagnostic tests, immunoperoxidase tests, immunohistochemical tests, for the *in*
30   *vitro* evaluation of spirochete invasion, to select candidate antigens for vaccine
development, protein isolation, and for screening genomic and cDNA libraries to select
appropriate gene sequences.

Immunodiagonostic detection of *C. pneumoniae* infections

The present invention also provides methods for detecting the presence or absence of *C. pneumoniae*, or antibodies reactive with it, in a biological sample. For instance, antibodies specifically reactive with *Chlamydia* can be detected *using* either

5   *Chlamydia* proteins or the isolates described here. The proteins and isolates can also be used to raise specific antibodies (either monoclonal or polyclonal) to detect the antigen in a sample. In addition, the nucleic acids disclosed and claimed here can be used to detect *Chlamydia*-specific sequences using standard hybridization techniques.

For a review of immunological and immunoassay procedures in general,

10   see *Basic and Clinical Immunology* (Stites & Terr ed., 7th ed. 1991)). The immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); Tijssen, *Laboratory Techniques in Biochem.stry and Molecular Biology* (1985)). For instance, the proteins and antibodies disclose I here are conveniently used in ELISA, immunoblot analysis and

15   agglutination assays.

In brief, immunoassays to measure anti-*Chlamydia* antibodies or antigens can be either competitive or noncompetitive binding assays. In competitive binding assays, the sample analyte (e.g., anti-*Chlamydia* antibodies) competes with a labeled analyte (e.g., anti-*Chlamydia* monoclonal antibody) for specific binding sites on a capture

20   agent (e.g., isolated *Chlamydia* protein) bound to a solid surface. The concentration of labeled analyte bound to the capture agent is inversely proportional to the amount of free analyte present in the sample.

Noncompetitive assays are typically sandwich assays, in which the sample analyte is bound between two analyte-specific binding reagents. One of the binding

25   agents is used as a capture agent and is bound to a solid surface. The second binding agent is labelled and is used to measure or detect the resultant complex by visual or instrument means.

A number of combinations of capture agent and labelled binding agent can be used. For instance, an isolated *Chlamydia* protein or culture can be used as the

30   capture agent and labelled anti-human antibodies specific for the constant region of human antibodies can be used as the labelled binding agent. Goat, sheep and other non-human antibodies specific for human immunoglobulin constant regions (e.g., γ or μ) are

well known in the art. Alternatively, the anti-human antibodies can be the capture agent and the antigen can be labelled.

Various components of the assay, including the antigen, anti-*Chlamydia* antibody, or anti-human antibody, may be bound to a solid surface. Many methods for immobilizing biomolecules to a variety of solid surfaces are known in the art. For instance, the solid surface may be a membrane (e.g., nitrocellulose), a microtiter dish (e.g., PVC or polystyrene) or a bead. The desired component may be covalently bound or noncovalently attached through nonspecific bonding.

Alternatively, the immunoassay may be carried out in liquid phase and a variety of separation methods may be employed to separate the bound labeled component from the unbound labelled components. These methods are known to those of skill in the art and include immunoprecipitation, column chromatography, adsorption, addition of magnetizable particles coated with a binding agent and other similar procedures.

An immunoassay may also be carried out in liquid phase without a separation procedure. Various homogeneous immunoassay methods are now being applied to immunoassays for protein analytes. In these methods, the binding of the binding agent to the analyte causes a change in the signal emitted by the label, so that binding may be measured without separating the bound from the unbound labelled component.

Western blot (immunoblot) analysis can also be used to detect the presence of antibodies to *Chlamydia* in the sample. This technique is a reliable method for confirming the presence of antibodies against a particular protein in the sample. The technique generally comprises separating proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the separated proteins. This causes specific target antibodies present in the sample to bind their respective proteins. Target antibodies are then detected using labeled anti-human antibodies.

The immunoassay formats described above employ labelled assay components. The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. A wide variety of labels may be used. The component may be labelled by any one of several methods. Traditionally a radioactive label incorporating ^{3}H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P was used. Non-radioactive labels

include ligands which bind to labelled antibodies, fluorophores, chemiluminescent agents, enzymes, and antibodies which can serve as specific binding pair members for a labelled ligand. The choice of label depends on sensitivity required, ease of conjugation with the compound, stability requirements, and available instrumentation.

5   Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, e.g., luminol. For a review of various labelling or
10   signal producing systems which may be used, see U.S. Patent No. 4,391,904, which is incorporated herein by reference.

          Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to an anti-ligand (e.g., streptavidin) molecule which is either inherently detectable or
15   covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. A number of ligands and anti-ligands can be used. Where a ligand has a natural anti-ligand, for example, biotin, thyroxine, and cortisol, it can be used in conjunction with the labelled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an
20   antibody.

          Some assay formats do not require the use of labelled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labelled and the presence of
25   the target antibody is detected by simple visual inspection.

Pharmaceutical Compositions

          The peptides or antibodies (typically monoclonal antibodies) of the present invention and pharmaceutical compositions thereof are useful for administration to mammals, particularly humans, to treat and/or prevent *Chlamydia* infections. Suitable
30   formulations are found in *Remington's Pharmaceutical Sciences*, Mack Publishing Company, Philadelphia, PA, 17th ed. (1985).

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The immunogenic peptides or antibodies of the invention are administered prophylactically or to an individual already suffering from the disease. The peptide compositions are administered to a patient in an amount sufficient to elicit an effective immune response to *Chlamydia*. An effective immune response is one that inhibits infection. An amount adequate to accomplish this is defined as "therapeutically effective dose" or "immunogenically effective dose." Amounts effective for this use will depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial immunization (that is for therapeutic or prophylactic administration) from about 0.1 mg to about 1.0 mg per 70 kilogram patient, more commonly from about 0.5 mg to about 0.75 mg per 70 kg of body weight. Boosting dosages are typically from about 0.1 mg to about 0.5 mg of peptide using a boosting regimen over weeks to months depending upon the patient's response and condition. A suitable protocol would include injection at time 0, 4, 2, 6, 10 and 14 weeks, followed by further booster injections at 24 and 28 weeks.

For therapeutic use, administration should begin at the first sign of infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In some circumstances, loading doses followed by boosting doses may be required. The resulting immune response helps to cure or at least partially arrest symptoms and/or complications. Vaccine compositions containing the peptides are administered prophylactically to a patient susceptible to or otherwise at risk of the infection.

The pharmaceutical compositions (containing either peptides or antibodies) are intended for parenteral or oral administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic polypeptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.4% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain

28

pharmaceutically acceptable auxiliary substances as required to approximate

physiological conditions, such as buffering agents, tonicity adjusting agents, wetting

agents and the like, for example, sodium acetate, sodium lactate, sodium chloride,

potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

5   The compositions may also comprise carriers to enhance the immune

response. Useful carriers are well known in the art, and include, e.g., KLH,

thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids

such as poly(lysine:glutamic acid), influenza, hepatitis B virus core protein, hepatitis B

virus recombinant vaccine and the like.

10   For solid compositions, conventional nontoxic solid carriers may be used

which include, for example, pharmaceutical grades of mannitol, lactose, starch,

magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium

carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic

composition is formed t y incorporating any of the normally employed excipients, such as

15   those carriers previously listed, and generally 10-95% of active ingredient, that is, one or

more peptides of the invention, and more preferably at a concentration of 25%-75%.

        As noted above, the peptide compositions are intended to induce an

immune response to *Chlamydia*. Thus, compositions and methods of administration

suitable for maximizing the immune response are preferred. For instance, peptides may

20   be introduced into a host, including humans, linked to a carrier or as a homopolymer or

heteropolymer of active peptide units from various *Chlamydia* proteins disclosed here.

Alternatively, a "cocktail" of polypeptides can be used. A mixture of more than one

polypeptide has the advantage of increased immunological reaction and, where different

peptides are used to make up the polymer, the additional ability to induce antibodies to a

25   number of epitopes.

        The compositions also include an adjuvant. As used here, number of

adjuvants are well known to one skilled in the art. Suitable adjuvants include incomplete

Freund's adjuvant, alum, aluminum phosphate, aluminum hydroxide,

N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP),

30   N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP),

N-acetylmuramyl-Lalanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-

glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE),

and RIBI, which contains three components extracted from bacteria, monophosphoryl

lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2%
squalene/Tween 80 emulsion. The effectiveness of an adjuvant may be determined by
measuring the amount of antibodies directed against the immunogenic peptide.

5   The concentration of immunogenic peptides of the invention in the
pharmaceutical formulations can vary widely, i.e. from less than about 0.1%, usually at
or at least about 2% to as much as 20% to 50% or more by weight, and will be selected
primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of
administration selected.

         The peptides of the invention can also be expressed by attenuated viral
10   hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus as a
vector to express nucleotide sequences that encode the peptides of the invention. Upon
introduction into a host, the recombinant vaccinia virus expresses the immunogenic
peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in
immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector
15   is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover et al. (*Nature*
351:456-460 (1991)). A wide variety of other vectors useful for therapeutic
administration or immunization of the peptides of the invention, e.g., *Salmonella typhi*
vectors and the like, will be apparent to those skilled in the art from the description
herein.

20   The DNA encoding one or more of the peptides of the invention can also
be administered to the patient. This approach is described, for instance, in Wolff *et. al.*,
Science 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466.

         In order to enhance serum half-life, the peptides may also be encapsulated,
introduced into the lumen of liposomes, prepared as a colloid, or other conventional
25   techniques may be employed which provide an extended serum half-life of the peptides.
A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et
al., *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), U.S. Pat. Nos. 4, 235,871, 4,501,728 and
4,837,028.

30   EXAMPLES
         The following examples are offered to illustrate, but no to limit the
claimed invention.
Example 1:

This example describes comparison of the *C. pneumoniae* genome disclosed here and the, previously sequenced, *C. trachomatis* genome (Stephens, *et al. Science* 282:754-759 (1998)).

The apparent low level of DNA homology between *C. trachomatis* and *C.*

5   *pneumoniae* (Campbell, *et al., J. Clin. Microbiol.* 25:1911-1916 (1987)) yet analogous cell structures and developmental cycles, predicts that comparative analysis of the two genomes will significantly enhance the understanding of both pathogens. Identification of genes that are present in one species but not the other are of particular importance for the mutually exclusive biological, virulence and pathogenesis capabilities of each.

10   Identification of genes shared between the two species strongly supports the requirement for these capabilities in a biological system that has, over its long-term association with mammalian host cells, evolved to reduce the metabolic capacities while optimizing survival, growth and transmission of these unique pathogens.

The previously sequenced *C. trachomatis* genome contains 1,042,519

15   nucleotides and 875 likely protein-coding genes. Similarity searching permitted the inferred functional assignment of sequences 636 (60%) genes disclosed here and 251 (23%) are similar to hypothetical genes for other bacterial organisms including those for *C. trachomatis*. The remaining 186 (17%) genes are not homologous to sequences deposited in GenBank.. Seventy *C. trachomatis* genes are not represented in the *C.*

20   *pneumoniae* genome. These are contained within blocks consisting of 2-17 genes and 19 single genes. Of the 70 *C. trachomatis* genes without homologs in *C. pneumoniae*, 60 are classified as encoding hypothetical proteins. The remaining genes not represented in *C. pneumoniae* consist of the tryptophan operon (*trpA,B,R*), *trpC*, two predicted thiol protease genes, and 4 genes assigned to the phospholipase-D superfamily.

25   It is evident that there is a high level of functional conservation between *C. pneumoniae* and *C. trachomatis* as orthologs to *C. trachomatis* genes were identified for 859 (80%) of the predicted coding sequences for *C. pneumoniae*. The level of similarity for individual encoded proteins spans a wide spectrum (22-95% amino acid identity) with an average of 62% amino acid identity between orthologs from the two species. The

30   percent amino acid identity between orthologous chlamydial proteins is similar among functional groups with the highest for proteins associated with translation and the lowest for proteins whose function in chlamydiae is uncharacterized and not related to proteins encoded by other organisms. The gene order of the homologous set of genes in *C.*

pneumoniae shows reorganization relative to the genome of *C. trachomatis*; however, there is a high level of synteny for the gene organization of the two genomes. We identified thirty-nine blocks of 2 or more genes whose gene organization is colinear with homologs to *C. trachomatis*, although some of these are inverted. The distribution of

5   genome reorganization is not evenly distributed on the chromosome as the region between *C. pneumoniae* coding sequences 0130-0300 contains substantially more reorganization than other areas of the genome. This region coincides with the predicted chromosome replication terminus.

        We identified orthologs of enzymes characterized in other bacteria that

10   account for the essential requirements for DNA replication, repair, transcription and translation including two predicted DNA helicases of the Swi2/Snf2 family found in *C. trachomatis*. Similar to *C. trachomatis*, alternative sigma subunits for RNA polymerase, σ^{28} and σ^{54}, were identified in addition to anti-σ regulatory system factors RsbV, a RsbW-like single-domain histidine kinase, and a RsbU-like protein phosphatase. These

15   findings suggest that the fundamental mechanisms of transcriptional regulation are conserved among *Chlamydia*. The *C. trachomatis* proteins containing SET and SWIB domains, and a SWIB domain fused to the C-terminus of the chlamydial topoisomerase I, not identified outside eukaryotes, are found in *C. pneumoniae* supporting their possible role in the chromatin condensation-decondensation characteristic of the biologically

20   unique chlamydial developmental cycle.

        The central metabolic pathways inferred from the *C. pneumoniae* genome sequence are the same as those identified for *C. trachomatis* *C. pneumoniae* has a glycolytic pathway and a linked tricarboxylic acid cycle, although likely functional, is incomplete as genes for citrate synthase, aconitase, and isocitrate dehydrogenase were not

25   identified. *C. pneumoniae* has a complete glycogen synthesis and degradation system supporting a role for glycogen synthesis and utilization of glucose-derivatives in chlamydial metabolism. Genes encoding essential functions in aerobic respiration are present and electron flux may be supported by pyruvate, succinate, glycerol-3-phosphate, and NADH dehydrogenases, NADH-ubiquinone oxidoreductase and cytochrome oxidase.

30   *C. pneumoniae* also contains the V (vacuolar)-type ATPase operon and the two ATP translocases found in *C. trachomatis*.

        The type-III secretion virulence system required for invasion by several pathogenic bacteria and found in the *C. trachomatis* genome in three chromosomal

locationsis also present in the *C. pneumoniae* genome. Each of the components is conserved and their relative genomic contexts are conserved. Genes such as a predicted serine/threonine protein kinase and other genes physically linked to genes encoding structural components of the type-III secretion apparatus, but without identified

5   homologs, are also highly similar between the two species suggesting the functional roles in modifying cellular biology are fundamentally conserved.

Chlamydia-encoded proteins that are not found in chlamydial organisms but localized to the intracellular chlamydial inclusion membrane are likely essential for the unique intracellular biology and perhaps differences in inclusion morphology

10   observed between species of *Chlamydia*. Several such proteins, termed IncA,B&C, have been characterized for a *C. psittaci* strain (Rockey, *et al. Mol. Microbiol.* 15:617-626 (1995); Rockey *et al. Infect. Immun.* 62:106-112 (1994)). *C. pneumoniae* and *C. trachomatis* encode orthologs to *C. psittaci* IncB and IncC and *C. trachomatis* also contains an ortholog to IncA. *C. pneumoniae* contains two genes that encode proteins

15   with similarity to IncA (CPn0186 and CPn0585), although the level of homology is low suggesting analogous but possibily altered functions.

The tryptophan biosynthesis operon (*trpA, trpB, trpR*) and *trpC* identified in *C. trachomatis* is conspicuously missing in the *C. pneumoniae* genome. This represents the entire repertoire of genes associated with tryptophan biosynthesis identified

20   in *C. trachomatis*. Seventeen genes adjacent to the *C. trachomatis* tryptophan operon also were not found in the *C. pneumoniae* genome. This region is the single largest loss of a contiguous genomic segment and includes 4 HKD superfamily encoding genes that encompass a family of proteins related to endonuclease and phospholipase D. These findings may be important for the ability of *Chlamydia* to persist in their hosts and cause

25   disease by eliciting potent, focal and persistent inflammatory responses thought to be essential for pathogenesis.

The *C. pneumoniae* genome contains 187,711 additional nucleotides compared to the *C. trachomatis* genome, and the 214 coding sequences not found in *C. trachomatis* account for most of the increased genome size. Eighty-eight of these genes

30   are found in blocks of >10 genes (11-30 genes/block), 41 are single genes, and the remainder are partnered with at least one other gene. Based upon the observation that ~70% of all the *C. pneumoniae* genes have an identifiable homolog in GenBank, exclusive of *C. trachomatis*, it would be expected that over 150 of the 214 genes should

have a homolog in GenBank, many associated with a function. However, only 28 coding sequences have similarity to genes from other organisms. Thus the majority of the genes that are mutually exclusive of *C. trachomatis* (186 of 214), and the 60 of 70 *C. trachomatis* genes that lacked an identifiable homolog in *C. pneumoniae*, do not have

5   detectable homologs to genes from other organisms. We predict that most of the unique genes are essential for specific attributes that define the differential biology, tropism and pathogenesis of *C. trachomatis* and *C. pneumoniae*. Moreover, this suggests that *C. pneumoniae* has more unique biological (i.e., virulence) capacity than *C. trachomatis*. The ability of *C. pneumoniae* to be more invasive and survive in a broader range of host

10   cell types than *C. trachomatis* is consistent with this hypothesis. Not all of the differences in biological capacity may be associated with mutually exclusive genes. One explanation for the significantly lower level of homology between protein sequences assigned as having *C. pneumoniae* and *C. trachomatis* orthologs but no identifiable orthologs in other organisms is that this set of proteins is not only associated with

15   biological requirements specific for *Chlamydia* but this polymorphism may account for differential biology between the two species. The determination of the genome sequence from a representative of the *C. psittaci* group will precisely delineate those genes that are mutually exclusive and specific for each species.

The major functionally identifiable addition to the *C. pneumoniae* genome

20   is a large expansion of genes encoding a new family of chlamydial polymorphic membrane proteins (Pmp), alone representing 22% of the increased coding capacity. While the *C. trachomatis* genome has 9 *pmp* genes, remarkably the *C. pneumoniae* genome contains 21 *pmp* genes. Most of these genes appear to be amplified in two regions of the genome with three stand-alone genes. Interestingly one of the stand-alone

25   genes is most closely related to the *C. trachomatis pmpD* which is the only stand-alone *pmp* gene in the *C. trachomatis* genome and it is located with the same relative genomic context, suggesting an essential and conserved function for this paralog. Six Pmp-coding genes are presumably not functional as five contain predicted coding frame-shifts and one is truncated. The amplification of this gene family and the confidently predicted frame-

30   shifts suggest a specific molecular mechanism to promote functional or antigenic diversity. The biological role of this protein family remains enigmatic, although at least one of the proteins in *C. psittaci* related to this family is exposed on the chlamydial surface.

While a function could not be assigned for most of the unique *C. pneumoniae* genes, several have significant similarity to genes from other organisms. Functional assignments could be made for genes encoding GMP synthetase, IMP dehydrogenase, UMP synthase, uridine kinase, biotin synthase pathway proteins,

5 methylthioadenosine nucleosidase, a DNA glycosylase and aromatic amino acid hydroxylase. Thus a complete pathway was identified for biotin biosynthesis. The additional purine and pyrimidine salvage pathway genes presumably reflect metabolic limitations in one of the cell types that *C. pneumoniae* infects or differences in the ability of *C. pneumoniae* to transport precursor nucleosides or nucleotides.

10 The addition of aromatic amino acid hydroxylase in *C. pneumoniae* is intriguing especially in light of the loss of tryptophan biosynthetic genes and the inability to synthesize other amino acids including phenylalanine. Aromatic amino acid hyroxlyases include three distinct enzymes that function to receptively oxidize phenylalanine to tyrosine, tyrosine to Dopa, and tryptophan to 5-hydroxytryptophan and

15 serotonin. Although the chlamydial protein is similar to proteins of this family and incrementally more closely related to tryptophan hydroxylase, its specific function could not be confidently predicted. We hypothesize that it may be involved in *C. pneumoniae* virulence. Tryptophan hydroxylase has not been previously identified in bacteria and the origin of the chlamydial gene appears to be from eukaryotes. The functional role of an

20 aromatic amino acid hydroxylase for *C. pneumoniae* is linked to the unique intracellular biology of this organism and may represent a key contribution to *C. pneumoniae* persistence and pathogenesis.

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof

25 will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

Table 1 provides functional assignments of *C. pneumoniae* nonprotein-

30 encoding genomic sequences. Table 2 provides functional assignments of protein coding sequences. Table 3 provides the amino acid sequences of the proteins corresponding to the coding sequences.

TABLE 1

type	SEQ ID NO:1 start position	SEQ ID NO:1 end position	Gene
Ori	841664	841396	(R) Putative Origin of Replica
tmRNA	138493	138074	(R) tmRNA
pRNA	607342	607649	Ribonuclease P RNA
rRNA	1000564	1002115	16S rRNA
rRNA	1002415	1005278	23S rRNA
rRNA	1005393	1005509	5S rRNA
tRNA	269070	269142	Ala tRNA_1
tRNA	164318	164389	Asn tRNA
tRNA	296224	296151	(R) Asp tRNA
tRNA	836191	836119	(R) Ala tRNA_2
tRNA	1030533	1030603	Cys tRNA
tRNA	784896	784822	(R) Glu tRNA
tRNA	781680	781610	(R) Gly tRNA_1
tRNA	961536	961607	Gly tRNA_2
tRNA	999949	1000023	His tRNA
tRNA	268992	269065	Ile tRNA
tRNA	672236	672318	Leu tRNA_1
tRNA	680178	680257	Leu tRNA_2
tRNA	715889	715971	Leu tRNA_3
tRNA	739403	739486	Leu tRNA_4
tRNA	1175863	1175944	Leu tRNA_5
tRNA	784994	784922	(R) Lys tRNA
tRNA	843926	843999	Pro tRNA_2
tRNA	409922	409848	(R) Pro tRNA_1
tRNA	631373	631445	Phe tRNA
tRNA	677337	677264	(R) Arg tRNA_2
tRNA	807413	807341	(R) Arg tRNA_3
tRNA	877473	877400	(R) Arg tRNA_4
tRNA	462141	462214	Arg tRNA_1
tRNA	1085605	1085676	Gln tRNA
tRNA	786780	786708	(R) Thr tRNA_3
tRNA	89728	89657	(R) Thr tRNA_1
tRNA	293477	293405	(R) Thr tRNA_2
tRNA	87522	87450	(R) Met tRNA_1
tRNA	199301	199229	(R) Met tRNA_2
tRNA	199390	199317	(R) Met tRNA_3
tRNA	626904	626987	Ser tRNA_1
tRNA	708359	708440	Ser tRNA_2
tRNA	1142034	1142117	Ser tRNA_3
tRNA	1230028	1229945	(R) Ser tRNA_4
tRNA	91070	90999	(R) Trp tRNA
tRNA	293399	293317	(R) Tyr tRNA
tRNA	296147	296075	(R) Val tRNA_1
tRNA	1137389	1137462	Val tRNA_2

TABLE 2

Gene #	From	To	Strand	Gene Function (C. trachomatis ortholog in parentheses)
CPn0001	282	4	R	CT001 hypothetical protein
CPn0002	573	875	F	gatC-Glu-tRNA Gln Amidotransferase (C subunit)-(CT002)
CPn0003	895	2370	F	gatA-Glu tRNA Gln Amidotransferase-(CT003)
CPn0004	2370	3411	F	gatB-(Penti2) Glu tRNA Gln Amidotransferase (B Subunit)-(CT004)
CPn0005	4127	6492	F	pmp_1-Polymorphic Outer Membrane Protein G Family
CPn0006	7293	7141	R	
CPn0007	7605	10496	F	
CPn0008	10975	11685	F	
CPn0009	11815	13119	F	
CPn0010	13435	14325	F	
CPn0010	14379	15746	F	frame-shift with 0010
CPn0011	15892	16614	F	
CPn0012	16644	18212	F	
CPn0013	18584	21106	F	pmp_2-Polymorphic Outer Membrane Protein G Family
CPn0014	21392	21922	F	pmp_3-Polymorphic Outer Membrane Protein G Family
CPn0015	21835	24174	F	pmp_3-PMP_3 (frame-shift with 0014)
CPn0016	24416	26188	F	pmp_4-Polymorphic Outer Membrane Protein G Family
CPn0017	26094	27170	F	pmp_4-PMP_4 (frame-shift with 0016)
CPn0018	27522	29003	F	pmp_5-Polymorphic Outer Membrane Protein G Family
CPn0019	29007	30356	F	pmp_5-PMP_5 (frame-shift with 0018)
CPn0020	32687	30603	R	Predicted OMP [leader (14) peptide: outer membrane]-(CT351)
CPn0021	34410	32707	R	Predicted OMP [leader (19) peptide]-(CT350)
CPn0022	34982	34395	R	maf-(CT349)
CPn0023	36603	35014	R	yjjK/alr-ABC Transporter Protein ATPase-(CT348)
CPn0024	37596	36661	F	xerC-Integrase/recombinase-(CT347)
CPn0025	38604	37684	R	elaC/atsA-Sulphohydrolase/Glycosulfatase-(CT346)
CPn0026	39625	38762	R	CT345 hypothetical protein-(CT345)
CPn0027	42234	39778	R	lon-Lon ATP-dependent Protease-(CT344)
CPn0028	43325	42543	R	
CPn0029	43755	43390	R	
CPn0030	43891	44529	F	gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343)
CPn0031	44711	44884	F	rs21-S21 Ribosomal Protein-(CT342)
CPn0032	44923	46098	F	dnaJ-Heat Shock Protein J-(CT341)
CPn0033	46138	48171	F	pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & Beta Fusion-(CT340)
CPn0034	49457	48210	R	
CPn0035	51029	49569	R	CT339 hypothetical protein
CPn0036	51002	51796	F	CT338 hypothetical protein
CPn0037	51792	52115	F	ptsH-PTS Phosphocarrier Protein Hpr-(CT337)
CPn0038	52119	53831	F	ptsI-PTS PEP Phosphotransferase-(CT336)
CPn0039	54250	53963	R	ybaB-(CT335)
CPn0040	55643	54318	R	dnaX_1-DNA Pol III Gamma and Tau_1-(CT334)
CPn0041	55996	57342	F	
CPn0042	57403	58182	F	
CPn0043	58447	60372	F	
CPn0044	60419	60778	F	
CPn0045	61069	62790	F	
CPn0046	62790	63263	F	
CPn0047	63455	63652	F	
CPn0048	63687	65801	F	*yqfF-Bs conserved hypothetical IM protein
CPn0049	66296	65817	R	
CPn0050	66813	66499	R	
CPn0051	66833	67111	F	
CPn0052	68005	67304	R	hemC-Porphobilinogen Deaminase-(CT299)
CPn0053	69344	67986	R	sms-Sms Protein-(CT298)
CPn0054	70023	69313	R	rnc-Ribonuclease III-(CT297)
CPn0055	70129	70590	F	CT296 hypothetical protein
CPn0056	70953	72746	F	.mrsA-Phosphomannomutase-(CT295)
CPn0057	72934	73554	F	sodM-Superoxide Dismutase (Mn)-(CT294)
CPn0058	73639	74562	F	accD-AcCoA Carboxylase/Transferase Beta-(CT293)
CPn0059	74616	75050	F	dut-dUTP Nucleotidohydrolase-(CT292)
CPn0060	75055	75528	F	ptsN_1-PTS IIA Protein-(CT291)
CPn0061	75534	76208	F	ptsN_2-PTS IIA Protein + HTH DNA-Binding Domain-(CT290)
CPn0062	76308	77690	F	CT289 hypothetical protein
CPn0063	78112	78267	F	
CPn0064	78346	78576	F	
CPn0065	78924	80651	F	CT288 hypothetical protein
CPn0066	80925	82655	F	

CPn0067	82953	84053	F	
CPn0068	84903	84331	R	CT360 hypothetical protein
CPn0069	85236	87086	F	
CPn0070	87378	87208	R	
CPn0071	88045	87599	R	CT325 hypothetical protein
CPn0072	89061	88057	R	CT324 hypothetical protein
CPn0073	89356	89574	F	infA-Initiation Factor IF-1-(CT323)
CPn0074	89774	90955	F	tufA-Elongation Factor Tu-(CT322)
CPn0075	91102	91350	F	secE-preprotein translocase-(CT321)
CPn0076	91358	91903	F	nusG-Transcriptional Antitermination-(CT320)
CPn0077	92013	92435	F	rl11-L11 Ribosomal Protein-(CT319)
CPn0078	92465	93160	F	rl1-L1 Ribosomal Protein-(CT318)
CPn0079	93179	93688	F	rl10-L10 Ribosomal Protein-(CT317)
CPn0080	93735	94121	F	rl7-L7/L12 Ribosomal Protein-(CT316)
CPn0081	94261	98016	F	rpoB-RNA Polymerase Beta-(CT315)
CPn0082	98043	102221	F	rpoC-RNA Polymerase Beta'-(CT314)
CPn0083	102332	103312	F	tal-Transaldolase-(CT313)
CPn0084	103362	103751	F	predicted ferredoxin-(CT312)
CPn0085	104506	103766	R	CT311 hypothetical protein
CPn0086	104904	105527	F	atpE-ATP Synthase Subunit E-(CT310)
CPn0087	105579	106376	F	CT309 hypothetical protein
CPn0088	106373	108145	F	atpA-ATP Synthase Subunit A-(CT308)
CPn0089	108153	109466	F	atpB-ATP Synthase Subunit B-(CT307)
CPn0090	109454	110080	F	atpD-ATP Synthase Subunit D-(CT306)
CPn0091	110074	112053	F	atpI-ATP Synthase Subunit I-(CT305)
CPn0092	112151	112573	F	atpK-ATP Synthase Subunit K-(CT304)
CPn0093	112509	113015	F	CT303 hypothetical protein
CPn0094	113152	115971	F	valS-Valyl tRNA Synthetase-(CT302)
CPn0095	116037	118790	F	pknD-S/T Protein Kinase-(CT301)
CPn0096	124314	118837	R	uvrA-Excinuclease ABC Subunit A-(CT333)
CPn0097	124555	126006	F	pyk-Pyruvate Kinase-(CT332)
CPn0098	127491	126091	R	htrB-Acyltransferase-(CT010)
CPn0099	127593	127865	F	
CPn0100	129141	127882	R	CT011 hypothetical protein
CPn0101	129932	129141	R	ybbP family hypothetical protein-(CT012)
CPn0102	130123	131466	F	cydA-Cytochrome Oxidase Subunit I-(CT013)
CPn0103	131480	132511	F	cydB-Cytochrome Oxidase Subunit II-(CT014)
CPn0104	133875	132676	R	CT017 hypothetical protein
CPn0105	134847	134029	R	CT016 hypothetical protein
CPn0106	135091	136374	F	phoH-ATPase-(CT015)
CPn0107	137162	136392	R	CT058 hypothetical protein_1
CPn0108	137857	137303	R	CT018
CPn0109	138655	141783	F	ileS-Isoleucyl-tRNA Synthetase-(CT019)
CPn0110	143734	141827	R	lepB-Signal Peptidase I-(CT020)
CPn0111	144686	143934	R	CT021 hypothetical protein
CPn0112	144767	145093	F	rl31-L31 Ribosomal Protein-(CT022)
CPn0113	145335	146405	F	pfrA-Peptide Chain Releasing Factor (RF-1)-(CT023)
CPn0114	146398	147261	F	hemK-A/G specific methylase-(CT024)
CPn0115	147279	148622	F	ffh-Signal Recognition Particle GTPase-(CT025)
CPn0116	148616	148972	F	rs16-S16 Ribosomal Protein-(CT026)
CPn0117	148989	150071	F	trmD-tRNA (guanine N-1)-Methyltransferase-(CT027)
CPn0118	150102	150464	F	rl19-L19 Ribosomal Protein-(CT028)
CPn0119	150523	151164	F	rnhB_1-Ribonuclease HII_1-(CT029)
CPn0120	151164	151778	F	gmk-GMP Kinase-(CT030)
CPn0121	151778	152068	F	CT031 hypothetical protein
CPn0122	152071	153723	F	metG-Methionyl-tRNA Synthetase-(CT032)
CPn0123	155969	153774	R	recD_1-Exodeoxyribonuclease V (Alpha Subunit)_1-(CT033)
CPn0124	156614	158068	F	
CPn0125	158096	158605	F	
CPn0126	158809	161085	F	
CPn0127	162143	161130	R	ytfF-Cationic Amino Acid Transporter-(CT034)
CPn0128	162277	163053	F	bpll-Biotin Protein Ligase-(CT035)
CPn0129	163717	163064	R	similarity to CT036
CPn0130	164245	163751	R	
CPn0131	164549	165580	F	
CPn0132	165587	166561	F	
CPn0133	167334	166564	R	CHLPS hypothetical protein-(CT109)
CPn0134	169098	167467	R	groEL_1-HSP-60_1-(CT110)
CPn0135	169448	169143	R	groES-10KDa Chaperonin-(CT111)
CPn0136	171401	169569	R	pepF-Oligopeptidase-(CT112)
CPn0137	172254	171502	R	ybgI-ACR family-(CT108)
CPn0138	174019	172700	R	hemL-Glutamate-1-semialdehyde-2,1-aminomutase-(CT210)

CPn0139	174656	174093	R	yqgE-(CT210)
CPn0140	175110	174673	R	yqdE-(CT212)
CPn0141	175802	175110	R	rpiA-Ribose-5-P Isomerase A-(CT213)
CPn0142	176091	175816	R	
CPn0143	177335	176214	R	*yxjG_Bs_1 Hypothetical Protein
CPn0144	177963	180560	F	clpB-Clp Protease ATPase-(CT113)
CPn0145	180777	182369	F	CT114 hypothetical protein
CPn0146	182613	183095	F	
CPn0147	183225	183671	F	
CPn0148	183846	185702	F	pkn1-S/T Protein Kinase-(CT145)
CPn0149	185715	187700	F	dnlJ-DNA Ligase-(CT146)
CPn0150	187834	192444	F	CT147 hypothetical protein
CPn0151	194142	192625	R	mhpA-Monooxygenase-(CT148)
CPn0152	195265	194318	R	CT149 hypothetical protein
CPn0153	195433	197892	F	leuS-Leucyl tRNA Synthetase-(CT209)
CPn0154	197892	199202	F	gseA-KDO Transferase-(CT208)
CPn0155	199691	199488	R	
CPn0156	200117	199770	R	
CPn0157	200723	200298	R	
CPn0158	201430	200894	R	
CPn0159	201772	201467	R	
CPn0160	203791	202127	R	pfkA_1-Fructose-6-P Phosphotransferase_1-(CT207)
CPn0161	204622	203798	R	predicted acyltransferase family-(CT206)
CPn0162	205828	204803	R	
CPn0163	206026	206394	F	
CPn0164	206498	206998	F	
CPn0165	206998	207582	F	
CPn0166	207630	207962	F	
CPn0167	208306	207977	R	
CPn0168	208641	208417	R	
CPn0169	209501	208710	R	
CPn0170	211026	210025	R	
CPn0171	212435	211149	R	*guaA-GMP Synthase
CPn0172	213177	212440	R	*guaB/impD-Inosine 5'-monophosphase dehydrogenase (COOH-terminal region only)
CPn0173	213987	213715	R	
CPn0174	214257	214724	F	
CPn0175	214898	215275	F	
CPn0176	215286	216518	F	CT153 hypothetical protein
CPn0177	217459	216608	R	
CPn0178	218052	217789	R	
CPn0179	218403	218056	R	
CPn0180	218851	218355	R	
CPn0181	219175	218777	R	
CPn0182	220695	219334	R	accC-Biotin Carboxylase-(CT124)
CPn0183	221195	220695	R	accB-Biotin Carboxyl Carrier Protein-(CT123)
CPn0184	221775	221221	R	efp_1-Elongation Factor P_1-(CT122)
CPn0185	222451	221765	R	rpe/araD-Ribulose-P Epimerase-(CT121)
CPn0186	222899	224068	F	*similarity to Cps IncA_1-(CT119)
CPn0187	224248	225045	F	predicted methylase-(CT133)
CPn0188	225111	226400	F	CT132 hypothetical protein
CPn0189	226400	229825	F	CT131 homolog-(Possible Transmembrane Protein)
CPn0190	229919	231274	F	
CPn0191	231991	231314	R	glnQ-ABC Amino Acid Transporter ATPase-(CT130)
CPn0192	232634	231984	R	glnP-ABC Amino Acid Transporter Permease-(CT129)
CPn0193	233126	232686	R	*argR-Arginine Repressor
CPn0194	233210	234241	F	gcp_2-O-Sialoglycoprotein Endopeptidase_2-(CT197)
CPn0195	234190	235785	F	oppA_1-Oligopeptide Binding Protein_1
CPn0196	235939	237519	F	oppA_2-Oligopeptide Binding Protein_2-(CT198)
CPn0197	237578	238882	F	oppA_3-Oligopeptide Binding Protein_3
CPn0198	239169	240746	F	oppA_4-Oligopeptide Binding Protein_4
CPn0199	241042	241983	F	oppB_1-Oligopeptide Permease_1-(CT199)
CPn0200	242017	242868	F	oppC_1-Oligopeptide Permease_1-(CT200)
CPn0201	242864	243715	F	oppD-Oligopeptide Transport ATPase-(CT201)
CPn0202	243715	244500	F	oppF-Oligopeptide Transport ATPase-(CT202)
CPn0203	245008	245802	F	
CPn0204	245817	246002	F	
CPn0205	246133	246327	F	
CPn0206	246409	247161	F	CT203 hypothetical protein
CPn0207	247208	248617	F	ybhI/sodiT1-Oxoglutarate/Malate Translocator-(CT204)
CPn0208	248953	250602	F	pfkA_2-Fructose-6-P Phosphotransferase_2-(CT205)
CPn0209	251036	251272	F	

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CPn0210	252384	251440	R	
CPn0211	252756	252463	R	
CPn0212	254066	252888	R	
CPn0213	254342	254190	R	
CPn0214	255657	254446	R	
CPn0215	257015	255759	R	
CPn0216	257608	257174	R	
CPn0217	257896	258579	F	ypdP-(CT140)
CPn0218	259058	258582	R	
CPn0219	259357	260472	F	tgt-Queuine tRNA Ribosyl Transferase-(CT193)
CPn0220	260696	261238	F	
CPn0221	261657	262064	F	
CPn0222	262504	262842	F	*weak similarity to Bacteriophage CHP1 (Orf4)
CPn0223	262956	263333	F	
CPn0224	263435	263674	F	
CPn0225	263873	264541	F	
CPn0226	264566	264967	F	
CPn0227	265416	265009	R	dsbB-Disulfide bond Oxidoreductase-(CT176)
CPn0228	266110	265412	R	dsbG-Disulfide Bond Chaperone-(CT177)
CPn0229	266328	267560	F	CT178 hypothetical protein
CPn0230	268253	267576	R	CT179 hypothetical protein
CPn0231	268957	268253	R	tauB-ABC Transport ATPase (Nitrate/Fe)-(CT180)
CPn0232	270122	269232	R	*similarity to 5'-Methylthioadenosine / S-Adenosylhomocysteine Nucleosidase
CPn0233	270424	270248	R	
CPn0234	271240	270548	R	CT181 hypothetical protein
CPn0235	271416	272177	F	kdsB-deoxyoctulonosic Acid Synthetase-(CT182)
CPn0236	272156	273766	F	pyrG-CTP Synthetase-(CT183)
CPn0237	273762	274214	F	yggF Family-(CT184)
CPn0238	274303	275838	F	zwf-Glucose-6-P Dehyrogenase-(CT185)
CPn0239	275899	276672	F	devB-Glucose-6-P Dehyrogenase (DevB family)-(CT186)
CPn0240	277861	276698	R	
CPn0241	279354	278203	R	
CPn0242	279918	279487	R	
CPn0243	280555	280133	R	
CPn0244	280918	281556	F	adk-Adenylate Kinase-(CT128)
CPn0245	281645	282499	F	ydhO-Polysaccharide Hydrolase-Invasin Repeat Family-(CT127)
CPn0246	282952	282551	R	rs9-S9 Ribosomal Protein-(CT126)
CPn0247	283415	282969	R	rl13-L13 Ribosomal Protein-(CT125)
CPn0248	284327	283650	R	ycfV/ybbA-ABC Transporter ATPase-(CT152)
CPn0249	285841	284333	R	CT151 hypothetical protein
CPn0250	286057	285902	R	rl33-L33 Ribosomal Protein-(CT150)
CPn0251	286060	287559	F	*conserved hypothetical protein
CPn0252	288112	287576	R	CT144 hypothetical protein (frame-shift with 0253?)
CPn0253	288456	287950	R	CT144 hypothetical protein_1
CPn0254	289262	288459	R	CT143 hypothetical protein_1
CPn0255	290165	289329	R	CT142 hypothetical protein_1
CPn0256	291264	290398	R	CT144 hypothetical protein_2
CPn0257	292127	291267	R	CT143 hypothetical protein_2
CPn0258	292534	292133	R	CT142 hypothetical protein (frame-shift with 0259?)
CPn0259	292986	292441	R	CT142 hypothetical protein_2
CPn0260	294045	293548	R	secA_1-Protein Translocase Subunit_1-(CT141)
CPn0261	294302	295033	F	ydaO-PP-Loop Superfamily ATPase-(CT217)
CPn0262	295091	295933	F	surE-SurE-like Acid Phosphatase-(CT218)
CPn0263	296249	297136	F	yqfU hypothetical protein-(CT221)
CPn0264	297730	297155	R	ubiD-Phenylacrylate Decarboxylase-(CT220)
CPn0265	298620	297730	R	ubiA-Benzoate Octaphenyltransferase-(CT219)
CPn0266	299184	299876	F	
CPn0267	300122	300910	F	
CPn0268	300935	301318	F	
CPn0269	302450	301476	R	Dipeptidase-(CT138)
CPn0270	303325	302468	R	ywlC-SuA5 Superfamily-related Protein-(CT137)
CPn0271	303634	304362	F	Lysophospholipase esterase-(CT136)
CPn0272	305233	304340	R	dnaX_2-DNA Pol III Gamma and Tau_2-(CT187)
CPn0273	305844	305227	R	tdk-Thymidylate Kinase-(CT188)
CPn0274	308353	305852	R	gyrA_1-DNA Gyrase Subunit A_1-(CT189)
CPn0275	310786	308372	R	gyrB_1-DNA Gyrase Subunit B_1-(CT190)
CPn0276	311137	310793	R	CT191 hypothetical protein
CPn0277	311910	311404	R	
CPn0278	312875	312060	R	*conserved outer membrane lipoprotein protein
CPn0279	313537	312875	R	*Possible ABC Transporter Permease Protein
CPn0280	314572	313550	R	dppF-Dipeptide Transporter ATPase-(CT689)

CPn0281	315057	316103	F	dhnA-Predicted 1.6-Fructose Biphosph..e Aldolase (dehydrin family)-(CT215)
CPn0282	316126	317529	F	xasA/gadC-Amino Acid Transporter-(CT216)
CPn0283	318497	317532	R	
CPn0284	319045	318551	R	
CPn0285	320595	319051	R	
CPn0286	322059	320650	R	mgtE-Mg++ Transporter (CBS Domain)-(CT194)
CPn0287	324221	322089	R	
CPn0288	325716	324571	R	CT195 hypothetical protein
CPn0289	325812	326996	F	aaaT-Neutral Amino Acid (Glutamate) Transporter-(CT230)
CPn0290	327042	328523	F	Na-dependent Transporter-(CT231)
CPn0291	328667	329194	F	incB-Inclusion Membrane Protein B-(CT232)
CPn0292	329228	329836	F	incC-Inclusion Membrane Protein C-(CT233)
CPn0293	329949	332723	F	CT234 hypothetical protein
CPn0294	333092	333502	F	cAMP-Dependent Protein Kinase Regulatory Subunit-(CT235)
CPn0295	333863	333627	R	acpP-Acyl Carrier Protein-(CT236)
CPn0296	334765	334022	R	fabG-Oxoacyl (Carrier Protein) Reductase-(CT237)
CPn0297	335697	334774	R	fabD-Malonyl Acyl Carrier Transcyclase-(CT238)
CPn0298	336721	335717	R	fabH-Oxoacyl Carrier Protein Synthase III-(CT239)
CPn0299	336816	337415	F	recR-Recombination Protein-(CT240)
CPn0300	337783	340152	F	yaeT-Omp85 Analog-(CT241)
CPn0301	340250	340762	F	(OmpH-Like Outer Membrane Protein)-(CT242)
CPn0302	340787	341866	F	lpxD-UDP Glucosamine N-Acyltransferase-(CT243)
CPn0303	342958	341921	R	CT244 hypothetical protein
CPn0304	343133	344158	F	pdhA/odpA-Pyruvate Dehydrogenase Alpha-(CT245)
CPn0305	344154	345137	F	pdhB/odpB-Pyruvate Dehydrogenase Beta-(CT246)
CPn0306	345145	346431	F	pdhC-Dihydrolipoamide Acetyltransferase-(CT247)
CPn0307	348986	346515	R	glgP-Glycogen Phosphorylase-(CT248)
CPn0308	349234	349596	F	similarity to CT249
CPn0309	350974	349595	R	dnaA_1-Replication Initiation Protein_1-(CT250)
CPn0310	353433	351049	R	60IM-60kDa Inner Membrane Protein-(CT251)
CPn0311	354438	353575	R	lgt-Prolipoprotein Diacylglycerol Transferase-(CT252)
CPn0312	354524	354976	F	CT101 hypothetical protein
CPn0313	354990	355355	F	acpS-Acyl-carrier Protein Synthase-(CT100)
CPn0314	356285	355353	R	trxB-Thioredoxin Reductase-(CT099)
CPn0315	356977	358716	F	rs1-S1 Ribosomal Protein-(CT098)
CPn0316	358820	360121	F	nusA-N Utilization Protein A-(CT097)
CPn0317	360081	362750	F	infB-Initiation Factor-2-(CT096)
CPn0318	362767	363126	F	rbfA-Ribosome Binding Factor A-(CT095)
CPn0319	363175	363879	F	truB-tRNA Pseudouridine Synthase-(CT094)
CPn0320	363860	364783	F	ribF-FAD Synthase-(CT093)
CPn0321	365858	364767	R	ychF-GTP Binding Protein-(CT092)
CPn0322	366249	367328	F	yscU-YopS Translocation Protein U -(CT091)
CPn0323	367331	369460	F	lcrD- Low Calcium Response D-(CT090)
CPn0324	369492	370688	F	lcrE- Low Calcium Response E-(CT089)
CPn0325	370708	371148	F	sycE-Secretion Chaperone-(CT088)
CPn0326	371148	372725	F	malQ-Glucanotransferase-(CT087)
CPn0327	372945	373211	F	rl28-L28 Ribosomal Protein-(CT086)
CPn0328	373241	374992	F	CT085 hypothetical protein
CPn0329	375088	376146	F	Phopholipase D Superfamily [leader (33) peptide]-(CT084)
CPn0330	376675	376202	R	CT083 hypothetical protein
CPn0331	378437	376701	R	CT082 hypothetical protein
CPn0332	378655	378536	R	CHLTR T2 Protein-(CT081)
CPn0333	379090	378800	R	ltuB-(CT080)
CPn0334	379311	379823	F	CT079 similarity
CPn0335	379817	380674	F	folD-Methylene Tetrahydrofolate Dehydrogenase-(CT078)
CPn0336	380650	381591	F	yojL-(CT077)
CPn0337	382027	381575	R	smpB- Small Protein B-(CT076)
CPn0338	382278	383375	F	dnaN-DNA Pol III (beta chain)-(CT075)
CPn0339	383420	384034	F	recF-ABC superfamily ATPase-(CT074)
CPn0340	383842	384156	F	(frame-shift with 0339)
CPn0341	384160	384495	F	(frame-shift with 0340)
CPn0342	384622	385062	F	predicted OMP [leader (19) peptide]-(CT073)
CPn0343	84999	385595	F	(frame-shift with 0342?)
CPn0344	387420	385558	R	yaeL-Metalloprotease-(CT072)
CPn0345	388572	387436	R	yaeM-(CT071)
CPn0346	389675	388704	R	troD/ytgD-Integral Membrane Protein-(CT070)
CPn0347	391021	389678	R	troC/ytgC-Integral Membrane Protein-(CT069)
CPn0348	391803	391027	R	troB/ytgB-ABC transporter ATPase-(CT068)
CPn0349	392770	391790	R	troA/ytgA-Solute Protein Binding Family-(CT067)
CPn0350	393181	393684	F	CT066 hypothetical protein
CPn0351	393888	395432	F	adt_1-ADP/ATP Translocase_1-(CT065)

CPn0352	395574	396830	F	
CPn0353	396893	397135	F	
CPn0354	397167	398507	F	
CPn0355	399889	398591	R	
CPn0356	400459	400109	R	
CPn0357	401317	400469	R	
CPn0358	401751	401578	R	
CPn0359	402012	403817	F	lepA-GTPase-(CT064)
CPn0360	405358	403922	R	gnd-6-Phosphogluconate Dehydrogenase-(CT063)
CPn0361	406647	405382	R	tyrS-tyrosyl tRNA Synthetase-(CT062)
CPn0362	407825	407055	R	fliA/rpsD-Sigma-28/WhiG Family-(CT061)
CPn0363	409688	407943	R	flhA-Flagellar Secretion Protein-(CT060)
CPn0364	409966	410238	F	fer4-Ferredoxin IV-(CT059)
CPn0365	410528	411544	F	
CPn0366	411976	412440	F	
CPn0367	413102	413836	F	
CPn0368	413790	414107	F	
CPn0369	414351	415562	F	CT058 hypothetical protein_2
CPn0370	415800	416912	F	CT058 hypothetical protein_3
CPn0371	417147	417503	F	
CPn0372	417687	418001	F	
CPn0373	418380	420218	F	gcpE-(CT057)
CPn0374	420218	420961	F	CT056 hypothetical protein
CPn0375	421121	421615	F	
CPn0376	421854	422294	F	
CPn0377	423438	422347	R	sucB_1-Dihydrolipoamide Succinyltransferase_1-(CT055)
CPn0378	426168	423445	R	sucA-Oxoglutarate Dehydrogenase-(CT054)
CPn0379	426322	426765	F	CT053 hypothetical protein
CPn0380	426758	427876	F	hemN_1-Coproporphyrinogen III Oxidase_1-(CT052)
CPn0381	429809	428037	R	CT326 similarity
CPn0382	430749	430036	R	yabC/yraL-SAM-Dependent Methytransferase-(CT048)
CPn0383	431693	430749	R	CT047 hypothetical protein
CPn0384	432377	431862	R	hctB-Histone-like Protein 2-(CT046)
CPn0385	434018	432522	R	pepA-Leucyl Aminopeptidase A-(CT045)
CPn0386	434525	434046	R	ssb-SS DNA Binding Protein-(CT044)
CPn0387	435196	434699	R	CT043 hypothetical protein
CPn0388	435329	437320	F	glgX-Glycogen Hydrolase (debranching)-(CT042)
CPn0389	438134	437319	R	CT041 hypothetical protein
CPn0390	439144	438134	R	ruvB-Holliday Junction Helicase-(CT040)
CPn0391	439692	439510	R	
CPn0392	439814	440383	F	dcd-dCTP Deaminase-(CT039)
CPn0393	440379	440723	F	CT038 hypothetical protein
CPn0394	440736	441968	F	tlyC_1-CBS Domain protein (Hemolysin Homolog)_1-(CT256)
CPn0395	441964	443175	F	CT257 hypothetical protein
CPn0396	444353	443241	R	yhfO-NifS-related protein-(CT258)
CPn0397	445115	444381	R	PP2C phosphatase family-(CT259)
CPn0398	445533	445700	F	
CPn0399	445879	446523	F	CT253 hypothetical protein
CPn0400	446536	447306	F	CT254 hypothetical protein
CPn0401	447884	447495	R	CT255 hypothetical protein
CPn0402	448994	447888	R	mutY-Adenine Glycosylase-(CT107)
CPn0403	449015	449710	F	yceC-predicted pseudouridine synthetase family-(CT106)
CPn0404	450887	449871	R	
CPn0405	451739	450966	R	CT105 hypothetical protein
CPn0406	451969	452865	F	fabI-Enoyl-Acyl-Carrier Protein Reductase-(CT104)
CPn0407	453742	452858	R	HAD superfamily hydrolase/phosphatase-(CT103)
CPn0408	454105	454581	F	CT102 hypothetical protein
CPn0409	454645	455127	F	CT260 hypothetical protein
CPn0410	455123	455833	F	dnaQ_1-DNA Pol III Epsilon Chain_1-(CT261)
CPn0411	455833	456609	F	CT262 hypothetical protein
CPn0412	456590	457246	F	CT263 hypothetical protein
CPn0413	459203	457227	R	msbA-Transport ATP Binding Protein-(CT264)
CPn0414	460143	459172	R	accA-AcCoA Carboxylase/Transferase Alpha-(CT265)
CPn0415	461498	460221	R	CT266 hypothetical protein
CPn0416	461856	461557	R	himD/ihfA-Integration Host Factor Alpha-(CT267)
CPn0417	463035	462244	R	amiA-N-Acetylmuramoyl Alanine Amidase-(CT268)
CPn0418	464401	462953	R	murE-N-Acetylmuramoylalanylglutamyl DAP Ligase-(CT269)
CPn0419	466834	464876	R	pbp3- transglycolase/transpeptidase-(CT270)
CPn0420	467108	466824	R	CT271 hypothetical protein
CPn0421	467998	467108	R	yabC-PBP2B Family methyltransferase-(CT272)
CPn0422	468242	468784	F	CT273 hypothetical protein
CPn0423	468791	469216	F	CT274 hypothetical protein

CPn0424	469612	470961	F	dnaA_2-Replication Initiation Factor_2-(CT275)
CPn0425	470980	471564	F	CT276 hypothetical proteins
CPn0426	472111	471536	R	CT277 similarity
CPn0427	472207	473715	F	nqr2-NADH (Ubiquinone) Dehydrogenase-(CT278)
CPn0428	473722	474681	F	nqr3-NADH (Ubiquinone) Oxidoreductase, Gamma-(CT279)
CPn0429	474681	475319	F	nqr4-NADH (Ubiquinone) Reductase 4-(CT280)
CPn0430	475326	476093	F	nqr5-NADH (Ubiquinone) Reductase 5-(CT281)
CPn0431	476483	476151	R	
CPn0432	476816	476514	R	
CPn0433	477273	476929	R	gcsH-Glycine Cleavage System H Protein-(CT282)
CPn0434	479462	477276	R	CT283 hypothetical protein
CPn0435	480902	479475	R	Phospholipase D superfamily [uncleavable leader peptide]-(CT284)
CPn0436	481618	480902	R	lplA-Lipoate Protein Ligase-Like Protein-(CT285)
CPn0437	481816	484350	F	clpC-ClpC Protease-(CT286)
CPn0438	485416	484334	R	ycbF-PP-loop superfamily ATPase-(CT287)
CPn0439	485553	486077	F	
CPn0440	486105	486740	F	
CPn0441	486891	487838	F	CT007 hypothetical protein
CPn0442	488013	488528	F	CT006 hypothetical protein
CPn0443	488729	489979	F	CT005 hypothetical protein
CPn0444	490287	494507	F	pmp_6-Polymorphic Outer Membrane Protein G/I Family
CPn0445	494772	497579	F	pmp_7-Polymorphic Outer Membrane Protein G Family
CPn0446	497626	500415	F	pmp_8-Polymorphic Outer Membrane Protein G Family
CPn0447	500568	503351	F	pmp_9-Polymorphic Outer Membrane Protein G/I Family
CPn0448	504810	503698	R	*yxjG_Bs_2 Hypothetical Protein
CPn0449	507231	505330	R	pmp_10-PMP_10 (Frame-shift with 0451)
CPn0450	508112	507180	R	pmp_10-Polymorphic Outer Membrane Protein G Family
CPn0451	508275	511058	F	pmp_11-Polymorphic Outer Membrane Protein G Family
CPn0452	511319	512860	F	pmp_12-Polymorphic Outer Membrane Protein A/I Family (truncated)
CPn0453	513234	516152	F	pmp_13 -Polymorphic Outer Membrane Protein G Family
CPn0454	516182	519115	F	pmp_14-Polymorphic Outer Membrane Protein H Family
CPn0455	520348	519458	R	
CPn0456	521532	520327	R	
CPn0457	523865	522120	R	
CPn0458	526320	524236	R	
CPn0459	527005	526619	R	
CPn0460	527840	526992	R	
CPn0461	528638	527844	R	
CPn0462	531052	529037	R	
CPn0463	532357	531191	R	
CPn0464	532842	532366	R	
CPn0465	533212	532871	R	
CPn0466	533724	536537	F	pmp_15-Polymorphic Outer Membrane Protein E Family
CPn0467	536633	539434	F	pmp_16-Polymorphic Outer Membrane Protein E Family
CPn0468	539632	540432	F	pmp_17-Polymorphic Outer Membrane Protein E Family
CPn0469	540399	541460	F	pmp_17-Polymorphic Outer Membrane Protein (Frame-shift with 0469)
CPn0470	541357	542532	F	pmp_17-Polymorphic Outer Membrane Protein (Frame-shift with 0470)
CPn0471	542564	545401	F	pmp_18-Polymorphic Outer Membrane Protein E/F Family
CPn0472	547905	545581	R	
CPn0473	549593	548070	R	
CPn0474	551573	549807	R	CT365 hypothetical protein
CPn0475	553844	551685	R	glgB-Glucan Branching Enzyme-(CT866)
CPn0476	554844	553858	R	CT865 hypothetical protein
CPn0477	556106	554844	R	*yqeV_Bs Hypothetical Protein
CPn0478	557625	556210	R	hflX-GTP Binding Protein-(CT379)
CPn0479	558425	557616	R	phnP-Metal Dependent Hydrolase-(CT380)
CPn0480	559303	558650	R	CT383 hypothetical protein
CPn0481	560946	559339	R	
CPn0482	561737	560961	R	artJ-Arginine Periplasmic Binding Protein-(CT381)
CPn0483	561836	564964	F	
CPn0484	564970	565824	F	aroG-Deoxyheptonate Aldolase-(CT382)
CPn0485	566038	566229	F	CT382.1 hypothetical protein
CPn0486	567784	566405	R	*hypothetical proline permease
CPn0487	569740	568112	R	CT384 hypothetical protein
CPn0488	570096	569767	R	hitA-HIT Family Hydrolase-(CT385)
CPn0489	570965	570096	R	CT386 hypothetical protein
CPn0490	571279	573333	F	CT387 hypothetical protein
CPn0491	574352	573336	R	CT389 hypothetical protein
CPn0492	574652	574804	F	
CPn0493	575004	574855	R	
CPn0494	575364	575146	R	
CPn0495	575603	576793	F	aspC-Aspartate Aminotransferase-(CT390)

CPn0496	576793	577812	F	CT391 hypothetical protein
CPn0497	578089	577820	R	CT388 hypothetical protein
CPn0498	579035	578085	R	
CPn0499	580359	579205	R	
CPn0500	580659	582362	F	proS-Prolyl tRNA Synthetase-(CT393)
CPn0501	582457	583650	F	hrcA-HTH Transcriptional Repressor-(CT394)
CPn0502	583650	584201	F	grpE-HSP-70 Cofactor-(CT395)
CPn0503	584234	586213	F	dnaK-HSP-70-(CT396)
CPn0504	586487	588514	F	vacB-ribonuclease family-(CT397)
CPn0505	588519	589106	F	*3-methyladenine DNA glycosylase
CPn0506	589172	589840	F	CT421 hypothetical protein
CPn0507	589961	590122	F	CT421.1 hypothetical protein
CPn0508	590142	590300	F	CT421.2 hypothetical protein
CPn0509	590335	590808	F	(predicted Metalloenzyme)-(CT422)
CPn0510	590813	591973	F	tlyC_2-CBS Domains (Hemolysin homolog)_2-(CT423)
CPn0511	592141	592488	F	rsbV_1-Sigma Regulatory Factor_1-(CT424)
CPn0512	592553	594412	F	CT425 hypothetical protein
CPn0513	594647	595753	F	Fe-S oxidoreductase_1-(CT426)
CPn0514	595729	596520	F	CT427 hypothetical protein
CPn0515	596492	597181	F	ubiE-Ubiquinone Methyltransferase-(CT428)
CPn0516	598814	597255	R	
CPn0517	599631	598795	R	
CPn0518	600803	599832	R	CT429 hypothetical protein
CPn0519	601674	600904	R	dapF-Diaminopimelate Epimerase-(CT430)
CPn0520	602218	601646	R	clpP-CLP Protease-(CT431)
CPn0521	603797	602241	R	glyA-Serine Hydroxymethyltransferase-(CT432)
CPn0522	603987	604655	F	CT433 hypothetical protein
CPn0523	604723	605052	F	
CPn0524	605103	606179	F	
CPn0525	606522	607283	F	CT398 hypothetical protein
CPn0526	608696	607710	R	yrbH-GutQ/KpsF Family Sugar-P Isomerase-(CT399)
CPn0527	609904	608726	R	sucB_2-Dihydrolipoamide Succinyltransferase_2-(CT400)
CPn0528	611162	609921	R	gltT-Glutamate Symport-(CT401)
CPn0529	612259	611165	R	ycaH-ATPase-(CT402)
CPn0530	613254	612460	R	spoU_1-rRNA Methylase_1-(CT403)
CPn0531	614069	613245	R	SAM dependent methyltransferase-(CT404)
CPn0532	614674	614075	R	ribC/risA-Riboflavin Synthase-(CT405)
CPn0533	614930	615385	F	CT406 hypothetical protein
CPn0534	615413	615784	F	dksA-DnaK Suppressor-(CT407)
CPn0535	615793	616296	F	lspA-Lipoprotein Signal Peptidase-(CT408)
CPn0536	616345	617691	F	dagA_1-D-Ala/Gly Permease_1-(CT409)
CPn0537	617833	618189	F	CT814.1 hypothetical protein
CPn0538	618212	618511	F	CT814 hypothetical protein
CPn0539	618705	621545	F	pmp_19-polymorphic outer membrane protein A Family -(CT412)
CPn0540	621694	626862	F	pmp_20-polymorphic outer membrane protein B Family-(CT413)
CPn0541	627170	628003	F	Solute binding protein (-yebL-Synechocystis Adhesin Homolog)-(CT415)
CPn0542	628003	628737	F	ABC Transporter ATPase-(CT416)
CPn0543	628725	629603	F	(Metal Transport Protein)-(CT417)
CPn0544	630529	629525	R	yhbZ-GTP binding protein-(CT418)
CPn0545	630884	630633	R	rl27-L27 ribosomal protein-(CT419)
CPn0546	631229	630912	R	rl21-L21 Ribosomal Protein-(CT420)
CPn0547	631661	632188	F	ygbB family-(CT434)
CPn0548	633231	632191	R	cysJ-Sulfite Reductase-(CT435)
CPn0549	633569	633255	R	rs10-S10 Ribosomal Protein-(CT436)
CPn0550	635661	633580	R	fusA-Elongation Factor G-(CT437)
CPn0551	636168	635698	R	rs7-S7 Ribosomal Protein-(CT438)
CPn0552	636587	636219	R	rs12-S12 Ribosomal Protein-(CT439)
CPn0553	637747	636812	R	
CPn0554	637854	638141	F	CT440 hypothetical protein
CPn0555	638298	640241	F	tsp-Tail-Specific Protease-(CT441)
CPn0556	640912	640325	R	crpA-15kDa Cysteine-Rich Protein-(CT442)
CPn0557	642861	641194	R	omcB-60kDa Cysteine-Rich Outer Membrane Complex Protein-(CT443)
CPn0558	643300	643031	R	omcA-9kDa-Cysteine-Rich Outer Membrane Complex Lipoprotein-(CT444)
CPn0559	643742	643927	F	CT441.1 hypothetical protein
CPn0560	645612	644098	R	gltX-Glutamyl-tRNA Synthetase-(CT445)
CPn0561	646404	645871	R	euo-CHLPS Euo Protein-(CT446)
CPn0562	648036	646918	R	*CHLPS 43 kDa protein homolog_1
CPn0563	650056	648293	R	recJ-ssDNA Exonuclease-(CT447)
CPn0564	654350	650145	R	secD&secF-Protein Export Proteins SecD/SecF (fusion)-(CT448)
CPn0565	655630	654533	R	CT449 hypothetical protein
CPn0566	656141	656890	F	yaeS family-(CT450)
CPn0567	656894	657817	F	cdsA-Phosphatidate Cytidylytransferase-(CT451)

CPn0568	657817	658464	F	cdsA-Phosphatidate Cytidylytransferase-(CT452)
CPn0569	658464	659099	F	plsC-Glycerol-3-P Acyltransferase-(CT453)
CPn0570	659107	660789	F	argS-Arginyl tRNA Transferase-(CT454)
CPn0571	662122	660749	R	murA-UDP-N-Acetylglucosamine Transferase-(CT455)
CPn0572	662352	664616	F	CT456 hypothetical protein
CPn0573	665404	664691	R	yebC family-(CT457)
CPn0574	665945	665394	R	
CPn0575	666494	665982	R	YhhY-Amino Group Acetyl Transferase-(CT458)
CPn0576	667543	666494	R	prfB-Peptide Chain Release Factor 2 (natural UGA frame-shift)-(CT459
CPn0576	667598	667530	R	prfB-(natural UGA frame-shift)
CPn0577	667895	668155	F	SWIB (YM74) complex protein-(CT460)
CPn0578	668406	669365	F	yaeI-phosphohydrolase-(CT461)
CPn0579	669361	669993	F	ygbP/yacM-Sugar Nucleotide Phosphorylase-(CT462)
CPn0580	669993	670793	F	truA-Pseudouridylate Synthase I-(CT463)
CPn0581	671434	670745	R	Phosphoglycolate Phosphatase-(CT464)
CPn0582	671503	672177	F	CT465 hypothetical protein
CPn0583	672400	672717	F	CT466 hypothetical protein
CPn0584	672707	673798	F	atoS/ntrB-2-Component Sensor-(CT467)
CPn0585	675817	673865	R	*similarity to Cps IncA_2
CPn0586	676026	677183	F	atoC/ntrC-2-Component Regulator-(CT468)
CPn0587	677441	678124	F	*yvyD_Bs conserved hypothetical protein
CPn0588	678084	678626	F	CT469 hypothetical protein
CPn0589	678640	679395	F	CT470 hypothetical protein
CPn0590	680112	679516	F	CT471 hypothetical protein
CPn0591	680373	681020	F	yagE family-(CT472)
CPn0592	681153	681461	F	yidD family-(CT473)
CPn0593	682476	681391	R	CT474 hypothetical protein
CPn0594	682583	684958	F	pheT-phenylalanyl tRNA Synthetase Beta-(CT475)
CPn0595	684958	685926	F	CT476 hypothetical protein
CPn0596	685939	686457	F	ada-methyltransferase-(CT477)
CPn0597	688215	686479	R	oppC_2-Oligopeptide Permease_2-(CT478)
CPn0598	689697	688219	R	oppB_2-Oligopeptide Permease_2-(CT479)
CPn0599	691802	689682	R	oppA_5-oligopeptide Binding Lipoprotein_5-(CT480)
CPn0600	692147	691827	R	
CPn0601	693053	692736	R	CT483 hypothetical protein
CPn0602	694105	693104	R	CT484 hypothetical protein
CPn0603	694205	695185	F	hemZ-Ferrochetalase-(CT485)
CPn0604	695945	695196	R	fliY-Glutamine Binding Protein-(CT486)
CPn0605	696707	696150	R	yhhF-Methylase -(CT487)
CPn0606	697444	696707	R	CT488 hypothetical protein
CPn0607	698895	697573	R	glgC-Glucose-1-P Adenyltransferase-(CT489)
CPn0608	699645	699016	R	*pyrF-Uridine 5'-Monophosphate Synthase (Ump Synthase)-truncated?
CPn0609	699705	699986	F	CT490 hypothetical protein
CPn0610	701420	700029	R	rho-Transcription Termination Factor-(CT491)
CPn0611	702025	701420	R	yacE-predicted phosphatase/kinase-(CT492)
CPn0612	704631	702022	R	polA-DNA Polymerase I-(CT493)
CPn0613	705656	704658	R	sohB-Protease-(CT494)
CPn0614	707402	705783	R	adt_2-ADP/ATP Translocase_2-(CT495)
CPn0615	708137	707634	R	pgsA_1-Glycerol-3-P Phosphatidyltransferase_1-(CT496)
CPn0616	708791	710137	F	dnaB-Replicative DNA Helicase-(CT497)
CPn0617	710484	712316	F	gidA-FAD-dependent oxidoreductase-(CT498)
CPn0618	712306	713010	F	lplA-Lipoate-Protein Ligase A-(CT499)
CPn0619	713444	713013	R	ndk-Nucleoside-2-P Kinase-(CT500)
CPn0620	714139	713519	R	ruvA-Holliday Junction Helicase-(CT501)
CPn0621	714647	714144	R	ruvC-Crossover Junction Endonuclease-(CT502)
CPn0622	715752	714793	R	CT503 hypothetical protein
CPn0623	716993	716163	R	CT504 hypothetical protein
CPn0624	718015	717011	R	gapA-Glyceraldehyde-3-P Dehyrogenase-(CT505)
CPn0625	718485	718060	R	rl17-L17 Ribosomal Protein-(CT506)
CPn0626	719616	718495	R	rpoA-RNA Polymerase Alpha-(CT507)
CPn0627	720038	719640	R	rs11-S11 Ribosomal Protein-(CT508)
CPn0628	720428	720063	R	rs13-S13 Ribosomal Protein-(CT509)
CPn0629	721857	720487	R	secY-Translocase-(CT510)
CPn0630	722316	721885	R	rl15-L15 Ribosomal Protein-(CT511)
CPn0631	722806	722312	R	rs5-S5 Ribosomal Protein-(CT512)
CPn0632	723195	722827	R	rl18-L18 Ribosomal Protein-(CT513)
CPn0633	723757	723209	R	rl6-L6 Ribosomal Protein-(CT514)
CPn0634	724185	723787	R	rs8-S8 Ribosomal Protein-(CT515)
CPn0635	724745	724206	R	rl5-L5 Ribosomal Protein-(CT516)
CPn0636	725082	724750	R	rl24-L24 Ribosomal Protein-(CT517)
CPn0637	725464	725099	R	rl14-L14 Ribosomal Protein-(CT518)
CPn0638	725747	725490	R	rs17-S17 Ribosomal Protein-(CT519)

CPn0639	725958	725743	R	rl29-L29 Ribosomal Protein-(CT520)
CPn0640	726377	725964	R	rl16-L16 Ribosomal Protein-(CT521)
CPn0641	727077	726409	R	rs3-S3 Ribosomal Protein-(CT522)
CPn0642	727428	727096	R	rl22-L22 Ribosomal Protein-(CT523)
CPn0643	727713	727450	R	rs19-S19 Ribosomal Protein-(CT524)
CPn0644	728573	727722	R	rl2-L2 Ribosomal Protein-(CT525)
CPn0645	728930	728598	R	rl23-L23 Ribosomal Protein-(CT526)
CPn0646	729621	728950	R	rl4-L4 Ribosomal Protein-(CT527)
CPn0647	730331	729657	R	rl3-L3 Ribosomal Protein-(CT528)
CPn0648	731603	730605	R	CT529 hypothetical protein
CPn0649	732672	731710	R	fmt-Methionyl tRNA Formyltransferase-(CT530)
CPn0650	733501	732665	R	lpxA-Acyl-Carrier UDP-GlcNAc -(CT531)
CPn0651	733975	733517	R	fabZ-Myristoyl-Acyl Carrier Dehydratase-(CT532)
CPn0652	734835	733990	R	lpxC-Myristoyl GlcNac Deacetylase-(CT533)
CPn0653	736490	734868	R	cutE-Apolipoprotein N-Acetyltransferase-(CT534)
CPn0654	736967	736503	R	vdlD/yciA-acyl-CoA Thioesterase-(CT535)
CPn0655	737847	737101	R	dnaQ_2-DNA Pol III Epsilon Chain_2-(CT536)
CPn0656	737872	738048	F	
CPn0657	738473	738051	R	yjeE (ATPase or Kinase)-(CT537)
CPn0658	739168	738455	R	CT538 hypothetical protein
CPn0659	739533	739838	F	trxA-Thioredoxin-(CT539)
CPn0660	740327	739860	R	spoU_2-rRNA Methylase_2-(CT540)
CPn0661	741100	740327	R	mip-FKBP-type peptidyl-prolyl cis-trans isomerase-(CT541)
CPn0662	742923	741172	R	aspS-Aspartyl tRNA Synthetase-(CT542)
CPn0663	744190	742901	R	hisS-Histidyl tRNA Synthetase-(CT543)
CPn0664	744757	744557	R	
CPn0665	745001	746365	F	uhpC-Hexosphosphate Transport -(CT544)
CPn0666	746388	750107	F	dnaE-DNA Pol III Alpha-(CT545)
CPn0667	751058	750177	R	predicted OMP [leader (17)-(CT546)
CPn0668	751209	752162	F	CT547 hypothetical protein
CPn0669	752179	752775	F	CT548 hypothetical protein
CPn0670	752765	753196	F	rsbW-sigma regulatory factor-histidine kinase-(CT549)
CPn0671	753630	753205	R	CT550 hypothetical protein
CPn0672	753741	755048	F	dacF(pbp5)-D-Ala-D-Ala Caroxypeptidase-(CT551)
CPn0673	755287	755463	F	CT552 hypothetical protein
CPn0674	756668	755577	R	fmu-RNA Methyltransferase-(CT553)
CPn0675	757919	756768	R	CT696 hypothetical protein
CPn0676	759217	758051	R'	homologous to CT695
CPn0677	760401	759256	R	
CPn0678	761320	760682	R	
CPn0679	762930	761725	R	pgk-Phosphoglycerate Kinase-(CT693)
CPn0680	764248	762971	R	ygo4-Phosphate Permease-(CT692)
CPn0681	764929	764258	R	CT691 hypothetical protein
CPn0682	764984	765955	F	dppD-ABC ATPase Dipeptide Transport-(CT690)
CPn0683	765948	766919	F	dppF-ABC ATPase Dipeptide Transport-(CT689)
CPn0684	768038	767181	R	spoJ/parB-Chromosome Partitioning Protein-(CT688)
CPn0685	768068	768217	F	
CPn0686	768361	768176	R	
CPn0687	768564	769214	F	CT482 hypothetical protein
CPn0688	769382	770137	F	CT481 hypothetical protein
CPn0689	771404	770187	R	yfhO_1-NifS-related Aminotransferase_1-(CT687)
CPn0690	772680	771436	R	ABC Transporter Membrane Protein-(CT686)
CPn0691	773452	772685	R	abcX-ABC Transporter ATPase-(CT685)
CPn0692	774912	773461	R	ABC Transporter-(CT684)
CPn0693	776256	775240	R	TPR Repeats (O-Linked GlcNAc Transferase similarity)-(CT683)
CPn0694	779599	776330	R	pbp2-PBP2-transglycolase/transpeptidase-(CT682)
CPn0695	780216	781382	F	ompA-Major Outer Membrane Protein-(CT681)
CPn0696	781769	782599	F	rs2-S2 Ribosomal Protein-(CT680)
CPn0697	782602	783447	F	tsf-Elongation Factor TS-(CT679)
CPn0698	783458	784201	F	pyrH-UMP Kinase-(CT679)
CPn0699	784182	784721	F	rrf-Ribosome Releasing Factor-(CT677)
CPn0700	785097	785609	F	CT676 hypothetical protein
CPn0701	785599	786672	F	karG-Arginine Kinase-(CT675)
CPn0702	789685	786929	R	yscC/gspD-Yop C/Gen Secretion Protein D-(CT674)
CPn0703	791190	789685	R	pkn5-S/T Protein Kinase-(CT673)
CPn0704	792321	791209	R	fliN- Flagellar Motor Switch Domain/YscQ family-(CT672)
CPn0705	793173	792334	R	CT671 hypothetical protein
CPn0706	793683	793180	R	CT670 hypothetical protein
CPn0707	795029	793704	R	yscN-Yop N (Flagellar-Type ATPase)-(CT669)
CPn0708	795705	795034	R	CT668 hypothetical protein
CPn0709	796188	795742	R	CT667 hypothetical protein
CPn0710	796661	796210	R	CT666 hypothetical protein

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CPn0711	796731	796486	R	CT665 hypothetical protein
CPn0712	799315	796781	R	FHA domain; homology to adenylate cyclase)-(CT664)
CPn0713	799721	799332	R	CT663 hypothetical protein
CPn0714	801107	800091	R	hemA-Glutamyl tRNA Reductase-(CT662)
CPn0715	801657	803462	F	gyrB_2-DNA Gyrase Subunit B_2-(CT661)
CPn0716	803469	804902	F	gyrA_2-DNA Gyrase Subunit A_2-(CT660)
CPn0717	805010	805306	F	CT656 hypothetical protein
CPn0718	805309	805626	F	CT657 hypothetical protein
CPn0719	805916	806890	F	sfhB-(Pseudouridine Synthase)-(CT658)
CPn0720	807003	807236	F	CT659 hypothetical protein
CPn0721	807683	808489	F	kdsA-KDO Synthetase-(CT655)
CPn0722	808489	808974	F	CT654 hypothetical protein
CPn0723	808984	809703	F	yhbG-ABC Transporter ATPase-(CT653)
_CPn0724	810527	809706	R	
CPn0725	810811	810587	R	CT652.1 hypothetical protein
CPn0726	813372	810880	R	CT620 hypothetical protein
CPn0727	813577	816192	F	CT619 hypothetical protein
CPn0728	818477	816525	R	CHLPN 76kDa Homolog_1 (CT622)
CPn0729	819857	818592	R	CHLPN 76kDa Homolog_2 (CT623)
CPn0730	821603	819963	R	mviN-Integral Membrane Protein-(CT624)
CPn0731	821587	821760	F	
CPn0732	822098	822976	F	nfo-Endonuclease IV-(CT625)
CPn0733	823727	823101	R	rs4-S4 Ribosomal Protein-(CT626)
CPn0734	823944	824915	F	yceA-(CT627)
CPn0735	825668	825003	R	*pyrH/udk-Uridine Kinase (Uridine Monophosphokinase) (Pyrimidine Ribonucleoside Kinase).
CPn0736	827686	825992	R	ygeD-Efflux Protein-(CT641)
CPn0737	827685	830756	F	recC-Exodeoxyribonuclease V, Gamma-(CT640)
CPn0738	830746	833895	F	recB-Exodeoxyribonuclease V, Beta-(CT639)
CPn0739	834871	833861	R	CT638 hypothetical protein
CPn0740	836048	834864	R	tyrB-Aromatic AA Aminotransferase-(CT637)
CPn0741	838350	836185	R	greA-Transcription Elongation Factor-(CT636)
CPn0742	838463	838888	F	CT635 hypothetical protein
CPn0743	838962	840362	F	nqrA-Ubiquinone Oxidoreductase, Alpha-(CT634)
CPn0744	841384	840389	R	hemB-Porphobilinogen Synthase-(CT633)
CPn0745	841903	841742	R	
CPn0746	841975	843567	F	CT632 hypothetical protein
CPn0747	843675	843740	F`	CT631 hypothetical protein
CPn0747	843725	843910	F	CT631 hypothetical protein (frame-shift)
CPn0748	844987	844121	R	ispA-Geranyl Transtransferase-(CT628)
CPn0749	845629	845006	R	glmU-UDP-GlcNAc Pyrophosphorylase-(CT629)
CPn0750	846411	845707	R	tctD/cpxR-HTH Transcriptional Regulatory Protein + Receiver Domain-(CT630)
CPn0751	846608	848434	F	CT651 hypothetical protein
CPn0752	848604	850082	F	recD_2-Exodeoxyribonuclease V, Alpha_2-(CT652)
CPn0753	851006	850161	R	
CPn0754	851336	851040	R	rs20-S20 Ribosomal Protein-(CT617)
CPn0755	851597	852799	F	CT616 hypothetical protein
CPn0756	852961	854676	F	rpoD-RNA Polymerase Sigma-66 -(CT615)
CPn0757	854733	855134	F	folX-Dihydroneopterin Aldolase-(CT614)
CPn0758	855110	856459	F	folP/dhpS-Dihydropteroate Synthase-(CT613)
CPn0759	856488	856997	F	folA-Dihydrofolate Reductase-(CT612)
CPn0760	856957	857694	F	CT611 hypothetical protein
CPn0761	857704	858375	F	CT610 hypothetical protein
CPn0762	859597	858539	R	recA-RecA recombination protein-(CT650)
CPn0763	860511	859972	R	ygfA-Formyltetrahydrofolate Cycloligase-(CT649)
CPn0764	861807	860524	R	CT648 hypothetical protein
CPn0765	862382	861801	R	CT647 hypothetical protein
CPn0766	863782	862394	R	CT646 hypothetical protein
CPn0767	863884	864177	F	CT645 hypothetical protein
CPn0768	864159	865163	F	yohI/nirJ-predicted oxidoreductase -(CT644)
CPn0769	867733	865121	R	topA-DNA Topoisomerase I-Fused to SWI Domain-(CT643)
CPn0770	868340	869131	F	CT642 hypothetical protein
CPn0771	870463	869144	R	rpoN-RNA Polymerase Sigma-54-(CT609)
CPn0772	872385	870469	R	uvrD-DNA Helicase-(CT608)
CPn0773	872488	873195	F	ung-Uracil DNA Glycosylase-(CT607)
CPn0774	873195	873425	F	CT606.1 hypothetical protein
CPn0775	874031	873414	R	yggV family-(CT606)
CPn0776	874246	875487	F	CT605 hypothetical protein
CPn0777	875601	877178	F	groEL_2-heat shock protein-60 -(CT604)
CPn0778	877505	878092	F	tsa/ahpC-Thio-specific Antioxidant (TSA) Peroxidase-(CT603)
CPn0779	878481	878095	R	CT602 hypothetical protein

CPn0780	879205	878591	R	papQ/amiB-N-Acetylmuramoyl-L-Ala Amidase-(CT601)
CPn0781	879773	879198	R	pal-Peptidoglycan-Associated Lipoprotein-(CT600)
CPn0782	881065	879773	R	tolB-polysaccharide transporter-(CT599)
CPn0783	881885	881100	R	CT598 hypothetical protein
CPn0784	882296	881892	R	exbD-Biopolymer Transport Protein-(CT597)
CPn0785	882991	882296	R	exbB/tolQ-polysaccharide transporter-(CT596)
CPn0786	883185	885293	F	dsbD/xprA-Thio:disulfide Interchange Protein-(CT595)
CPn0787	885619	886401	F	yabD/ycfH-PHP superfamily (urease/pyrimidinase) hydrolase-(CT594)
CPn0788	886542	887432	F	sdhC-Succinate Dehydrogenase-(CT593)
CPn0789	887439	889316	F	sdhA-Succinate Dehydrogenase-(CT592)
CPn0790	889330	890103	F	sdhB-Succinate Dehydrogenase-(CT591)
CPn0791	893050	890111	R	CT590 hypothetical protein
CPn0792	894919	893108	R	CT589 hypothetical protein
CPn0793	896823	894919	R	rbsU-sigma regulatory family protein—PP2C phosphatase (RsbW antagonist)-(CT588)
CPn0794	897174	898004	F	
CPn0795	898128	899195	F	
CPn0796	899301	901340	F	
CPn0797	901600	902694	F	
CPn0798	902846	903856	F	
CPn0799	904986	903940	R	
CPn0800	906532	905249	R	eno-Enolase-(CT587)
CPn0801	908697	906727	R	uvrB-Exinuclease ABC Subunit B-(CT586)
CPn0802	909740	908709	R	trpS-Tryptophanyl tRNA Synthetase-(CT585)
CPn0803	910303	909752	R	CT584 hypothetical protein
CPn0804	911059	910310	R	gp6D-CHLTR Plasmid Paralog-(CT583)
CPn0805	911831	911067	R	minD-chromosome partitioning ATPase-CHLTR plasmid protein GP5D-(CT582)
CPn0806	913771	911867	R	thrS-Threonyl tRNA Synthetase-(CT581)
CPn0807	913971	914879	F	CT580 hypothetical protein
CPn0808	916287	914956	R	CT579 hypothetical protein
CPn0809	917785	916307	R	CT578 hypothetical protein
CPn0810	918184	917825	R	CT577 hypothetical protein
CPn0811	918900	918208	R	lcrH_1-Low Ca Response Protein H_1-(CT576)
CPn0812	919123	920862	F	mutL-DNA Mismatch Repair-(CT575)
CPn0813	920870	921934	F	pepP-Aminopeptidase P-(CT574)
CPn0814	922107	923357	F	CT573 hypothetical protein
CPn0815	923361	925622	F	gspD/pilQ-Gen. Secretion Protein D-(CT572)
CPn0816	925615	927102	F	gspE-Gen. Secretion Protein E-(CT571)
CPn0817	927115	928287	F	gspF-Gen. Secretion Protein F-(CT570)
CPn0818	928314	928682	F	predicted OMP [leader (16) peptide]-(CT569)
CPn0819	928689	929132	F	CT568 hypothetical protein
CPn0820	929120	929659	F	CT567 hypothetical protein
CPn0821	929667	930668	F	CT566 hypothetical protein
CPn0822	930756	931229	F	CT565 hypothetical protein
CPn0823	932367	931501	R	yscT/spaR-YopT Tranlocation T-(CT564)
CPn0824	932662	932378	R	yscS/fliQ-YopS/fliQ Translocation Protein-(CT563)
CPn0825	933594	932677	R	yscR-Yop Translocation R-(CT562)
CPn0826	934310	933612	R	yscL-Yop Translocation L-(CT561)
CPn0827	935264	934434	R	CT560 hypothetical protein
CPn0828	936271	935267	R	yscJ-Yop Translocation J-(CT559)
CPn0829	936744	937298	F	
CPn0830	937444	937959	F	
CPn0831	938267	938434	F	
CPn0832	939747	938827	R	lipA-Lipoate Synthetase-(CT558)
CPn0833	941129	939747	R	lpdA-Lipoamide Dehydrogenase-(CT557)
CPn0834	941553	942014	F	CT556 hypothetical protein
CPn0835	945689	942045	R	motl_1-SWI/SNF family helicase_1-(CT555)
CPn0836	946879	945722	R	brnQ-Amino Acid (Branched) Transport-(CT554)
CPn0837	947771	947145	R	nth-Enodnuclease III-(CT697)
CPn0838	949106	947781	R	thdF-Thiophene/Furan Oxidation Protein-(CT698)
CPn0839	949257	950159	F	psdD-Phosphatidylserine Decarboxylase-(CT699)
CPn0840	950222	951544	F	CT700 hypothetical protein
CPn0841	951731	954640	F	secA_2-Translocase SecA_2-(CT701)
CPn0842	954883	954710	R	CT702 hypothetical protein (frame-shift with 0843)
CPn0843	955191	954994	R	CT702 hypothetical protein
CPn0844	956730	955270	R	yphC-GTPase/GTP-binding protein-(CT703)
CPn0845	958079	956650	R	pcnB_1-Poly A Polymerase_1-(CT704)
CPn0846	959374	958112	R	clpX-CLP Protease ATPase-(CT705)
CPn0847	959995	959387	R	clpP-CLP Protease Subunit-(CT706)
CPn0848	961502	960177	R	tig/murI-Trigger Factor-peptidyl-prolyl isomerase-(CT707)
CPn0849	961788	965285	F	motl_2-SWI/SNF family helicase_2-(CT708)
CPn0850	965293	966390	F	mreB-Rod Shape Protein-Sugar Kinase-(CT709)

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CPn0851	966396	968195	F	pckA-Phosphoenolpyruvate Carboxykinase-(CT710)
CPn0852	968316	970613	F	CT711 hypothetical protein
CPn0853	970637	971803	F	CT712 hypothetical protein
CPn0854	972837	971806	R	ompB-Outer Membrane Protein B-(CT713)
CPn0855	973995	972994	R	gpdA-Glycerol-3-P Dehydrogenase-(CT714)
CPn0856	975377	973995	R	AgX-1 Homolog-UDP-Glucose Pyrophosphorylase-(CT715)
CPn0857	975757	975392	R	CT716 hypothetical protein
CPn0858	977055	975757	R	fliI-Flagellum-specific ATP Synthase-(CT717)
CPn0859	977588	977055	R	CT718 hypothetical protein
CPn0860	978630	977608	R	fliF-Flagellar M-Ring Protein-(CT719)
CPn0861	979722	978925	R	nifU-NifU-related protein-(CT720)
CPn0862	980873	979722	R	yfhO_2-NifS-related protein_2-(CT721)
CPn0863	981514	980831	R	pgmA-Phosphoglycerate Mutase-(CT722)
CPn0864	981670	982374	F	yjbC-predicted pseudouridine synthase-(CT723)
CPn0865	982418	982942	F	CT724 hypothetical protein
CPn0866	983491	982916	R	birA-Biotin Synthetase-(CT725)
CPn0867	983423	984667	F	rodA-Rod Shape Protein-(CT726)
CPn0868	986643	984670	R	zntA/cadA-Metal Transport P-type ATPase-(CT727)
CPn0869	987401	986658	F	CT728 hypothetical protein
CPn0870	988728	987448	F	serS-Seryl tRNA Synthetase_2-(CT729)
CPn0871	988772	989899	F	ribD-Riboflavin Deaminase-(CT730)
CPn0872	989963	991216	F	ribA&ribB-GTP Cyclohydratase & DHBP Synthase -(CT731)
CPn0873	991233	991694	F	ribE-Ribityllumazine Synthase-(CT732)
CPn0874	993107	991749	F	CT733 hypothetical protein
CPn0875	993372	994022	F	CT734 hypothetical protein
CPn0876	994144	995517	F	dagA_2-D-Alanine/Glycine Permease_2-(CT735)
CPn0877	995533	995982	F	ybcL family-(CT736)
CPn0878	996654	995992	F	SET Domain protein-(CT737)
CPn0879	997439	996645	R	yycJ-metal dependent hydrolase-(CT738)
CPn0880	999861	997444	R	ftsK-Cell Division Protein FtsK-(CT739)
CPn0881	1005667	1006209	F	
CPn0882	1006268	1007404	F	
CPn0883	1008865	1007573	R	dmpP/nqr6-Phenolhydrolase/NADH ubiquinone oxidoreductase-(CT740)
CPn0884	1009359	1009009	R	CT741 hypothetical protein
CPn0885	1010635	1009433	R	ygcA-rRNA Methyltransferse-(CT742)
CPn0886	1011276	1010908	R	hctA-Histone-Like Developmental Protein-(CT743)
CPn0887	1011692	1014157	F	CHLTR possible phosphoprotein-(CT744)
CPn0888	1015423	1014119	R	hemG-protoporphyrinogen Oxidase-(CT745)
CPn0889	1016835	1015462	R	hemN_2-Coproporphyrinogen III Oxidase_2-(CT746)
CPn0890	1017805	1016819	R	hemE-Uroporphyrinogen Decarboxylase-(CT747)
CPn0891	1021073	1017819	R	mfd-Transcription-Repair Coupling-(CT748)
CPn0892	1023661	1021046	R	alaS-Alanyl tRNA Synthetase-(CT749)
CPn0893	1023894	1025888	F	tktB-Transketolase-(CT750)
CPn0894	1026766	1025888	R	amn-AMP Nucleosidase-(CT751)
CPn0895	1026988	1027557	F	efp_2-Elongation Factor P_2-(CT752)
CPn0896	1027595	1027822	F	CT753 hypothetical protein
CPn0897	1028737	1027853	R	(possible phosphohydrolase)-(CT754)
CPn0898	1030460	1028904	R	Mitochondrial HSP60 Chaperonin Homolog-(CT755)
CPn0899	1030875	1032215	F	murF-Muramoyl-DAP Ligase-(CT756)
CPn0900	1032235	1033281	F	mraY-Muramoyl-Pentapeptide Transferase-(CT757)
CPn0901	1033287	1034537	F	murD-Muramoylalanine-Glucamate Ligase-(CT758)
CPn0902	1034543	1035241	F	nlpD-Muramidase (invasin repeat family)-(CT759)
CPn0903	1035263	1036417	F	ftsW-Cell Division Protein FtsW-(CT760)
CPn0904	1036326	1037396	F	murG-Peptidoglycan Transferase-(CT761)
CPn0905	1037409	1039835	F	murC&ddlA-Muramate-Ala Ligase & D-Ala-D-Alam Ligase-(CT762)
CPn0906	1040340	1039915	R	CT763 hypothetical protein
CPn0907	1040780	1040445	R	*cutA Periplasmic Divalent Cation Tolerance Protein CutA (C-Type Cytochrome Biogenesis Protein)
CPn0908	1041589	1040780	R	CT764 hypothetical protein
CPn0909	1041637	1041966	F	rsbV_2-Sigma Factor Regulator_2-(CT765)
CPn0910	1041979	1043004	F	miaA-tRNA Pyrophosphate Transferase-(CT766)
CPn0911	1044043	1042985	R	Fe-S cluster oxidoreductase_2-(CT767)
CPn0912	1044129	1045760	F	CT768 hypothetical protein
CPn0913	1045760	1045945	F	
CPn0914	1045999	1046397	F	
CPn0915	1046461	1046817	F	ybeB-iojap superfamily ortholog-(CT769)
CPn0916	1046837	1048084	F	fabF-Acyl Carrier Protein Synthase-(CT770)
CPn0917	1048090	1048539	F	hydrolase/phosphatase homolog-(CT771)
CPn0918	1049223	1048579	R	ppa-Inorganic Pyrophosphatase-(CT772)
CPn0919	1049378	1050430	F	ldh-Leucine Dehydrogenase-(CT773)
CPn0920	1051405	1050431	R	cysQ-Sulfite Synthesis/biphosphate phosphatase-(CT774)
CPn0921	1051535	1052293	F	snGlycerol-3-P Acyltransferase-(CT775)

CPn0922	1052314	1053927	F	aas-Acylglycerophosphoethanolamine Acyltransferase-(CT776)
CPn0923	1053984	1055093	F	bioF_1-Oxononanoate Synthase_1-(CT777)
CPn0924	1057274	1055028	R	priA-Primosomal Protein N' -(CT778)
CPn0925	1057900	1057226	R	CT779 hypothetical protein
CPn0926	1058060	1058557	F	Thioredoxin Disulfide Isomerase-(CT780)
CPn0927	1059809	1058670	R	*CHLPS 43 kDa protein homolog_2
CPn0928	1061008	1059884	R	*CHLPS 43 kDa protein homolog_3
CPn0929	1062292	1061186	R	*CHLPS 43 kDa protein homolog_4
CPn0930	1062857	1063330	F	
CPn0931	1064138	1065718	F	lysS-Lysyl tRNA Synthetase-(CT781)
CPn0932	1067142	1065721	R	cysS-Cysteinyl tRNA Synthetase-(CT782)
CPn0933	1067535	1068578	F	predicted disulfide bond isomerase-(CT783)
CPn0934	1068942	1068526	R	rnpA-Ribonuclease P Protein Component-(CT784)
CPn0935	1069091	1068957	R	rl34-L34 Ribosomal Protein-(CT785)
CPn0936	1069336	1069470	F	rl36-L36 Ribosomal Protein-(CT786)
CPn0937	.1069496	1069798	F	rs14-S14 Ribosomal Protein-(CT787)
CPn0938	1070322	1069849	R	CT788 hypothetical protein -[leader (60) peptide-periplasmic]
CPn0939	1070728	1071195	F	CT790 hypothetical protein
CPn0940	1073012	1071204	R	uvrC-Excinuclease ABC, Subunit C-(CT791)
CPn0941	1075501	1073018	R	mutS-DNA Mismatch Repair-(CT792)
CPn0942	1075985	1077754	F	dnaG/priM-DNA Primase-(CT794)
CPn0943	1077978	1078238	F	CT794.1 hypothetical protein
CPn0944	1078512	1078997	F	
CPn0945	1079070	1079660	F	CT795 hypothetical protein
CPn0946	1082786	1079745	R	glyQ-Glycyl tRNA Synthetase-(CT796)
CPn0947	1083442	1084059	F	pgsA_2-Glycerol-3-P-Phosphatydyltransferase_2-(CT797)
CPn0948	1085474	1084047	R	glgA-Glycogen Synthase-(CT798)
CPn0949	1085929	1086483	F	ctc-General Stress Protein-(CT799)
CPn0950	1086488	1087027	F	pth-Peptidyl tRNA Hydrolase-(CT800)
CPn0951	1087122	1087457	F	rs6-S6 Ribosomal Protein-(CT801)
CPn0952	1087478	1087723	F	rs18-S18 Ribosomal Protein-(CT802)
CPn0953	1087742	1088248	F	rl9-L9 Ribosomal Protein-(CT803)
CPn0954	1088286	1088708	F	ychB-Predicted Kinase-(CT804)
CPn0955	1088612	1089175	F	(frame-shift with 0954)
CPn0956	1089560	1090909	F	CT805 hypothetical protein
CPn0957	1093788	1090963	R	ide/ptr-Insulinase family/Protease III-(CT806)
CPn0958	1094785	1093793	R	plsB-Glycerol-3-P Acyltransferase-(CT807)
CPn0959	1096343	1094799	R	cafE-Axial Filament Protein-(CT808)
CPn0960	1096764	1097102	F	CT809 hypothetical protein
CPn0961	1097118	1097297	F	rl32-L32 Ribosomal Protein-(CT810)
CPn0962	1097316	1098275	F	plsX-FA/Phospholipid Synthesis Protein-(CT811)
CPn0963	1098398	1103224	F	pmp_21-Polymorphic Outer Membrane Protein D Family-(CT812)
CPn0964	1104758	1103301	R	
CPn0965	1106736	1104925	R	lpxB-Lipid A Disaccharide Synthase-(CT411)
CPn0966	1108037	1106748	R	pcnB_2-PolyA Polymerase_2-(CT410)
CPn0967	1108512	1109885	F	mrsA/pgm-Phosphoglucomutase-(CT815)
CPn0968	1109895	1111721	F	glmS-Glucosamine-Fructose-6-P Aminotransferase-(CT816)
CPn0969	1111812	1112999	F	0969-tyrP_1-Tyrosine Transport_1-(CT817) tyrP_1-Tyrosine Transport_1-(CT817)
CPn0970	1113461	1114648	F	0970-tyrP_2-Tyrosine Transport_2-(CT818) tyrP_2-Tyrosine Transport_2-(CT818)
CPn0971	1114702	1115415	F	yccA-Transport Permease-(CT819)
CPn0972	1116299	1115430	R	ftsY-Cell Division Protein FtsY-(CT820)
CPn0973	1116370	1117527	F	sucC-Succinyl-CoA Synthetase, Beta-(CT821)
CPn0974	1117544	1118422	F	sucD-Succinyl-CoA Synthetase, Alpha-(CT822)
CPn0975	1119104	1119637	F	
CPn0976	1120082	1121185	F	
CPn0977	1121371	1122402	F	
CPn0978	1122665	1123693	F	
CPn0979	1123980	1125443	F	htrA-DO Serine Protease-(CT823)
CPn0980	1126982	1125504	R	*similarity to Saccharomyces serevisiae hypothetical 52.9KD protein
CPn0981	1127031	1129952	F	Zinc Metalloprotease (insulinase family)-(CT824)
CPn0982	1131194	1129962	R	yigN family-(CT825)
CPn0983	1132000	1131206	R	pssA-Glycerol-Serine Phosphatidyltransferase-(CT826)
CPn0984	1132379	1135510	F	nrdA-Ribonucleoside Reductase, Large Chain-(CT827)
CPn0985	1135534	1136571	F	nrdB-Ribonucleoside Reductase, Small Chain-(CT828)
CPn0986	1136724	1137395	F	yggH-predicted rRNA Methylase-(CT829)
CPn0987	1137516	1138115	F	ytgB-like predicted rRNA methylase-(CT830)
CPn0988	1138986	1138075	R	murB-UDP-N-Acetylenolpyruvoylglucosamine Reductase-(CT831)
CPn0989	1139495	1139016	R	CT832 hypothetical protein
CPn0990	1139883	1140440	F	infC-Initiation Factor 3-(CT833)
CPn0991	1140421	1140612	F	rl35-L35 Ribosomal Protein-(CT834)

CPn0992	1140634	1140996	F	rl20-L20 Ribosomal Protein-(CT835)
CPn0993	1141014	1142030	F	pheS-Phenylalanyl tRNA Synthetase, Alpha-(CT836)
CPn0994	1142398	1144440	F	CT837 hypothetical protein
CPn0995	1145512	1144415	R	CT838 hypothetical protein
CPn0996	1146589	1145519	R	CT839 hypothetical protein
CPn0997	1146708	1147664	F	mesJ-PP-loop superfamily ATPase-(CT840)
CPn0998	1147855	1150584	F	ftsH-ATP-dependent zinc protease-(CT841)
CPn0999	1152847	1150766	R	pnp-Polyribonucleotide Nucleotidyltransferase-(CT842)
CPn1000	1153157	1152891	R	rs15-S15 Ribosomal Protein-(CT843)
CPn1001	1153405	1153869	F	yfhC-cytosine deaminase-(CT844)
CPn1002	1153862	1154089	F	CT845 hypothetical protein
CPn1003	1154796	1154092	R	CT846 hypothetical protein
CPn1004	1155397	1154879	R	CT847 hypothetical protein
CPn1005	1155933	1155415	R	CT848 hypothetical protein
CPn1006	1156472	1155990	R	CT849 hypothetical protein
CPn1007	1156689	1156907	F	CT849.1 hypothetical protein
CPn1008	1156928	1158223	F	CT850 hypothetical protein
CPn1009	1159058	1158186	R	map-Methionine Aminopeptidase-(CT851)
CPn1010	1159672	1159067	R	CT852 hypothetical protein
CPn1011	1160306	1159902	R	CT853 hypothetical protein
CPn1012	1162193	1160421	R	yzeB-ABC transporter permease-(CT854)
CPn1013	1162245	1163624	F	fumC-Fumarate Hydratase-(CT855)
CPn1014	1165426	1163732	R	ychM-Sulfate Transporter-(CT856)
CPn1015	1165634	1166893	F	CT857 hypothetical protein (possible IM protein)
CPn1016	1167042	1168898	F	CT858 hypothetical protein
CPn1017	1169006	1169935	F	lytB-Metalloprotease-(CT859)
CPn1018	1169898	1170629	F	
CPn1019	1172128	1170638	R	CT860 hypothetical protein
CPn1020	1173679	1172150	R	CT861 hypothetical protein
CPn1021	1174213	1173698	R	lcrH_2-Low Calcium Response_2-(CT862)
CPn1022	1175673	1174216	R	CT863 hypothetical protein
CPn1023	1176035	1176331	F	
CPn1024	1177236	1176334	R	xerD-Integrase/recombinase-(CT864)
CPn1025	1177302	1178879	F	pgi-Glucose-6-P Isomerase-(CT378)
CPn1026	1178997	1179137	F	ltuA-(CT377)
CPn1027	1179175	1180755	F	
CPn1028	1181016	1181999	F	mdhC-Malate Dehyrogenase-(CT376)
CPn1029	1182008	1182844	F	
CPn1030	1183886	1182843	R	predicted D-amino acid dehyrogenase-(CT375)
CPn1031	1185552	1184098	R	arcD-Arginine/Ornithine Antiporter-(CT374)
CPn1032	1186150	1185566	R	CT373 hypothetical protein
CPn1033	1187500	1186187	R	CT372 hypothetical protein
CPn1034	1188517	1187732	R	Predicted OMP_1 (CT371) [leader (18) peptide]
CPn1035	1190000	1188570	R	AroE-Shikimate 5-Dehyrogenase-(CT370)
CPn1036	1191135	1189984	R	AroB-Dehyroquinate Synthase-(CT369)
CPn1037	1192199	1191123	R	AroC-Chorismate Synthase-(CT368)
CPn1038	1192726	1192199	R	aroL-Shikimate Kinase II-(CT367)
CPn1039	1193999	1192665	R	aroA-Phosphoshikimate Vinyltransferase-(CT366)
CPn1040	1194741	1194073	R	
CPn1041	1195994	1194726	R	*bioA-Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase
CPn1042	1196590	1195934	R	*bioD-dethiobiotin synthetase
CPn1043	1197717	1196572	R	bioF_2-Oxononanoate Synthase_2
CPn1044	1198691	1197699	R	*bioB-Biotin Synthase
CPn1045	1199590	1198901	R	*conserved hypothetical bacterial membrane protein
CPn1046	1200675	1199590	R	*Tryptophan Hyroxylase
CPn1047	1200552	1201343	F	dapB-Dihydrodipicolinate Reductase-(CT364)
CPn1048	1201606	1202604	F	asd-Aspartate Dehydrogenase-(CT363)
CPn1049	1202595	1203914	F	lysC-Aspartokinase III-(CT362)
CPn1050	1203926	1204798	F	dapA-Dihydrodipicolinate Synthase-(CT361)
CPn1051	1204962	1205270	F	
CPn1052	1205417	1206169	F	
CPn1053	1206153	1206701	F	
CPn1054	1207034	1209466	F	
CPn1055	1209694	1210521	F	
CPn1056	1210527	1211228	F	
CPn1057	1211497	1213596	F	CT356 hypothetical protein
CPn1058	1213748	1214836	F	CT355 hypothetical protein
CPn1059	1214848	1215678	F	kgsA-Dimethyladenosine Transferase-(CT354)
CPn1060	1217658	1215727	R	dxs/tkt-Transketolase-(CT331)
CPn1061	1217920	1217666	R	CT330 hypothetical protein
CPn1062	1219820	1218159	R	xseA-Exodoxyribonuclease VII-(CT329)
CPn1063	1219951	1220712	F	tpiS-Triosephosphate Isomerase-(CT328)

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CPn1064	1220719	1220895	F	
CPn1065	1221095	1220928	R	
CPn1066	1221135	1221488	F	
CPn1067	1221735	1222292	F	def-Polypeptide Deformylase-(CT353)
CPn1068	1223258	1222365	R	rnhB_2-Ribonuclease HII_2-(CT008)
CPn1069	1223513	1223941	F	yfgA-HTH Transcriptional Regulator-(CT009)
CPn1070	1225511	1224144	R	
CPn1071	1227324	1225885	R	
CPn1072	1227969	1228835	F	
CPn1073	1229011	1229832	F	Predicted OMP_2 -(CT371)

Table 2 (Supplemental Data) Functional Assignments of *C. pneumoniae* Coding Sequences. *C. trachomatis* genes are shown in parentheses.

Amino Acid Biosynthesis

Aromatic Family

1039	(CT366)	aroA	Phosphoshikimate Vinyltransferase
1036	(CT369)	aroB	Dehyroquinate Synthase
1037	(CT368)	aroC	Chorismate Synthase
1035	(CT370)	aroE	Shikimate 5-Dehyrogenase
0484	(CT382)	aroG	Deoxyheptonate Aldolase
1038	(CT367)	aroL	Shikimate Kinase II
0740	(CT637)	tyrB	Aromatic AA Aminotransferase

Aspartate Family (lysine)

1048	(CT363)	asd	Aspartate Dehydrogenase
1050	(CT361)	dapA	Dihydrodipicolinate Synthase
1047	(CT364)	dapB	Dihydrodipicolinate Reductase
0519	(CT430)	dapF	Dian inopimelate Epimerase
1049	(CT362)	lysC	Aspa tokinase III

Serine Family

0433	(CT282)	gcsH	Glyc ne Cleavage System H Protein
0521	(CT432)	glyA	Serine Hydroxymethyltransferase

Base & Nucleotide Metabolism

0171		guaA	GMP Synthase
0172		guaB	Inosine 5'-Monophosphase Dehydrogenase
0608			Uridine 5'-Monophosphate Synthase
0735			Uridine Kinase
0244	(CT128)	adk	Adenylate Kinase
0894	(CT751)	amn	AMP Nucleosidase
0568	(CT452)	cmk	CMP Kinase
0392	(CT039)	dcd	dCTP Deaminase
0059	(CT292)	dut	dUTP Nucleotidohydrolase
0120	(CT030)	gmk	GMP Kinase
0619	(CT500)	ndk	Nucleoside-2-P Kinase
0984	(CT827)	nrdA	Ribonucleoside Reductase, Large Chain
0985	(CT828)	nrdB	Ribonucleoside Reductase, Small Chain
0236	(CT183)	pyrG	CTP Synthetase
0698	(CT678)	pyrH	UMP Kinase
0273	(CT188)	tdk	Thymidylate Kinase
0659	(CT539)	trxA	Thioredoxin
0314	(CT099)	trxB	Thioredoxin Reductase
1001	(CT844)	yfhC	Cytosine Deaminase

Biosynthesis of Cofactors

Biotin, Lipoate & Ubiquinone

1041		bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase
1044		bioB	Biotin Synthase
1042		bioD	Dethiobiotin Synthetase
0923	(CT777)	bioF_1	Oxononanoate Synthase_1
1043	(CT777)	bioF_2	Oxononanoate Synthase_2
0866	(CT725)	birA	Biotin Synthetase
0748	(CT628)	ispA	Geranyl Transtransferase
0832	(CT558)	lipA	Lipoate Synthetase

0265	(CT219)	ubiA	Benzoate Octaphenyltransferase
0264	(CT220)	ubiD	Phenylacrylate Decarboxylase
0515	(CT428)	ubiE	Ubiquinone Methyltransferase

Folic Acid

0759	(CT612)	folA	Dihydrofolate Reductase
0335	(CT078)	folD	Methylene Tetrahydrofolate Dehydrogenase
0758	(CT613)	folP	Dihydropteroate Synthase
0757	(CT614)	folX	Dihydroneopterin Aldolase
0763	(CT649)	ygfA	Formyltetrahydrofolate Cycloligase

Porphyrin

0714	(CT662)	hemA	Glutamyl tRNA Reductase
0744	(CT633)	hemB	Porphobilinogen Synthase
0052	(CT299)	hemC	Porphobilinogen Deaminase
0890	(CT747)	hemE	Uroporphyrinogen Decarboxylase
0888	(CT745)	hemG	protoporphyrinogen Oxidase
0138	(CT210)	hemL	Glutamate-1-Semialdehyde-2,1-Aminomutase
0380	(CT052)	hemN_1	Coproporphyrinogen III Oxidase_1
0889	(CT746)	hemN_2	Coproporphyrinogen III Oxidase_2
0603	(CT485)	hemZ	Ferrochetalase

Riboflavin

0872	(CT731)	nbA&ribB	GTP Cyclohydratase & DHBP Synthase
0532	(CT405)	ribC	Riboflavin Synthase
0871	(CT730)	ribD	Riboflavin Deaminase
0873	(CT732)	ribE	Ribityllumazine Synthase
0320	(CT093)	ribF	FAD Synthase

Cell Envelope

Fatty Acid & Phospholipid Metabolism

0161	(CT206)		(predicted acyltransferase family)
0922	(CT776)	aas	Acylglycerophosphoethanolamine Acyltransferase
0414	(CT265)	accA	AcCoA Carboxylase/Transferase Alpha
0183	(CT123)	accB	Biotin Carboxyl Carrier Protein
0182	(CT124)	accC	Biotin Carboxylase
0058	(CT293)	accD	AcCoA Carboxylase/Transferase Beta
0295	(CT236)	acpP	Acyl Carrier Protein
0313	(CT100)	acpS	Acyl-carrier Protein Synthase
0567	(CT451)	cdsA	Phosphatidate Cytidylyltransferase
0297	(CT238)	fabD	Malonyl Acyl Carrier Transcyclase
0916	(CT770)	fabF	Acyl Carrier Protein Synthase
0296	(CT237)	fabG	Oxoacyl (Carrier Protein) Reductase
0298	(CT239)	fabH	Oxoacyl Carrier Protein Synthase III
0406	(CT104)	fabI	Enoyl-Acyl-Carrier Protein Reductase
0651	(CT532)	fabZ	Myristoyl-Acyl Carrier Dehydratase
0098	(CT010)	htrB	Acyltransferase
0271	(CT136)		Lysophospholipase Esterase
0615	(CT496)	pgsA_1	Glycerol-3-P Phosphatidyltransferase_1
0947	(CT797)	pgsA_2	Glycerol-3-P Phosphatydyltransferase_2
0958	(CT807)	plsB	Glycerol-3-P Acyltransferase
0569	(CT453)	plsC	Glycerol-3-P Acyltransferase
0962	(CT811)	plsX	FA/Phospholipid Synthesis Protein
0839	(CT699)	psdD	Phosphatidylserine Decarboxylase
0983	(CT826)	pssA	Glycerol-Serine Phosphatidyltransferase
0921	(CT775)		snGlycerol-3-P Acyltransferase
0654	(CT535)	yciA	Acyl-CoA Thioesterase
0877	(CT736)	ybcL	CT736 Hypothetical Protein

LPS

	0154	(CT208)	gseA	KDO Transferase
	0721	(CT655)	kdsA	KDO Synthetase
	0235	(CT182)	kdsB	Deoxyoctulonosic Acid Synthetase
	0650	(CT531)	lpxA	Acyl-Carrier UDP-GlcNAc O-Acyltransferase
5	0965	(CT411)	lpxB	Lipid A Disaccharide Synthase
	0652	(CT533)	lpxC	Myristoyl GlcNac Deacetylase
	0302	(CT243)	lpxD	UDP Glucosamine N-Acyltransferase

Membrane Proteins, Lipoproteins & Porins

	0310	(CT251)	60IM	60kDa Inner Membrane Protein
10	0556	(CT442)	crpA	15kDa Cysteine-Rich Protein
	0653	(CT534)	cutE	Apolipoprotein N-Acetyltransferase
	0311	(CT252)	lgt	Prolipoprotein Diacylglycerol Transferase
	0558	(CT444)	omcA	9kDa-Cysteine-Rich Lipoprotein
	0557	(CT443)	omcB	60kDa Cysteine-Rich OMP
15	0695	(CT681)	ompA	Major Outer Membrane Protein
	0854	(CT713)	ompB	Outer Membrane Protein B
	0781	(CT600)	pal	Peptidoglycan-Associated Lipoprotein
	0300	(CT241)	yaeT	Omp85 Homolog

Peptidoglycan

	0417	(CT268)	amiA	N-Acetylmuramoyl Alanine Amidase
20	0780	(CT601)	amiB	N-Acetylmuramoyl-L-Ala Amidase
	0672	(CT551)	dacF	D-Ala-D-Ala Caroxypeptidase
	0968	(CT816)	glmS	Glucosamine-Fructose-6-P Aminotransferase
	0749	(CT629)	glmU	UDP-GlcNAc Pyrophosphorylase
25	0900	(CT757)	mraY	Muramoyl-Pentapeptide Transferase
	0571	(CT455)	murA	UDP-N-Acetylglucosamine Transferase
	0988	(CT831)	murB	UDP-N-Acetylenolpyruvoylglucosamine Reductase
	0905	(CT762)	murC&ddlA	Muramate-Ala Ligase & D-Ala-D-Alam Ligase
	0901	(CT758)	murD	Muramoylalanine-Glutamate Ligase
30	0418	(CT269)	murE	N-Acetylmuramoylalanylglutamyl DAP Ligase
	0899	(CT756)	murF	Muramoyl-DAP Ligase
	0904	(CT761)	murG	Peptidoglycan Transferase
	0902	(CT759)	nlpD	Muramidase (invasin repeat family)
	0694	(CT682)	pbp2	PBP2-Transglycolase/Transpeptidase
35	0419	(CT270)	pbp3	Transglycolase/Transpeptidase
	0421	(CT272)	yabC	PBP2B Family Methyltransferase

Cellular Processes

Cell Division

	0959	(CT808)	cafE	Axial Filament Protein
40	0880	(CT739)	ftsK	Cell Division Protein FtsK
	0903	(CT760)	ftsW	Cell Division Protein FtsW
	0972	(CT820)	ftsY	Cell Division Protein FtsY
	0617	(CT498)	gidA	FAD-dependent Oxidoreductase
45	0805	(CT582)	minD	Chromosome Partitioning ATPase
	0850	(CT709)	mreB	Rod Shape Protein-Sugar Kinase
	0867	(CT726)	rodA	Rod Shape Protein
	0684	(CT688)	parB	Chromosome Partitioning Protein

Detoxification

50	0057	(CT294)	sodM	Superoxide Dismutase (Mn)
	0778	(CT603)	ahpC	Thio-specific Antioxidant (TSA) Peroxidase

Signal Transduction

	0148	(CT145)		S/T Protein Kinase
	0584	(CT467)	atoS	Two-Component Sensor
55	0294	(CT235)		cAMP-Dependent Protein Kinase Regulatory Subunit
	0712	(CT664)		(FHA domain)

	0478	(CT379)	hflX	GTP Binding Protein
	0703	(CT673)		S/T Protein Kinase
	0095	(CT301)		S/T Protein Kinase
	0397	(CT259)		PP2C Phosphatase Family
5	0037	(CT337)	ptsH	PTS Phosphocarrier Protein Hpr
	0038	(CT336)	ptsI	PTS PEP Phosphotransferase
	0060	(CT291)	ptsN_1	PTS IIA Protein_1
	0061	(CT290)	ptsN_2	PTS IIA Protein + HTH DNA-Binding Domain
	0262	(CT218)	surE	SurE-like Acid Phosphatase
10	0838	(CT698)	thdF	Thiophene/Furan Oxidation Protein
	0693	(CT683)		TPR Repeats-CT683 Hypothetical Protein
	0321	(CT092)	ychF	GTP Binding Protein
	0544	(CT418)	yhbZ	GTP binding protein
	0844	(CT703)	yphC	GTPase/GTP-binding protein

15 *Standard Protein Secretion*

	0115	(CT025)	ffh	Signal Recognition Particle GTPase
	0363	(CT060)	flhA	Flagellar Secretion Protein
	0858	(CT717)	fliI	Flagellum-specific ATP Synthase
	0704	(CT672)	fliN	Flagellar Motor Switch Domain/YscQ family
20	0815	(CT572)	gspD	Gen. Secretion Protein D
	0816	(CT571)	gspE	Gen. Secretion Protein E
	0817	(CT570)	gspF	Gen. Secretion Protein F
	0359	(CT064)	lepA	GTPase
	0110	(CT020)	lepB	Signal Peptidase I
25	0535	(CT408)	lspA	Lipoprotein Signal Peptidase
	0260	(CT141)	secA_1	Protein Translocase Subunit_1
	0841	(CT701)	secA_2	Translocase SecA_2
	0564	(CT448)	secD&secF	Protein Export Proteins SecD/SecF (fusion)
	0075	(CT321)	secE	Preprotein Translocase
30	0629	(CT510)	secY	Translocase
	0848	(CT707)	tig	Trigger Factor-Peptidyl-prolyl Isomerase

Transport-Related Proteins

	0486			Hypothetical Proline Permease
	0289	(CT230)	aaaT	Neutral Amino Acid (Glutamate) Transporter
35	0691	(CT685)	abcX	ABC Transporter ATPase
	1031	(CT374)	arcD	Arginine/Ornithine Antiporter
	0482	(CT381)	artJ	Arginine Periplasmic Binding Protein
	0836	(CT554)	brnQ	Amino Acid (Branched) Transport
	0536	(CT409)	dagA_1	D-Ala/Gly Permease_1
40	0876	(CT735)	dagA_2	D-Alanine/Glycine Permease_2
	0682	(CT690)	dppD	ABC ATPase Dipeptide Transport
	0683	(CT689)	dppF	ABC ATPase Dipeptide Transport
	0280	(CT689)	dppF	Dipeptide Transporter ATPase
	0785	(CT596)	exbB	Macromolecule Transporter
45	0784	(CT597)	exbD	Biopolymer Transport Protein
	0604	(CT486)	fliY	Glutamine Binding Protein
	0192	(CT129)	glnP	ABC Amino Acid Transporter Permease
	0191	(CT130)	glnQ	ABC Amino Acid Transporter ATPase
	0528	(CT401)	gltT	Glutamate Symport
50	0286	(CT194)	mgtE	Mg^{++} Transporter (CBS Domain)
	0413	(CT264)	msbA	Transport ATP Binding Protein
	0290	(CT231)		Na^{+}-dependent Transporter
	0195	(CT198)	oppA_1	Oligopeptide Binding Protein_1
	0196	(CT198)	oppA_2	Oligopeptide Binding Protein_2
55	0197	(CT139)	oppA_3	Oligopeptide Binding Protein_3
	0198	(CT175)	oppA_4	Oligopeptide Binding Protein_4

0599	(CT480)	oppA_5	Oligopeptide Binding Lipoprotein_5
0199	(CT199)	oppB_1	Oligopeptide Permease_1
0598	(CT479)	oppB_2	Oligopeptide Permease_2
0200	(CT200)	oppC_1	Oligopeptide Permease_1
0597	(CT478)	oppC_2	Oligopeptide Permease_2
0201	(CT201)	oppD	Oligopeptide Transport ATPase
0202	(CT202)	oppF	Oligopeptide Transport ATPase
0231	(CT180)	tauB	ABC Transport ATPase (Nitrate/Fe)
0782	(CT599)	tolB	Macromolecule Transporter
0969	(CT817)	tyrP_1	Tyrosine Transport_1
0970	(CT818)	tyrP_2	Tyrosine Transport_2
0665	(CT544)	uhpC	Hexosphosphate Transport
0282	(CT216)	xasA	Amino Acid Transporter
0207	(CT204)	ybhI	dicarboxylate Translocator
0971	(CT819)	yccA	Transport Permease
0248	(CT152)	ycfV	ABC Transporter ATPase
1014	(CT856)	ychM	Sulfate Transporter
0736	(CT641)	ygeD	Efflux Protein
0680	(CT692)	ygo4	Phosphate Permease
0723	(CT653)	yhbG	ABC Transporter ATPase
0023	(CT348)	yjjK	ABC Transporter Protein ATPase
0127	(CT034)	yrfF	Cationic Amino Acid Transporter
0349	(CT067)	ytgA	Solute Protein Binding Family
0348	(CT068)	ytgB	ABC Transporter ATPase
0347	(CT069)	ytgC	Integral Membrane Protein
0346	(CT070)	ytgD	Integral Membrane Protein
1012	(CT854)	yzeB	ABC Transporter Permease
0868	(CT727)	zntA	Metal Transport P-type ATPase
0279			Possible ABC Transporter Permease Protein
0543	(CT417)		(Metal Transport Protein)
0692	(CT684)		ABC Transporter
0542	(CT416)		ABC Transporter ATPase
0690	(CT686)		ABC Transporter Membrane Protein
0541	(CT415)		solute binding protein

Type-III Secretion

0323	(CT090)	lcrD	Low Calcium Response D
0324	(CT089)	lcrE	Low Calcium Response E
0811	(CT576)	lcrH_1	Low Ca Response Protein H_1
1021	(CT862)	lcrH_2	Low Calcium Response_2
0325	(CT088)	sycE	Secretion Chaperone
0702	(CT674)	yscC	Yop C/Gen Secretion Protein D
0828	(CT559)	yscJ	Yop Translocation J
0826	(CT561)	yscL	Yop Translocation L
0707	(CT669)	yscN	Yop N (Flagellar-Type ATPase)
0825	(CT562)	yscR	Yop Translocation R
0824	(CT563)	yscS	YopS Translocation Protein
0823	(CT564)	yscT	YopT Tranlocation T
0322	(CT091)	yscU	Yop Translocation Protein U

Central Intermediary Metabolism

Glycogen Metabolism

0856	(CT715)		UDP-Glucose Pyrophosphorylase
0948	(CT798)	glgA	Glycogen Synthase
0475	(CT866)	glgB	Glucan Branching Enzyme
0607	(CT489)	glgC	Glucose-1-P Adenyltransferase
0307	(CT248)	glgP	Glycogen Phosphorylase
0388	(CT042)	glgX	Glycogen Hydrolase (debranching)

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| | 0326 | (CT087) | malQ | Glucanotransferase |
| | 0851 | (CT710) | pckA | Phosphoenolpyruvate Carboxykinase |

Phosphorous & Sulfur

	0548	(CT435)	cysJ	Sulfite Reductase
5	0920	(CT774)	cysQ	Sulfite Synthesis/Biphosphate Phosphatase
	0025	(CT346)	atsA	Sulphohydrolase
	0918	(CT772)	ppa	Inorganic Pyrophosphatase

DNA Replication, Modification, Repair & Recombination

DNA Mismatch Repair

	0505			3-Methyladenine DNA Glycosylase
	0812	(CT575)	mutL	DNA Mismatch Repair
	0941	(CT792)	mutS	DNA Mismatch Repair
	0402	(CT107)	mutY	Adenine Glycosylase
15	0732	(CT625)	nfo	Endonuclease IV
	0837	(CT697)	nth	Enodnuclease III

DNA Modification

	0596	(CT477)	ada	Methyltransferase
	0114	(CT024)	hemK	A/G-specific Methylase
20	0891	(CT748)	mfd	Transcription-Repair Coupling
	0620	(CT501)	ruvA	Holliday Junction Helicase
	0390	(CT040)	ruvB	Holliday Junction Helicase
	0621	(CT502)	ruvC	Crossover Junction Endonuclease
	0053	(CT298)	sms	Sms Protein
25	0773	(CT607)	ung	Uracil DNA Glycosylase
	1062	(CT329)	xseA	Exodoxyribonuclease VII

DNA Recombination

	0762	(CT650)	recA	RecA Recombination Protein
	0738	(CT639)	recB	Exodeoxyribonuclease V, Beta
30	0737	(CT640)	recC	Exodeoxyribonuclease V, Gamma
	0123	(CT033)	recD_1	Exodeoxyribonuclease V (Alpha Subunit)_1
	0752	(CT652)	recD_2	Exodeoxyribonuclease V, Alpha_2
	0339	(CT074)	recF	ABC Superfamily ATPase
	0340	(CT074)		(frame-shift with 0339)
35	0563	(CT447)	recJ	ssDNA Exonuclease
	0299	(CT240)	recR	Recombination Protein

DNA Replication

	0309	(CT250)	dnaA_1	Replication Initiation Protein_1
	0424	(CT275)	dnaA_2	Replication Initiation Factor_2
40	0616	(CT497)	dnaB	Replicative DNA Helicase
	0666	(CT545)	dnaE	DNA Pol III Alpha
	0942	(CT794)	dnaG	DNA Primase
	0338	(CT075)	dnaN	DNA Pol III (Beta)
	0410	(CT261)	dnaQ_1	DNA Pol III Epsilon Chain_1
45	0655	(CT536)	dnaQ_2	DNA Pol III Epsilon Chain_2
	0040	(CT334)	dnaX_1	DNA Pol III Gamma and Tau_1
	0272	(CT187)	dnaX_2	DNA Pol III Gamma and Tau_2
	0149	(CT146)	dnlJ	DNA Ligase
	0274	(CT189)	gyrA_1	DNA Gyrase Subunit A_1
50	0716	(CT660)	gyrA_2	DNA Gyrase Subunit A_2
	0275	(CT190)	gyrB_1	DNA Gyrase Subunit B_1
	0715	(CT661)	gyrB_2	DNA Gyrase Subunit B_2
	0416	(CT267)	himD	Integration Host Factor Alpha
	0612	(CT493)	polA	DNA Polymerase I
55	0924	(CT778)	priA	Primosomal Protein N'
	0386	(CT044)	ssb	SS DNA Binding Protein

0835	(CT555)		SWI/SNF family helicase_1
0849	(CT708)		SWI/SNF family helicase_2
0769	(CT643)	topA	DNA Topoisomerase I-Fused to SWI Domain
0024	(CT347)	xerC	Integrase/recombinase
1024	(CT864)	xerD	Integrase/recombinase

Eukaryotic-Type Chromatin Factors

0886	(CT743)	hctA	Histone-Like Developmental Protein
0384	(CT046)	hctB	Histone-like Protein 2
0878	(CT737)		SET Domain protein
0577	(CT460)		SWIB (YM74) Complex Protein

UVR Exinuclease Repair System

0096	(CT333)	uvrA	Excinuclease ABC Subunit A
0801	(CT586)	uvrB	Exinuclease ABC Subunit B
0940	(CT791)	uvrC	Excinuclease ABC. Subunit C
0772	(CT608)	uvrD	DNA Helicase

Energy Metabolism

Aerobic

0855	(CT714)	gpdA	Glycerol-3-P Dehydrogenase
0743	(CT634)	nqrA	Ubiquinone Oxidoreductase. Alpha
0427	(CT278)	nqr2	NADH (Ubiquinone) Dehydrogenase
0428	(CT279)	nqr3	NADH (Ubiquinone) Oxidoreductase. Gamma
0429	(CT280)	nqr4	NADH (Ubiquinone) Reductase 4
0430	(CT281)	nqr5	NADH (Ubiquinone) Reductase 5
0883	(CT740)	nqr6	Phenolhydrolase/NADH (Ubiquinone) Oxidoreductase 6

ATP Biogenesis and metabolism

0351	(CT065)	adt_1	ADP/ATP Translocase_1
0614	(CT495)	adt_2	ADP/ATP Translocase_2
0088	(CT308)	atpA	ATP Synthase Subunit A
0089	(CT307)	atpB	ATP Synthase Subunit B
0090	(CT306)	atpD	ATP Synthase Subunit D
0086	(CT310)	atpE	ATP Synthase Subunit E
0091	(CT305)	atpI	ATP Synthase Subunit I
0092	(CT304)	atpK	ATP Synthase Subunit K
0860	(CT719)	fliF	Flagellar M-Ring Protein

Electron Transport Chain

0102	(CT013)	cydA	Cytochrome Oxidase Subunit I
0103	(CT014)	cydB	Cytochrome Oxidase Subunit II
0364	(CT059)		Ferredoxin
0084	(CT312)		Predicted Ferredoxin

Glycolysis & Gluconeogenesis

0281	(CT215)	dhnA	Predicted 1,6-Fructose Biphosphate Aldolase
0800	(CT587)	eno	Enolase
0624	(CT505)	gapA	Glyceraldehyde-3-P Dehyrogenase
0056	(CT295)	mrsA	Phosphomannomutase
0967	(CT815)	pgm	Phosphoglucomutase
0160	(CT207)	pfkA_1	Fructose-6-P Phosphotransferase_1
0208	(CT205)	pfkA_2	Fructose-6-P Phosphotransferase_2
1025	(CT378)	pgi	Glucose-6-P Isomerase
0679	(CT693)	pgk	Phosphoglycerate Kinase
0863	(CT722)	pgmA	Phosphoglycerate Mutase
0097	(CT332)	pyk	Pyruvate Kinase
1063	(CT328)	tpiS	Triosephosphate Isomerase

Pentose Phosphate Pathway

0239	(CT186)	devB	Glucose-6-P Dehyrogenase (DevB family)
1060	(CT331)	dxs	Transketolase

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	0360	(CT063)	gnd	6-Phosphogluconate Dehydrogenase
	0185	(CT121)	rpe	Ribulose-P Epimerase
	0141	(CT213)	rpiA	Ribose-5-P Isomerase A
	0083	(CT313)	tal	Transaldolase
5	0893	(CT750)	tktB	Transketolase
	0238	(CT185)	zwf	Glucose-6-P Dehyrogenase

Pyruvate Dehydrogenase

	0833	(CT557)	lpdA	Lipoamide Dehydrogenase
	0436	(CT285)	lplA_1	Lipoate Protein Ligase-Like Protein
10	0618	(CT499)	lplA_2	Lipoate-Protein Ligase A
	0033	(CT340)	pdhA&B	Oxoisovalerate Dehydrogenase α/β Fusion
	0304	(CT245)	pdhA	Pyruvate Dehydrogenase Alpha
	0305	(CT246)	pdhB	Pyruvate Dehydrogenase Beta
	0306	(CT247)	pdhC	Dihydrolipoamide Acetyltransferase

15 *TCA Cycle*

	0495	(CT390)	aspC	Aspartate Aminotransferase
	1013	(CT855)	fumC	Fumarate Hydratase
	1028	(CT376)	mdhC	Malate Dehydrogenase
	0789	(CT592)	sdhA	Succinate Dehydrogenase
20	0790	(CT591)	sdhB	Succinate Dehydrogenase
	0788	(CT593)	sdhC	Succinate Dehydrogenase
	0378	(CT054)	sucA	Oxoglutarate Dehydrogenase
	0377	(CT055)	sucB_1	Dihydrolipoamide Succinyltransferase_1
	0527	(CT400)	sucB_2	Dihydrolipoamide Succinyltransferase_2
25	0973	(CT821)	sucC	Succinyl-CoA Synthetase, Beta
	0974	(CT822)	sucD	Succinyl-CoA Synthetase, Alpha

Protein Folding, Assembly & Modification

Chaperones

30	0949	(CT799)	ctc	General Stress Protein
	0534	(CT407)	dksA	DnaK Suppressor
	0032	(CT341)	dnaJ	Heat Shock Protein J
	0503	(CT396)	dnaK	Hsp-70
	0134	(CT110)	groEL_1	Hsp-60_1
35	0777	(CT604)	groEL_2	Hsp-60_2
	0898	(CT755)	groEL_3	Hsp-60_3
	0135	(CT111)	groES	10KDa Chaperonin
	0502	(CT395)	grpE	HSP-70 Cofactor
	0661	(CT541)	mip	FKBP-type Peptidyl-prolyl Cis-Trans Isomerase

40 *Proteases*

	0144	(CT113)	clpB	Clp Protease ATPase
	0437	(CT286)	clpC	ClpC Protease
	0520	(CT431)	clpP_1	CLP Protease
	0847	(CT706)	clpP_2	CLP Protease Subunit
45	0846	(CT705)	clpX	CLP Protease ATPase
	0269	(CT138)		Dipeptidase
	0998	(CT841)	ftsH	ATP-dependent Zinc Protease
	0030	(CT343)	gcp_1	O-Sialoglycoprotein Endopeptidase_1
	0194	(CT197)	gcp_2	O-Sialoglycoprotein Endopeptidase_2
50	0979	(CT823)	htrA	DO Serine Protease
	0957	(CT806)	ide	Insulinase family/Protease III
	0027	(CT344)	lon	Lon ATP-dependent Protease
	1017	(CT859)	lytB	Metalloprotease
	1009	(CT851)	map	Methionine Aminopeptidase
55	0385	(CT045)	pepA	Leucyl Aminopeptidase A
	0136	(CT112)	pepF	Oligopeptidase

0813	(CT574)	pepP	Aminopeptidase P
0613	(CT494)	sohB	Protease
0555	(CT441)	tsp	Tail-Specific Protease
0344	(CT072)	yaeL	Metalloprotease
0981	(CT824)		Zinc Metalloprotease (insulinase family)

Protein Isomerases

0227	(CT176)	dsbB	Disulfide bond Oxidoreductase
0786	(CT595)	dsbD	Thio:disulfide Interchange Protein
0228	(CT177)	dsbG	Disulfide Bond Chaperone
0933	(CT783)		Predicted Disulfide Bond Isomerase
0926	(CT780)		Thioredoxin Disulfide Isomerase

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Transcription

RNA Degradation

	0999	(CT842)	pnp	Polyribonucleotide Nucleotidyltransferase
5	0054	(CT297)	rnc	Ribonuclease III
	0119	(CT029)	rnhB_1	Ribonuclease HII_1
	1068	(CT008)	rnhB_2	Ribonuclease HII_2
	0934	(CT784)	rnpA	Ribonuclease P Protein Component
	0504	(CT397)	vacB	Ribonuclease Family

RNA Elongation & Termination Factors

10	0741	(CT636)	greA	Transcription Elongation Factor
	0316	(CT097)	nusA	N Utilization Protein A
	0076	(CT320)	nusG	Transcriptional Antitermination
	0845	(CT704)	pcnB_1	Poly A Polymerase_1
15	0966	(CT410)	pcnB_2	PolyA Polymerase_2
	0610	(CT491)	rho	Transcription Termination Factor

RNA Methylases

	0674	(CT553)	fmu	RNA Methyltransferase
	1059	(CT354)	kgsA	Dimethyladenosine Transferase
20	0187	(CT133)		Predicted Methylase
	0530	(CT403)	spoU_1	rRNA Methylase_1
	0660	(CT540)	spoU_2	rRNA Methylase_2
	0117	(CT027)	trmD	tRNA (Guanine N-1)-Methyltransferase
	0885	(CT742)	ygcA	rRNA Methyltransferse
25	0986	(CT829)	yggH	Predicted rRNA Methylase
	0987	(CT830)	ytgB	Predicted rRNA Methylase

RNA Modification

	0649	(CT530)	fmt	Methionyl tRNA Formyltransferase
	0910	(CT766)	miaA	tRNA Pyrophosphate Transferase
30	0719	(CT658)	sfhB	Predicted Pseudouridine Synthase
	0219	(CT193)	tgt	Queuine tRNA Ribosyl Transferase
	0580	(CT463)	truA	Pseudouridylate Synthase I
	0319	(CT094)	truB	tRNA Pseudouridine Synthase
	0403	(CT106)	yceC	Predicted Pseudouridine Synthetase Family
35	0864	(CT723)	yjbC	Predicted Pseudouridine Synthase

RNA Polymerase & Transcription Regulators

	0586	(CT468)	atoC	Two-Component Regulator
	0362	(CT061)	rpsD	Sigma-28/WhiG Family
	0501	(CT394)	hrcA	HTH Transcriptional Repressor
40	0793	(CT588)	rbsU	Sigma Regulatory Family Protein—PP2C Phosphatase (RsbW Antagonist)
	0626	(CT507)	rpoA	RNA Polymerase Alpha
	0081	(CT315)	rpoB	RNA Polymerase Beta
	0082	(CT314)	rpoC	RNA Polymerase Beta'
	0756	(CT615)	rpoD	RNA Polymerase Sigma-66
45	0771	(CT609)	rpoN	RNA Polymerase Sigma-54
	0511	(CT424)	rsbV_1	Sigma Regulatory Factor_1
	0909	(CT765)	rsbV_2	Sigma Factor Regulator_2
	0670	(CT549)	rsbW	Sigma Regulatory Factor-Histidine Kinase
	0750	(CT630)	tctD	HTH Transcriptional Regulatory Protein + Receiver Doman
50	1069	(CT009)	yfgA	HTH Transcriptional Regulator

Translation

Amino Acyl tRNA Synthesis

	0892	(CT749)	alaS	Alanyl tRNA Synthetase
55	0570	(CT454)	argS	Arginyl tRNA Transferase
	0662	(CT542)	aspS	Aspartyl tRNA Synthetase

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0932	(CT782)	cysS	Cysteinyl tRNA Synthetase
0003	(CT003)	gatA	Glu tRNA Gln Amidotransferase (A subunit)
0004	(CT004)	gatB	Glu tRNA Gln Amidotransferase (B Subunit)
0002	(CT002)	gatC	Glu tRNA Gln Amidotransferase (C subunit)
0560	(CT445)	gltX	Glutamyl-tRNA Synthetase
0946	(CT796)	glyQ	Glycyl tRNA Synthetase
0663	(CT543)	hisS	Histidyl tRNA Synthetase
0109	(CT019)	ileS	Isoleucyl-tRNA Synthetase
0153	(CT209)	leuS	Leucyl tRNA Synthetase
0931	(CT781)	lysS	Lysyl tRNA Synthetase
0122	(CT032)	metG	Methionyl-tRNA Synthetase
0993	(CT836)	pheS	Phenylalanyl tRNA Synthetase, Alpha
0594	(CT475)	pheT	Phenylalanyl tRNA Synthetase Beta
0500	(CT393)	proS	Prolyl tRNA Synthetase
0870	(CT729)	serS	Seryl tRNA Synthetase_2
0806	(CT581)	thrS	Threonyl tRNA Synthetase
0802	(CT585)	trpS	Tryptophanyl tRNA Synthetase
0361	(CT062)	tyrS	Tyrosyl tRNA Synthetase
0094	(CT302)	valS	Valyl tRNA Synthetase

Peptide Chain Initiation, Elongation & Termination

1067	(CT353)	def	Polypeptide Deformylase
0184	(CT122)	efp_1	Elongation Factor P_1
0895	(CT752)	efp_2	Elongation Factor P_2
0550	(CT437)	fusA	Elongation Factor G
0073	(CT323)	infA	Initiation Factor IF-1
0317	(CT096)	infB	Initiation Factor-2
0990	(CT833)	infC	Initiation Factor 3
0113	(CT023)	pfrA	Peptide Chain Releasing Factor 1
0576	(CT459)	prfB	Peptide Chain Release Factor 2
0950	(CT800)	pth	Peptidyl tRNA Hydrolase
0318	(CT095)	rbfA	Ribosome Binding Factor A
0699	(CT677)	rrf	Ribosome Releasing Factor
0697	(CT679)	tsf	Elongation Factor TS
0074	(CT322)	tufA	Elongation Factor Tu

Ribosomal Proteins

0078	(CT318)	rl1	L1 Ribosomal Protein
0644	(CT525)	rl2	L2 Ribosomal Protein
0647	(CT528)	rl3	L3 Ribosomal Protein
0646	(CT527)	rl4	L4 Ribosomal Protein
0635	(CT516)	rl5	L5 Ribosomal Protein
0633	(CT514)	rl6	L6 Ribosomal Protein
0080	(CT316)	rl7	L7/L12 Ribosomal Protein
0953	(CT803)	rl9	L9 Ribosomal Protein
0079	(CT317)	rl10	L10 Ribosomal Protein
0077	(CT319)	rl11	L11 Ribosomal Protein
0247	(CT125)	rl13	L13 Ribosomal Protein
0637	(CT518)	rl14	L14 Ribosomal Protein
0630	(CT511)	rl15	L15 Ribosomal Protein
0640	(CT521)	rl16	L16 Ribosomal Protein
0625	(CT506)	rl17	L17 Ribosomal Protein
0632	(CT513)	rl18	L18 Ribosomal Protein
0118	(CT028)	rl19	L19 Ribosomal Protein
0992	(CT835)	rl20	L20 Ribosomal Protein
0546	(CT420)	rl21	L21 Ribosomal Protein
0642	(CT523)	rl22	L22 Ribosomal Protein
0645	(CT526)	rl23	L23 Ribosomal Protein

	0636	(CT517)	rl24	L24 Ribosomal Protein
	0545	(CT419)	rl27	L27 ribosomal protein
	0327	(CT086)	rl28	L28 Ribosomal Protein
	0639	(CT520)	rl29	L29 Ribosomal Protein
5	0112	(CT022)	rl31	L31 Ribosomal Protein
	0961	(CT810)	rl32	L32 Ribosomal Protein
	0250	(CT150)	rl33	L33 Ribosomal Protein
	0935	(CT785)	rl34	L34 Ribosomal Protein
	0991	(CT834)	rl35	L35 Ribosomal Protein
10	0936	(CT786)	rl36	L36 Ribosomal Protein
	0315	(CT098)	rs1	S1 Ribosomal Protein
	0696	(CT680)	rs2	S2 Ribosomal Protein
	0641	(CT522)	rs3	S3 Ribosomal Protein
	0733	(CT626)	rs4	S4 Ribosomal Protein
15	0631	(CT512)	rs5	S5 Ribosomal Protein
	0951	(CT801)	rs6	S6 Ribosomal Protein
	0551	(CT438)	rs7	S7 Ribosomal Protein
	0634	(CT515)	rs8	S8 Ribosomal Protein
	0246	(CT126)	rs9	S9 Ribosomal Protein
20	0549	(CT436)	rs10	S10 Ribosomal Protein
	0627	(CT508)	rs11	S11 Ribosomal Protein
	0552	(CT439)	rs12	S12 Ribosomal Protein
	0628	(CT509)	rs13	S13 Ribosomal Protein
	0937	(CT787)	rs14	S14 Ribosomal Protein
25	1000	(CT843)	rs15	S15 Ribosomal Protein
	0116	(CT026)	rs16	S16 Ribosomal Protein
	0638	(CT519)	rs17	S17 Ribosomal Protein
	0952	(CT802)	rs18	S18 Ribosomal Protein
	0643	(CT524)	rs19	S19 Ribosomal Protein
30	0754	(CT617)	rs20	S20 Ribosomal Protein
	0031	(CT342)	rs21	S21 Ribosomal Protein

35 **Other Categories**

Chlamydia-Specific Proteins

	0561	(CT446)	Euo	CHLPS Euo Protein
	0804	(CT583)	Gp6D	CHLTR Plasmid Paralog
	0186	(CT119)		Similarity to IncA_1
40	0291	(CT232)	incB	Inclusion Membrane Protein B
	0292	(CT233)	incC	Inclusion Membrane Protein C
	1026	(CT377)		LtuA Protein
	0333	(CT080)		LtuB Protein
	0005	(CT871)	pmp_1	Polymorphic Outer Membrane Protein G Family
45	0013	(CT871)	pmp_2	Polymorphic Outer Membrane Protein G Family
	0014	(CT871)	pmp_3	Polymorphic Outer Membrane Protein G Family
	0015	(CT871)	pmp_3	PMP_3 (frame-shift with 0014)
	0016	(CT874)	pmp_4	Polymorphic Outer Membrane Protein G Family
	0017	(CT871)	pmp_4	PMP_4 (frame-shift with 0016)
50	0018	(CT874)	pmp_5	Polymorphic Outer Membrane Protein G Family
	0019	(CT871)	pmp_5	PMP_5 (frame-shift with 0018)
	0444	(CT871)	pmp_6	Polymorphic Outer Membrane Protein G/I Family
	0445	(CT871)	pmp_7	Polymorphic Outer Membrane Protein G Family
	0446	(CT871)	pmp_8	Polymorphic Outer Membrane Protein G Family
55	0447	(CT871)	pmp_9	Polymorphic Outer Membrane Protein G/I Family
	0450	(CT871)	pmp_10	Polymorphic Outer Membrane Protein G Family
	0449	(CT871)	pmp_10	PMP_10 (Frame-shift with 0450)

0451	(CT871)	pmp_11	Polymorphic Outer Membrane Protein G Family
0452	(CT874)	pmp_12	Polymorphic Outer Membrane Protein (truncated) A/I Family
0453	(CT871)	pmp_13	Polymorphic Outer Membrane Protein G Family
0454	(CT872)	pmp_14	Polymorphic Outer Membrane Protein H Family
0466	(CT869)	pmp_15	Polymorphic Outer Membrane Protein E Family
0467	(CT869)	pmp_16	Polymorphic Outer Membrane Protein E Family
0468	(CT869)	pmp_17	Polymorphic Outer Membrane Protein E Family
0469	(CT869)	pmp_17	PMP_17 (Frame-shift with 0468)
0470	(CT869)	pmp_17	PMP_17 (Frame-shift with 0469)
0471	(CT870)	pmp_18	Polymorphic Outer Membrane Protein E/F Family
0539	(CT412)	pmp_19	Polymorphic Membrane Protein A Family
0540	(CT413)	pmp_20	Polymorphic Membrane Protein B Family
0963	(CT812)	pmp_21	Polymorphic Membrane Protein D Family
0562			CHLPS 43 kDa Protein Homolog_1
0927			CHLPS 43 kDa Protein Homolog_2
0928			CHLPS 43 kDa Protein Homolog_3
0929			CHLPS 43 kDa Protein Homolog_4
0728	(CT622)		CHLPN 76kDa Homolog_1 (CT622)
0729	(CT623)		CHLPN 76kDa Homolog_2 (CT623)
0133	(CT109)		CHLPS Hypothetical Protein
0332	(CT081)		CHLPR T2 Protein

Miscellaneous Enzymes/Conserved Proteins

0193		argR	Possible Arginine Repressor
1046			Aromatic Amino Acid Hydroxylase
0232			Similarity to 5'-Methylthioadenosine Nucleosidase
0128	(CT035)		Biotin Protein Ligase
0513	(CT426)		Fe-S Oxidoreductase_1
0911	(CT767)		Fe-S Oxidoreductase_2
0373	(CT057)	gcpE	GcpE Protein
0407	(CT103)		HAD Superfamily Hydrolase/Phosphatase
0917	(CT771)		Hydrolase/Phosphatase Homolog
0488	(CT385)	ycfF	HIT Family Hydrolase
0701	(CT675)	karG	Arginine Kinase
0526	(CT399)	kpsF	GutQ/KpsF Family Sugar-P Isomerase
0919	(CT773)	ldh	Leucine Dehydrogenase
0022	(CT349)	maf	Maf protein
0997	(CT840)	mesJ	PP-loop superfamily ATPase
0151	(CT148)	mhpA	Monooxygenase
0730	(CT624)	mviN	Integral Membrane Protein
0861	(CT720)		NifU-Related Protein
0479	(CT380)	phnP	Metal Dependent Hydrolase
0106	(CT015)	phoH	ATPase
0329	(CT084)		Phopholipase D Superfamily
0435	(CT284)		Phospholipase D Superfamily
0581	(CT464)		Phosphoglycolate Phosphatase
0897	(CT754)		Predicted Phosphohydrolase
0509	(CT422)		Predicted Metalloenzyme
1030	(CT375)		Predicted D-Amino Acid Dehyrogenase
0531	(CT404)		SAM Dependent Methyltransferase
0337	(CT076)	smpB	Small Protein B
0394	(CT256)	tlyC_1	CBS Domain Protein (Hemolysin Homolog)_1
0510	(CT423)	tlyC_2	CBS Domains (Hemolysin Homolog)_2
0382	(CT048)	yabC	SAM-Dependent Methytransferase
0787	(CT594)	yabD	PHP Superfamily (Urease/Pyrimidinase) Hydrolase
0611	(CT492)	yacE	Predicted Phosphatase/Kinase
0579	(CT462)	yacM	Sugar Nucleotide Phosphorylase
0578	(CT461)	yael	Phosphohydrolase

0345	(CT071)	yaeM	CT071 Hypothetical Protein
0566	(CT450)	yaeS	YaeS family Hypothetical Protein
0591	(CT472)	yagE	YagE family
0039	(CT335)	ybaB	YbaB family Hypothetical Protein
0101	(CT012)	ybbP	YbbP family Hypothetical Protein
0915	(CT769)	ybeB	iojap Superfamily Ortholog
0137	(CT108)	ybgI	ACR family
0529	(CT402)	ycaH	ATPase
0438	(CT287)	ycbF	PP-loop Superfamily ATPase
0734	(CT627)	yceA	YceA Hypothetical Protein
0954	(CT804)	ychB	Predicted Kinase
0261	(CT217)	ydaO	PP-Loop Superfamily ATPase
0245	(CT127)	ydhO	Polysaccharide Hydrolase-Invasin Repeat Family
0573	(CT457)	yebC	YebC Family Hypothetical Protein
0689	(CT687)	yfhO_1	NifS-related Aminotransferase_1
0862	(CT721)	yfhO_2	NifS-related Aminotransferase_2
0547	(CT434)	ygbB	YgbB Family Hypothetical Protein
0237	(CT184)	yggF	YggF Family Hypothetical Protein
0775	(CT606)	yggV	YggV Family Hypothetical Protein
0396	(CT258)	yhfO_3	NifS-related Aminotransferase_3
0605	(CT487)	yhhF	Predicted Methylase
0575	(CT458)	yhhY	Amino Group Acetyl Transferase
0592	(CT473)	yidD	YidD Family
0982	(CT825)	yigN	YigN Family Hypothetical Protein
0657	(CT537)	yjeE	YjeE Hypothetical Protein
0768	(CT644)	yohI	YohI Predicted Oxidoreductase
0336	(CT077)	yojL	YojL Hypothetical Protein
0217	(CT140)	ypdP	YpdP Hypothetical Protein
0140	(CT212)	yqdE	YqdE Hypothetical Protein
0263	(CT221)	yqfU	YqfU Hypothetical Protein
0139	(CT211)	yqgE	YqgE Hypothetical Protein
0270	(CT137)	ywlC	SuA5 Superfamily-related Protein
0879	(CT738)	yycJ	Metal Dependent Hydrolase

Homologs to CHLTR Hypothetical Coding Genes

0001	(CT001)	CT001 Hypothetical Protein
0020	(CT351)	CT351 Hypothetical Protein
0021	(CT350)	CT350 Hypothetical Protein
0026	(CT345)	CT345 Hypothetical Protein
0035	(CT339)	CT339 Hypothetical Protein
0036	(CT338)	CT338 Hypothetical Protein
0055	(CT296)	CT296 Hypothetical Protein
0062	(CT289)	CT289 Hypothetical Protein
0065	(CT288)	CT288 Hypothetical Protein
0068	(CT360)	CT360 Hypothetical Protein
0071	(CT325)	CT325 Hypothetical Protein
0072	(CT324)	CT324 Hypothetical Protein
0085	(CT311)	CT311 Hypothetical Protein
0087	(CT309)	CT309 Hypothetical Protein
0093	(CT303)	CT303 Hypothetical Protein
0100	(CT011)	CT011 Hypothetical Protein
0104	(CT017)	CT017 Hypothetical Protein
0105	(CT016)	CT016 Hypothetical Protein
0107	(CT058)	CT058 Hypothetical Protein_1
0108	(CT018)	CT018 Similarity
0111	(CT021)	CT021 Hypothetical Protein
0121	(CT031)	CT031 Hypothetical Protein

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	0129	(CT036)	CT036 Similarity
	0145	(CT114)	CT114 Hypothetical Protein
	0150	(CT147)	CT147 Hypothetical Protein
	0152	(CT149)	CT149 Hypothetical Protein
5	0176	(CT153)	CT153 Hypothetical Protein
	0188	(CT132)	CT132 Hypothetical Protein
	0189	(CT131)	CT131 Hypothetical Protein
	0206	(CT203)	CT203 Hypothetical Protein
	0229	(CT178)	CT178 Hypothetical Protein
10	0230	(CT179)	CT179 Hypothetical Protein
	0234	(CT181)	CT181 Hypothetical Protein
	0249	(CT151)	CT151 Hypothetical Protein
	0253	(CT144)	CT144 Hypothetical Protein_1
	0254	(CT143)	CT143 Hypothetical Protein_1
15	0255	(CT142)	CT142 Hypothetical Protein_1
	0256	(CT144)	CT144 Hypothetical Protein_2
	0257	(CT143)	CT143 Hypothetical Protein_2
	0259	(CT142)	CT142 Hypothetical Protein_2
	0276	(CT191)	CT191 Hypothetical Protein
20	0288	(CT195)	CT195 Hypothetical Protein
	0293	(CT234)	CT234 Hypothetical Protein
	0301	(CT242)	CT368 Hypothetical Protein
	0303	(CT244)	CT244 Hypothetical Protein
	0308	(CT249)	CT249 Similarity
25	0312	(CT101)	CT101 Hypothetical Protein
	0328	(CT085)	CT085 Hypothetical Protein
	0330	(CT083)	CT083 Hypothetical Protein
	0331	(CT082)	CT082 Hypothetical Protein
	0334	(CT079)	CT079 Similarity
30	0342	(CT073)	CT073 Hypothetical Protein
	0343	(CT073)	(frame-shift with 0342?)
	0350	(CT066)	CT066 Hypothetical Protein
	0369	(CT058)	CT058 Hypothetical Protein_2
	0370	(CT058)	CT058 Hypothetical Protein_3
35	0374	(CT056)	CT056 Hypothetical Protein
	0379	(CT053)	CT053 Hypothetical Protein
	0381	(CT326)	CT326 Similarity
	0383	(CT047)	CT047 Hypothetical Protein
	0387	(CT043)	CT043 Hypothetical Protein
40	0389	(CT041)	CT041 Hypothetical Protein
	0393	(CT038)	CT038 Hypothetical Protein
	0395	(CT257)	CT257 Hypothetical Protein
	0399	(CT253)	CT253 Hypothetical Protein
	0400	(CT254)	CT254 Hypothetical Protein
45	0401	(CT255)	CT255 Hypothetical Protein
	0405	(CT105)	CT105 Hypothetical Protein
	0408	(CT102)	CT102 Hypothetical Protein
	0409	(CT260)	CT260 Hypothetical Protein
	0411	(CT262)	CT262 Hypothetical Protein
50	0412	(CT263)	CT263 Hypothetical Protein
	0415	(CT266)	CT266 Hypothetical Protein
	0420	(CT271)	CT271 Hypothetical Protein
	0422	(CT273)	CT273 Hypothetical Protein
	0423	(CT274)	CT274 Hypothetical Protein
55	0425	(CT276)	CT276 Hypothetical Proteins
	0426	(CT277)	CT277 Similarity
	0434	(CT283)	CT283 Hypothetical Protein

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0441	(CT007)	CT007 Hypothetical Protein
0442	(CT006)	CT006 Hypothetical Protein
0443	(CT005)	CT005 Hypothetical Protein
0474	(CT365)	CT365 Hypothetical Protein
0476	(CT865)	CT865 Hypothetical Protein
0480	(CT383)	CT383 Hypothetical Protein
0485	(CT382)	CT382.1 Hypothetical Protein
0487	(CT384)	CT384 Hypothetical Protein
0489	(CT386)	CT386 Hypothetical Protein
0490	(CT387)	CT387 Hypothetical Protein
0491	(CT389)	CT389 Hypothetical Protein
0496	(CT391)	CT391 Hypothetical Protein
0497	(CT388)	CT388 Hypothetical Protein
0506	(CT421)	CT421 Hypothetical Protein
0507	(CT421)	CT421.1 Hypothetical Protein
0508	(CT421)	CT421.2 Hypothetical Protein
0512	(CT425)	CT425 Hypothetical Protein
0514	(CT427)	CT427 Hypothetical Protein
0518	(CT429)	CT429 Hypothetical Protein
0522	(CT433)	CT433 Hypothetical Protein
0525	(CT398)	CT398 Hypothetical Protein
0533	(CT406)	CT406 Hypothetical Protein
0537	(CT814)	CT814.1 Hypothetical Protein
0538	(CT814)	CT814 Hypothetical Protein
0554	(CT440)	CT440 Hypothetical Protein
0559	(CT441)	CT441.1 Hypothetical Protein
0565	(CT449)	CT449 Hypothetical Protein
0572	(CT456)	CT456 Hypothetical Protein
0582	(CT465)	CT465 Hypothetical Protein
0583	(CT466)	CT466 Hypothetical Protein
0588	(CT469)	CT469 Hypothetical Protein
0589	(CT470)	CT470 Hypothetical Protein
0590	(CT471)	CT471 Hypothetical Protein
0593	(CT474)	CT474 Hypothetical Protein
0595	(CT476)	CT476 Hypothetical Protein
0601	(CT483)	CT483 Hypothetical Protein
0602	(CT484)	CT484 Hypothetical Protein
0606	(CT488)	CT488 Hypothetical Protein
0609	(CT490)	CT490 Hypothetical Protein
0622	(CT503)	CT503 Hypothetical Protein
0623	(CT504)	CT504 Hypothetical Protein
0648	(CT529)	CT529 Hypothetical Protein
0658	(CT538)	CT538 Hypothetical Protein
0667	(CT546)	CT546 Hypothetical Protein
0668	(CT547)	CT547 Hypothetical Protein
0669	(CT548)	CT548 Hypothetical Protein
0671	(CT550)	CT550 Hypothetical Protein
0673	(CT552)	CT552 Hypothetical Protein
0675	(CT696)	CT696 Hypothetical Protein
0676	(CT695)	CT695 Similarity
0681	(CT691)	CT691 Hypothetical Protein
0687	(CT482)	CT482 Hypothetical Protein
0688	(CT481)	CT481 Hypothetical Protein
0700	(CT676)	CT676 Hypothetical Protein
0705	(CT671)	CT671 Hypothetical Protein
0706	(CT670)	CT670 Hypothetical Protein
0708	(CT668)	CT668 Hypothetical Protein

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	0709	(CT667)	CT667 Hypothetical Protein
	0710	(CT666)	CT666 Hypothetical Protein
	0711	(CT665)	CT665 Hypothetical Protein
	0713	(CT663)	CT663 Hypothetical Protein
5	0717	(CT656)	CT656 Hypothetical Protein
	0718	(CT657)	CT657 Hypothetical Protein
	0720	(CT659)	CT659 Hypothetical Protein
	0722	(CT654)	CT654 Hypothetical Protein
	0725	(CT652)	CT652.1 Hypothetical Protein
10	0726	(CT620)	CT620 Hypothetical Protein
	0727	(CT619)	CT619 Hypothetical Protein
	0739	(CT638)	CT368 Hypothetical Protein
	0742	(CT635)	CT635 Hypothetical Protein
	0746	(CT632)	CT632 Hypothetical Protein
15	0747	(CT631)	CT631 Hypothetical Protein
	0751	(CT651)	CT651 Hypothetical Protein
	0755	(CT616)	CT616 Hypothetical Protein
	0760	(CT611)	CT611 Hypothetical Protein
	0761	(CT610)	CT610 Hypothetical Protein
20	0764	(CT648)	CT648 Hypothetical Protein
	0765	(CT647)	CT647 Hypothetical Protein
	0766	(CT646)	CT646 Hypothetical Protein
	0767	(CT645)	CT645 Hypothetical Protein
	0770	(CT642)	CT642 Hypothetical Protein
25	0774	(CT606)	CT606.1 Hypothetical Protein
	0776	(CT605)	CT605 Hypothetical Protein
	0779	(CT602)	CT602 Hypothetical Protein
	0783	(CT598)	CT598 Hypothetical Protein
	0791	(CT590)	CT590 Hypothetical Protein
30	0792	(CT589)	CT589 Hypothetical Protein
	0803	(CT584)	CT584 Hypothetical Protein
	0807	(CT580)	CT580 Hypothetical Protein
	0808	(CT579)	CT579 Hypothetical Protein
	0809	(CT578)	CT578 Hypothetical Protein
35	0810	(CT577)	CT577 Hypothetical Protein
	0814	(CT573)	CT573 Hypothetical Protein
	0818	(CT569)	CT569 Hypothetical Protein
	0819	(CT568)	CT568 Hypothetical Protein
	0820	(CT567)	CT567 Hypothetical Protein
40	0821	(CT566)	CT566 Hypothetical Protein
	0822	(CT565)	CT565 Hypothetical Protein
	0827	(CT560)	CT560 Hypothetical Protein
	0834	(CT556)	CT556 Hypothetical Protein
	0840	(CT700)	CT700 Hypothetical Protein
45	0842	(CT702)	CT702 Hypothetical Protein
	0843	(CT702)	CT702 Hypothetical Protein
	0852	(CT711)	CT711 Hypothetical Protein
	0853	(CT712)	CT712 Hypothetical Protein
	0857	(CT716)	CT716 Hypothetical Protein
50	0859	(CT718)	CT718 Hypothetical Protein
	0865	(CT724)	CT724 Hypothetical Protein
	0869	(CT728)	CT728 Hypothetical Protein
	0874	(CT733)	CT733 Hypothetical Protein
	0875	(CT734)	CT734 Hypothetical Protein
55	0884	(CT741)	CT741 Hypothetical Protein
	0887	(CT744)	CHLTR Possible Phosphoprotein
	0896	(CT753)	CT753 Hypothetical Protein

	0906	(CT763)	CT763 Hypothetical Protein
	0908	(CT764)	CT764 Hypothetical Protein
	0912	(CT768)	CT768 Hypothetical Protein
	0925	(CT779)	CT779 Hypothetical Protein
5	0938	(CT788)	CT788 Hypothetical Protein
	0939	(CT790)	CT790 Hypothetical Protein
	0943	(CT794)	CT794.1 Hypothetical Protein
	0945	(CT795)	CT795 Hypothetical Protein
	0956	(CT805)	CT805 Hypothetical Protein
10	0960	(CT809)	CT809 Hypothetical Protein
	0989	(CT832)	CT832 Hypothetical Protein
	0994	(CT837)	CT837 Hypothetical Protein
	0995	(CT838)	CT838 Hypothetical Protein
	0996	(CT839)	CT839 Hypothetical Protein
15	1002	(CT845)	CT845 Hypothetical Protein
	1003	(CT846)	CT846 Hypothetical Protein
	1004	(CT847)	CT847 Hypothetical Protein
	1005	(CT848)	CT848 Hypothetical Protein
	1006	(CT849)	CT849 Hypothetical Protein
20	1007	(CT849)	CT849.1 Hypothetical Protein
	1008	(CT850)	CT850 Hypothetical Protein
	1010	(CT852)	CT852 Hypothetical Protein
	1011	(CT853)	CT853 Hypothetical Protein
	1015	(CT857)	CT857 Hypothetical Protein
25	1016	(CT858)	CT858 Hypothetical Protein
	1019	(CT860)	CT860 Hypothetical Protein
	1020	(CT861)	CT861 Hypothetical Protein
	1022	(CT863)	CT863 Hypothetical Protein
	1032	(CT373)	CT373 Hypothetical Protein
30	1033	(CT372)	CT372 Hypothetical Protein
	1034	(CT371)	CT371 Hypothetical Protein
	1057	(CT356)	CT356 Hypothetical Protein
	1058	(CT355)	CT355 Hypothetical Protein
	1061	(CT330)	CT330 Hypothetical Protein
35	1073	(CT371)	CT371 Hypothetical Protein

Coding Genes Not in _C. trachomatis_

	0486		Hypothetical Proline Permease
	0279		Possible ABC Transporter Permease Protein
40	0505		3-Methyladenine DNA Glycosylase
	0193	argR	Similarity to Arginine Repressor
	1041	bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase
	1044	bioB	Biotin Synthase
	1042	bioD	Dethiobiotin synthetase
45	0585		Similarity to Cps IncA_2
	0562		CHLPS 43 kDa Protein Homolog_1
	0927		CHLPS 43 kDa Protein Homolog_2
	0928		CHLPS 43 kDa Protein Homolog_3
	0929		CHLPS 43 kDa Protein Homolog_4
50	1045		Conserved Hypothetical Membrane Protein
	0251		Conserved Hypothetical Protein
	0278		Conserved Outer Membrane Lipoprotein Protein
	0907		CutA-like Periplasmic Divalent Cation Tolerance Protein
	0171	guaA	GMP Synthase
55	0172	guaB	Inosine 5'-Monophosphase Dehydrogenase
	0608		Uridine 5'-Monophosphate Synthase
	0735		Uridine Kinase

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0980			Similar to *Saccharomyces cerevisiae* 52.9KDa Protein
0232			Similarity to 5'-Methylthioadenosine Nucleosidase
1046			Tryptophan Hydroxylase
0477	yqeV_Bs		Conserved Hypothetical Protein
0048	yqfF-Bs		Conserved Hypothetical IM Protein
0587	yvyD_Bs		Conserved Hypothetical Protein
0143	yxjG_Bs_1		Conserved Hypothetical Protein
0448	yxjG_Bs_2		Conserved Hypothetical Protein

0006	0180	0440	0977
0007	0181	0455	0978
0008	0190	0456	1018
0009	0203	0457	1023
0010	0204	0458	1027
0011	0205	0459	1029
0012	0209	0460	1040
0028	0210	0461	1051
0029	0211	0462	1052
0034	0212	0463	1053
0041	0213	0464	1054
0042	0214	0465	1055
0043	0215	0472	1056
0044	0216	0473	1064
0045	0218	0481	1065
0046	0220	0483	1066
0047	0221	0492	1070
0049	0222	0493	1071
0050	0223	0494	1072
0051	0224	0498	
0063	0225	0499	
0064	0226	0516	
0066	0233	0517	
0067	0240	0523	
0069	0241	0524	
0070	0242	0553	
0099	0243	0574	
0124	0266	0600	
0125	0267	0656	
0126	0268	0664	
0130	0277	0677	
0131	0283	0678	
0132	0284	0685	
0142	0285	0686	
0146	0287	0724	
0147	0352	0731	
0155	0353	0745	
0156	0354	0753	
0157	0355	0794	
0158	0356	0795	
0159	0357	0796	
0162	0358	0797	
0163	0365	0798	
0164	0366	0799	
0165	0367	0829	
0166	0368	0830	
0167	0371	0831	
0168	0372	0881	
0169	0375	0882	

0170	0376	0913
0173	0391	0914
0174	0398	0930
0175	0404	0944
0177	0431	0964
0178	0432	0975
0179	0439	0976

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Chlamydia pneumoniae Genome Encoded Proteins

CPn_0001   130   4
CT001 hypothetical protein
KRLKDEIKYTSLRRKAMLGKIIRGLSSLIVILCALNVGLIGITHNKLNIIAKLCCGVSTP
ATQITYIIIGIAGVICLLSFCPFCSKKSRHSHGDSCSSGCHSHHSDKN

CPn_0002   570   975
...
...
MHVVNVEDLREDSVTSDFNREEFLRNVPESLGCGLVKVPAVIK

CPn_0003   889   2370
gatA-Glu tRNA Gln Amidotransferae
KIMYRYSALELAKAVTLGELTATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAELIDK
KRSRCGEPLGKLAGVPVGIKDNIHVTGLKTTCASRVLENYQPPFDATVVERIKKEDGIILG
KLNMDEFAMGSTTLYSAFHPTHNPWDLSRVPGGSSGGSAAAVSARFCPVALGSDTGGSIR
QPAAFCGVVGFKPSYGAVSRYGLVAFASSLDQIGPLANTVEDVALMMDVFSGRDPKDATS
REFFRDSFMSKLSTEVPKVIGVPRTFLEGLRDDIRENFFSSLAIFEGEGTHLVDVELDIL
SHAVSIYYILASAEAATNLARFDGVRYGYRSPQAHTISQLYDLSRGEGFGKEVMRRILLG
NYVLSAERQNVYYKKATAVRAKIVKAFRTAFEKCEILAMPVCSSPAFEIGEILDPVTLYL
QDIYTVAMNLAYLPAIAVPSGFSKEGLPLGLQIIGQQGQDQQVCQVGYSFQEHAQIKQLF
SKRYAKSVVLGGQS

CPn_0004   2334   3833
gatB-(Pet112) Glu tRNA Gln Amidotransferase (B Subunit)
EICQKCCSRRSIMSAVYADWESVIGLEVHVELNTASKLFSSALNRFGDEPNTNISTVCTG
LPGSLPVLNQSAVEKAVLFGCAVEGEISLLSRFDRKSYFYPDSPRNFQITQFEHPIIRGG
RIKAIVQGEERYFELAQTHIEDDAGMLKHFGEFAGVDYNRAGVPLIEIVSKPCMFCPEDA
VAYATSLVSLLDYIGISDCNMEEGSIRFDVNVSVRPKGSPELRNKVEIKNMNSFAFMAQA
LEAEKQRQIDEYLNQPNKDPKLVIPAATYRWDPEKKKTVLMRLKESAEDYKYFPEPDLPT
LQLTESYIERIRKTLPELPYDKYHRYIQEYGLSEDIASILISDKNIATFFEVACKDCKNF
RSLSNMVTVEFGGRCKTLGVKLPSSGIFPEGVAQLVNAIDQGVITGKIAKEIADLMMESP
GKNPEEILKEXPELLPMSDEGELQKIIAEVVLANPESIVDYKNGKTKALGFLVGQIMKRT
AGKAPPKRVNELLLLELDKG

CPn_0005   4097   6892
pmp_1-Polymorphic Outer Membrane Protein
SDIHFDLGTKMRFSLCGFPLVFSFTLLSVFDTSLSATTISLTPEDSFHGDSQNAERSYNV
QAGDVSLTGDVSISNVDNSALNKACFNVTSGSVTFAGNHRGLYFNNISSGTTKEGAVLC
CQDPQATARFSGFSTLSFIQSPGDIKEQGCLYSKNALMLLNNYVVRFEQNQSKTKGGAIS
GANVTIVQGNVSNONAATFGGAIHSSGPLQIAVNQAEIRFAGNTAKNGSGGALYSDG
DIDIDQNAYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIM
GGGAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFGQNRT
SLPFLNGIHLLQNAKFLKLQARNGYSIEFYDPITSEADGSTQLNINGDPKNKEYTGTILF
SGEKSLANDPRDFKSTIPQNVNLSAGYLVIKEGAEVTVSKFTQSPGSHLVLDLGTKLIAS
KEDIAITGLAIDIDSLSSSTAAVIKANTANKQISVTDSIELISPTGNAYEDLRMRNSQT
FPLLSLEPGAGGSVTVTAGDFLPVSPHYGFGGNWKLAWTGTGNKVGEFFWDKINYKPRPE
KEGNLVPNILWGNAVDVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHN
SGGYVLSVNNEITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRY
ASRNPNVNVGILSRRFLQNPLMIFHFLCAYGHATNDMKTDYANFPMVKNSWRNNCWAIEC
GGSMPLLVFENGRLFQGAIPFMKLQLVYAYQGDFKETTADGRRFSNGSLTSISVPLGIRF
EKLALSQDVLYDFSFSYIPDIFRKDPSCEEAALVISGDSWLVPAAHVSRHAFVGSGTGRYH
FNDYTELLCRGSIECRPHARNYNINCGSKFRF

CPn_0006   7299   7141
No robust homolog present in Genebank/EMBL as of 11/7/98
KQLQEPLRSALLERLSEWLVLLGVPSPETTRSTPEKDANQLPKDSRNRTLESL

CPn_0007   7488   10496
No robust homolog present in Genebank/EMBL as of 11/7/98
KSFRYNLSLIFSFLVVIPLTDSTTSSLSTSLLDEGNPQSMRKLRILAIVLIALSIILIAG
GVVLLTVAIPGLSSVISSPAGMGACALGCVMLALGIDVLLKKREVPIVLASVTTTPGTGS
PRSGISISGADSTIRSLPTYLLDEGHPQSMRKLRILAIVLIVFSIILIASGVVLLTVAIP
GLSSVISSPAGMGACALGCVMLALGIDVLLKKREVPIVLASVTTTPGTGSPRSGISISGA
DSTIRSLPTYPLDEGHPQSMRKLRILAIVLIVFSIILIASGVVLLTVAIPGLSSIISSPA
EMGACALGCVMLALGIDVLLKKREVPIVVPAPIPEEVVIDDIDEESIRLQOEAEAALARL
PEEMSAFESYIKVVESHLENMKSLPYDGHGLEEKTKHQIRVVRRSLRKHQFKLYPEFLDIRRIF
EEEEFFFLSARKRLIDLATTLVERKILTEQLERNNLRKAFSYLYQDSIFKKIIDNFEKLA
WKFMILSKSICRFTIIFENHEHGVAKSLLHNAVLLEKVIYRSLQKSYRDIGHSSAKMKI
LHGNPFFSLEDNKKTIMKEHAEMLESLSSYRKVFLALSDENVVDTPSDPKKWDLSGIPCR
CALSEISRDEQWQKKAHLKHQESLYTQARDRLTDQSSKENQKELEKAEQEYISSWERVKK
FEIERVQERIRAIQKLYPNILEREEETTGQETVTPTVQGTTASSDLTDILGRIEVSSRED
NQNQESCVKVLRSHEVEMSWEVKQEYGPKKKEFQDQMGSLERFFTEHIEELEVLQKDYSK
HLSYFKKVNNKKEVQYAKFRLKVLESDLEGILAQTESAESLLTQEELPILATRCGALEKAV
FKGSLCCALASKAKPYFEEDPRFQDSDTQLRALTLRLQEAKASLEEEIKRFSNLENDIAE
ERRLLKESKQTFERAGLGVLREIAVESTYDLRSLTNTWEGTPESEKVYFSMYLNYYNEEK
RRAKTRLVEMTQRYRDFKMALEAMQFNEEALLQEELSIQAPSE

CPn_0008   10780   11685
No robust homolog present in Genebank/EMBL as of 11/7/98
CKYSYLLNYPPPPRRSLGVSCSKLRGLSITLLVLGVLLLTLGIPGLTAGISFCAGLGFSA
LCGVLVISGLLFLLVVRREVPTVRSEIPRGVSVTPEEPALEKAQKEPETKKILDRLGWK
LDOLDTYIQEVFACLERLKDPKYEDRGLLTEAKEKLRVFDVVEKSMMSEFLDIQRVLNEE
AYYVEHCQDPLENIAYEIFSSQELRDYYCAGVCGYLPSGDARADRLKRSVKEVMDRFMRV
TWKSWEASVMLDHSYGVARELFKKAVGVLEESVYKILFKSYRDAFYECEKAKIQRDGRFK
WL

CPn_0009   11689   13119
No robust homolog present in Genebank/EMBL as of 11/7/98
GTSAHAFQRFRDINQWEDLKQTIFWVGEIIDCTDIETVRKCCMWLDRYADKFILREKEEK
MERHELFHATMVRKASCHAYAKAKAAFEKERCNENQRKVKDVEKWLSKGLAEFRNQESRR
ARERLRELCTLYPEVSVEERVLERQRTKKVNLENLYADIEKKYHICVREQEHYWKEVENK
EAEYREMIEKVILAEEVSECLQRLEDCLETWCKILKAEESVFEMKFDATEKLANKVLSD
VTNRLEILIEDAEEMIFRIEEIEMTLRMVELPLLFMKNTFEKASLQYNCKEMLAKVEPO
CREGPTYRICGERLENLRQDIATYATNCOERLQIFCDLECSKVRTCROILRCMKHFEVOGG
IJHFINEELLWMIAELFTQARLDLVATVPYMEFYLQYIHIKREKVROCWMAKTERYREIRO
AFOZRVMKEPLLAECTILKEEDYWLIRDDWLLRDERKNHQRRLTCNKIAAACQRVKGF

CPn_0010   11124   14125
No robust homolog present in Genebank/EMBL as of 11/7/98

CRYFYLRGYPPPPCHSVTG.   GKLRVLAITFLVFGMLLLIGGALFLTLGIPGLSAAIS
FGLGIGLSALGGVLMISGLLCLLVKREIPTVRPEEIPEGVSLAPSEEPALQAACKTLAGL
PKELDQLDTDIQEVFAGLRKLKDSKVESRSFLNDAKKEGLRVFDFVTEDTLTEIEELRQIV
AQEGWDLNFLINCGRSLXMMTAESESLDLFHVSKRLGYLPSGOVRCECLXKSAKEEVARLM
SLHCEIHKVAVAFORNSYAMAEKAFAKALGALEESVYRSLTQSYRDKFLESERAKIPWNG
HITWLRDDAKSGCAEKKLGMPRNVGRNLGKQSFG

CPn_0010.:   14268   15746
...
KFAPDAGKWKKYEFFAYECHTFNLIED.DNLILWTMAGNDSLDMDRFTIDHIEHTPTGITT
FLKRLHRKCALAKTTFEKKFSKKNLQAVEEANARRLKYVRDWYDQEFQKACERLEKLHAL
YPEVSVSIRENKIQETRSNLEKAYEAIEENYRCCVREQEDYWKEEEKREAEFRERGNKIL
SPEELESSLEQFDHGLKNFSEKLMELEGHILKLQKEATAEVENKILSDAESRLEIVFEDV
KEMPCRIEEIEKTLRMAELPLLPTKKAFEKACSOYNSCAEMLEKVKPYCKESLAYVTSKE
RLVSLDEDLRRAYTECQKRFQGDSGLESEVRACREQLRERIQEFETQGLDLVEKELLCVS
SRLRNTECDCVSGVKKEAPPGKKFYAQYYDEIYRVRVQSRWMTMSERLREGVQACNKMLK
AGLSEEDKVLKEEEYWLYREERKNKEKRLVGTKIVATQQRIQEFQPSDIVESSNEKVSLM
DKARFLFNREDHS

CPn_0011   15877   16614
gatB-(Pet112) Glu tRNA Gln Amidotransferase (B Subunit)
FWYSIMTAAPAILHVSPTPPEETKFVIPKDSKSRALGITLLVVGILLVVCGAIVLSGVIS
GLSALIVCGLGISTISLGVVLFVLGLILLLRKRELTLEQIEAKQIAETFADELKELEMYI
QSTEKSLEKIEGSRYSDQGFLNRATQKILDLESSLSSITSEFRDLRQLFDEEKIELLSGE
RLLEFIAANLFKQGRDVYLNLGNLADIRAYMGPNNYKVAMVIEKAKAVVHEFIVLTTMAR
ELEFFF

CPn_0012   16596   18212
gatB-(Pet112) Glu tRNA Gln Amidotransferase (B Subunit)
GIRVFFLKNKYGLLKGMYQENLRLLERLLYNSVQKSYADRLFSYEXTKMVHDTPLIPWEE
DKEXCAEAEKAFLEQQKILLDYGKSIFWLNENDEINLNDPWSWGLNTVRTRKVFQEVDDS
ERWNHKVLIQDKEDDYEKLLEESSKESTEANKKLLSDLVDRLEDAKTKFFLKQEEVETR
VKDLRARYGGTVDPKQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIYWKEQDVKDL
ARTQELEEDDIEAKREEAAEDLRSLNERLKKSKTMLDRAKWHIENAEDSITWNTSQIEMX
DMKARLKILKEDITSVLPEIDEIETCLSLEELPLLTTRELLTKSYLRFKICSETLLKMTS
VFENNIYVQEYEVQLQNLGFKLQGISQRFGKKQDDFANLEEQVALQKKRLRELTQNFEIQ
GFNFMKEDFKAAAKDLYIRSTAEQKMNFDVPCMELFRRYHEEVNKPLLELMYNCADSYRD
AKKRLCSLRLDEKELLQKEIKKEEFYQKKQQRHADRSRHTTYQKLRIAEELALELKKKI

CPn_0013   18509   21106
pmp_2-Polymorphic Outer Membrane Protein
LRDRLAFFIYLLYWKESPLREKKVVMKIPLRFLLISLVPTLSHSNLLGAATTEELSASNS
FDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGETQSTSCFKNDAAAGDLNFLGG
GFSFTFSNIDATTASGAAIGSEAANKTVTLSGFSALSFLKSPASTVTNGLGAINVKGNLS
LLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGG
ETLFQGNTAPTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSA
KITALRAAQGHTIYFYGGPITVTGSTSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAEA
KDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLIMDLGTSLVANTESIELT
NLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESFYQNGFLNEDHSYDGILELD
AGKDIVISADSRSIDAVQSPYGYGGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPN
LLAGSFIDVRSFQNFIELGTEGAPYEKRFWVAGISNVLHRSGRENQRKFRHVSGGAVVGA
STRMPGGDTLSLGFAQLFARDKDYFMVTNFAKTYAGSLRLQHDASLYSVVSILLGEGGLR
EILLPYVSKTLPCSFYGQLSYGHTDHRHKTESLPPPPPTLSTDHTSWGGYVWAGELGTRY
AVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISRDFSDSHLYNLAIPLGIKLEKRF
AEQYYHVVAMYSPDVCRSNPKCTTTLLSNQGSWKTKGSNLARQAGIVQASGFRSLGAAAE
LFGNFGFEWRGSSRSYNVDAGSKIKF

CPn_0014   21365   21922
pmp_3-Polymorphic Outer Membrane Protein
IQNQSIYFTMKSSFPKFVFSTFAIFPLSMIATETVLDSSASFDGNKNGNFSVRESQEDAG
TTYLFKGNVTLENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFCTVDAGTVAGAAVNSS
VVDKSTTFIGFSSLSFIASPGSSITTGKGAVSCSTGSLSLTKMSVCSSAKTFQRIMAVLS
PQKLFH

CPn_0015   21935   24174
pmp_3-PMP_3 (frame-shift with 0014)
LEFDKNVSLLFSKNFSTDNGGAITAKTLSLTGTTMSALFSENTSSKKGGAIQTSDALTIT
GNQGEVSFSDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAY
KTSTDTKVTLTGNQMLLFSNNTSTTAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGA
IAIEDSGELSLSADSGDVFLGNTVTSTTPGTNRSSIDLGTSAKMTALRSAAGRAIYFYD
PITTGSTTVTDVLKVNETPADSALOYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLS
GGTLSLKHGVTLQTQAFTQOADSRLEMDVGTTLEPADTSTINNLVINISSIDGAKKAKIE
TKATSKNLTLSGTITLLDPTGTFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEK
FHYGYQGTWGPIVWCTGASTTATFNWTKTGYIPNPERIGSLVPNSLWNAFIDISSLHYLM
ETANEGLQGDRAFWCAGLSNFFHKDSTKTRRGFRHLSGGYVICGNLHTCSDKILSAAFCQ
LFGRDRDYFVAKNQGTVVGGTLTYQHNETYISLPCKLRPCSLSYVPTEIPVLFSGNLSYT
HTDNDLKTKYTTYPTVKGSWGNDSFALEFCGRAPICLDESALFEQYMPFMKLQFVYAHQE
GFKEQGTEAREFGSSRLVNLALPIGIRFDKESDCQODATYNLTLGYTVDLVRSNPDCTTTL
RISGDSWKTFGTNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF

CPn_0016   24383   26188
pmp_4-Polymorphic Outer Membrane Protein
RSDFALKRGCHMRSSFSLLLISSSLAFPLLMSVSADAADLTLGSRDSYNGDTSTTEFTPK
AATSDAGTTYILDGDVSISQAGKGTSLTTSCFSNTAGNLTFLGNSFSLHFDNIISSTVA
GVVVSNTAASGITKFSGFSTLRMLAAPRTTTKGAIKITDGLVFESIGNLDLNENASSENG
GAINTKTLSLTGSTRFVAFLGNSSSQQGGAIYASGDSVISENAGILSFGNNSATTSGGAI
GAECNLVISNNQNIFFDGCKATTIFKGAIDCNKAGANPDPILTLGGNESLHFLNNTAGNSG
GAIYTKKLVLSSGRGGVLFSNNYAANATPKGGAIAILDSGEISISADLGNIIFEGNTTST
TGGPAGVTRNAIDLASNAKFLNLPATRGHFVIFYDPITSCXATDKLSLHKADAGSGNTYE
GYIVFCGEKLSEEELKKPDNLKCTFFQAVELAVGALVLKDKVTVVANTITQVEISKVVMD
GYTTFFACAHIVTLNKLAINIDCLGTTUPAIIKATAACKDVALAIPIMLVDVAQGNYYRHH
RLXQQVFILIELGAQSTMTTTGLIDTFLIJTTNIGYGYQGNWRINKIAGGSNKNKKCYLN
LD

CPn_0017   26094   27170
pmp_4-PMP_4 (frame-shift with 0016)
ILRITMGIKGNLIVWYDPATAPTKNATLTWTKTGYKFNPERQIFLVMHEILWFIFVDVRS
IGCLMGRCTSCLLSSSTRLMVSIIALFLIJELONRQRCTRGLCGNVAUZXKFTALIENFPN
FAFVUFYDKDULVAKRIFHIVYACAMGYRHLAESCPTLAKIL22INGCLPFVHIARFAYG
HTLRRNFRTKYTGYTVKGSWANLAPRIEVCTSALVVAGKRRGWVITFFFLNLFMIYAHQ
HDFKRYTTKRGFQGEDAFNLAVIPACIFFEKRCDRCTTYDLLLAYYTMVIRNHGYTTTLM

VGGDGWGNGGGLSRQALLVRAGNHHAFAGNFE.   .FEVELRGSGRSYAIDLGGRFGF

CPn_0018   27513   29003
pmp_5-Polymorphic Outer Membrane Protein
EYNMKTSVSMLLALLCSGASSIVLHAATTPLNPEDGFIGEGNTNTFSPKSTTDAAGTTYS
UTGEVLYIDPGKGGSITGTCFVETAGDLTFLGNGNTLKFLSVDAGANIAVAHVGGSKNLS
FTDFLSLVITESPKGAVTTGKGSLVSLGAVQLQDINTLVLTSNASVEDGGVIKGNSCLIQ
GIKGIGAIFGGNTGSSKKGGAIGTTGGLTIENNLGTLKFNENKAVTSGGALDLGAASTFTAN
  . . . .
  . . . .
VGDIVFEGNGVTTTAPNATTKRNVIHLESTAKWTGLAASQGNAIYFYDPITTNDTGASDN
LRINEVSANQKLSGSIVFSGERLSTAEAIAENLTSRINQPVTLVEGSLVLKQGVTLITQG
FSQEPESTLLLDLGTSL

CPn_0019   29007   30356
pmp_5-PMP_5 (frame-shift with 0018)
ASTEDIVITNLSINADTIYGKNPINIVASAANKNITLTGTLALVNADGAFYENHTLQDSQ
DYSFVKLSPGAGGTIITQDASQKPLEVAPSRPHYGYQGHWNQVIPGTGTQPSQANLEMV
RTGYLPNPEROGSLVPNSLWGSFVDQRAIQEIMVNSSQILCQERGVWGAGIANFLHRDKI
NEHGYRHSGVGYLVGVGTHAFSDATINAAFCQLFSRDKDYVVSKNHGTSYSGVVFLEDTL
EFRSPQGFYTDSSSEACCNQVVTIDMQLSYSHRNNDMKTKYTTYPEAQGSWANDVFGLEF
GATTYYYPNSTFLFDYYSPFLRLQCTYAHQEDFKETGGEVRHFTSGDLFNLAVPIGVKFE
RFSDCKRGSYELTLAYVPDVIRKDPKSTATLASGATWSTHGNNLSRQGLQLRLGNHCLIN
PGIEVFSHGAIELRGSSRNYNINLGGKYRF

CPn_0020   32717   30603
Predicted OMP (leader (14) peptide: outer membrane]
KLWSNPNLRLMKRCFLFLASFVLMGSSADALTHQEAVKKKNSYLSHFKSVSGIVTIEDGV
LNIHNNLRIQANKVYVENTVGQSLKLVAHGNVMVNYRAKTLVCDYLEYYSDTDSCLLTNG
RFAMYPWFLGGSMITLTPETIVIRKGYISTSEGPKKDLCLSGDYLEYSSDSLLSIGKTTL
RVCRIPILFLPPFSIMPMEIPKPPINFRGGTGGFLGSYLGMSYSPISRKHFSSTFFLDSF
FKHGVGMGFNLHCSQKQVPENVFNMKSYYAHRLAIDMAEAHDRYRLHGDFCFTHKHVNFS
GEYHLSDSWETVADIFPNNFMLKNTGPTRVDCTWNDNYFEGYLTSSVKVNSFQNANQELP
YLTLRQYPISIYNTGVYLENIVECGYLNFAFSDHIVGENFSSLRLAARPKLHKTVPLPIG
TLSSTLGSSLIYYSDVPEISSRHSQLSAKLQLDYRFLLHKSYIQRRHIIEPFVTFITETR
PLAKNEDHYIFSIQDAFHSLNLLKAGIDTSVLSKTNPRFPRIHAKLWTTHILSNTESKPT
FPKTACELSLPFGKKNTVSLDAEWIWKKHCWDHMNIRWEWIGNDNVAMTLESLHRSKYSL
IKCDRENFILDVSRPIDQLLDSPLSDHRNLILGKLFVRPHPCWNYRLSLRYGWHRQDTPN
YLEYQMILGTKIFEHWQLYGVYERREADSRFFFFLKLDKPKKPPF

CPn_0021   34470   32707
Predicted OMP (leader (19) peptide]
CSRSPYPNIEILARGVEHRSMGLFHLTLFGLLLCSLPISLVAKFPESVGHKILYISTQST
QQALATYLEALDAYGDHDFFVLRKIGEDYLKQSIHSSDPQTRKSTIIGAGLAGSSEALDV
LSQAMETADPLQQLLVLSAVSGHLGKTSDDLLFKALASPYPVIRLEAAYRLANLKNTKVI
DHLHSFIHKLPEEIQCLSAAIFLRLETEESDAYIRDLLAAKKSAIRSATALQIGEYQQKR
FLPTLRNLLTSASPQDQEAILYALGKLKDQGSYYNIKKQLQKPDVDVTLAAAQALIALGK
EEDALPVIKKQALEERPRALYALRHLPSEIGIPIALPIFLKTKNSEAKLNVALALLELGC
DTPKLLEYITERLVQPHYNETLALSFSKGRTLQNWKRVNIIVPQDPQERERLLSTTRGLE
EQILTLFFRLPKEAYLPCIYKLLASQKTQLATTAISFLSHTSHQEALDLLFQAAKLPGEP
IIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPSMPYLRYQVTPES
RTKLMLDILETLATSKSSEDIRLLIQLMTEGDAKNFPVLAGLLIKIVE

CPn_0022   35042   34395
maf
TILQVISNCCNVSNTRSFYSMSLPLVLGSSSPRRKFILEKFRVPFTVIPSNFDESKVSYS
GDPIAYTQELAAQKAYAVSELHSPCDCIILQTDVTIVSYDGRIFTKPQDKADAIQMLKTLR
NQTHDVVTSIAVLHKGKLLTGSETSQISLTMIPDHRIESYIDTVGTLNNCGAYDVCHGGL
ILKKVHGCVYNVQGLPIQTLKYLLEELNIDLWDYSI

CPn_0023   36657   35014
yjjK/alr-ABC Transporter Protein ATPase
ENRAKLLYSKQHFVMLSAMSIVLDKIGKSLGTRILFDDVSVVFNPGNCYGLTGPNGAGKS
TLLKIIMGMIEPTRGSISLPKKVGILRQNIDSFHDTTVLDCVIMGNTRLWEALQRRDNLY
LQEFTDAIGMELGEIEEIIGEENGYRADSEAEELLTGIGIPNEMFDKMAMIPIDLQFRV
LLCQALFGHPEALLLLDEPTNHLDLYSINWLGNFLKDYGGTVIVVSHDRHFLNTITTHIAD
IDYDTIIIYPGNYDDMVEMKTASREQEKADIKSKEKKISQLKEFVAKFGAGSRASQVOSR
LREIKKLQPQELKKSNIQRPYIRFPLSDKSSGKVVLSLEAITKDYGDHQVIHPFSLEIYQ
GDKLGIIGNNGLGKTTLMKLLAGVEAPSSGSIKLGHQAICSYFPQNHSDVLADCGQETLF
EWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGGETARLLMAGMMLENHNVLILD
EANNHLDDLESVSALSWAINDYKGTAIFVSHDRGLIQDCATKLLIFDKDKITFFDGTMVDY
TAGHKQLL

CPn_0024   37605   36661
xerC-Integrase/recombinase
REVMIASIYSFLDYLKMVKSASPHTLRNYCLDLNGLKIFLEERGNLAPSSPLQLATEKRK
VSELPFSLFTKEHVRMYIAKLIENGKAKRTIKRCLSSIKSFAHYCVIQKILLENPAETIH
GPRLPKELPSPMTYAOVEVLMATPDISKYHGLRDRCLMELFYSSGLRISEIVAVNKQDFD
LSTHLIRIRGKGKKERIIPVTSNAIQWIQIYLNHPDRKRLEKDPQAIFLNRFGRRISTRS
IDRSFQEYLRRSGLSGHITPHTIRHTIATHWLESGMDLKTIQALLGHSSLETTTVYTQVS
VKLKKQTHQEAHPHA

CPn_0025   38610   37684
elaC/atsA-Sulphohydrolase/Glycosulfatase
ILMSSRELIILGCSSQQPTRTPNQGAYLFRWNGEGLLFDPGECTQROFIFANIAPTTVNR
IFVSHFHGDHCLGLGSMLMRLNLDKVSHPIHCYYPASGKKYFDRLRYGTIYHETIQVVEH
PISEEGIVEDFGSFRIEAQRLQHQVDTLGWRITEPDTIKFLPKELESRCIRGLIIODLIR
DQEISIGGSTVYLSDVSYVRKGDSIAIIADTLPCOAAIDLAKNSCMMLCESTYLEQHRHL
AESHFHMTAKQAATLAKRAATQKLILTHFSARYLNLDDFYKEAGAVFPNVSVAQEYRSYP
FPKNPLLHK

CPn_0026   19637   18762
CT145 hypothetical protein
SNFAMGILLPSLIHEVTSYFHKPQPLKOAAPGKGIRGICNIAYLLIICVLVFFFLVGAML
CMFIISVGILFGLGGIALLVLLSIFNDCLIMWISTPKPTKEIAFKDASESQPTFSAGRKGS
IQLSIHHLHIEFKNFTRTOLEKGVNVVTNKFKSGEEGFHIIGDEHHGPRQGKGGGIEINGS
GGPIEIJPFAKGGKAMHTATTKEGGKPTTTEGGKKKKKTKIGGLIRTTGGIHKRGAPKPMVPGK
KHKIVGJLKKTVPLPIEDLGHQGGGNFGGSDGGGSPPIVQRKAILFWFGKQPTGGP

CPn_0027   4252   19778
Lon-Lom ATP-dependent Protease

PSIRTIVDSTTNSDSPILD.   .VEKLLDESEEESEDQSTERLLPSELFILFLNKRPFF
PGMAAPILIESGPYYEVLKVVLAKGGOKTIGLVLTKKENADILKVSFNQLHKTGVAARILR
IMPIECGSAQVLESIEERIRITIEPIKGKGTEKARVSTHADNKELTEELKAYSSTDVSYIKD
CLLKLNPLFKEELQIFLCHGDFTEFGKEADFSVALTTATREELQEVLETTNMHBRIDMALI
LLKKELDLSRLQSSINQKIEATITKSCKEFFLKEQLKTIKKELGLEKEDRAIDIEKFSER
LRKRHVPDYAMEVICDEIEKLCTLETSSAEYTVCRNYLDWLTIIPWGIQSKEYHDLKKAE
IVLNKDHYGLDEIKQRILELISVGKLSKGLKGSICLVGPPGVGVCKTSIGRSIAKVLHRKF
FRFSVGGMRDEAEIKGHRRTYIGAMPGKMVQALKQSQAMNPVIMIDEVDKIGASYHGDPA
  . . . .
  . . . .
LKIVGNQEKPKSKKITFKLGSKNLJTTLKNFIFSSJDRFYESTPVGVATGLAWTSLCGATL
YIESVQVSSLKTDMHLTGQAGEVMKESSGIAWTYLHSALHRYAPGYTFFPKSQVHIHPE
GATPKDGPSAGITMVTSLLSLLLETPVVNNLGMTGEITLTGRVLGVGGIREKLIAARRSR
LNILIFPEDNRRDYEELPAYLKTGLKIHFVSHYDDVLKVAFPKLK

CPn_0028   43328   42543
No robust homolog present in Genebank/EMBL as of 11/7/98
RMFLQFFHPIVFSDQSLSFLPYLCKSSGIIEKCSNIVEHYLHLGGDTSVIITGVSGATFL
SVDHALPISKSEKIIKILSYILILPLILALFIKIVLRIILFFKYRGLILDVKKEDLKKTL
TPDQENLSLPLPSPTTLKKIHALHILVRSGKTYNELIQEGFSFTKITDLGQAPSPKQDIG
FSYNSLLPNFYFHSLVSVNISGEERALNYHKEQQEEMAVKLKTMQACSFVFRSLHLPSM
QTKDKKAGFGLLTFFPWKIYPL

CPn_0029   43839   43390
No robust homolog present in Genebank/EMBL as of 11/7/98
SNKNERNENIYCFNLFRYIRFFAALNIRMNDGLRFCYSYILLRPMLLDSSLLRKGGOELL
KKFQIKLRTTSIKSSLISLRQQLGKREATQSDILYGTSRFQYLNSFEIEDPRIPPTMAAQ
LQEITWSRSVMELKIKFYVVLNSERNKTKP

CPn_0030   43840   44529
gcp-O-Sialoglycoprotein Endopeptidase
LKGVCWYSLFFYIKNRRMYFYKYVIIDTSGYYPFLACVDNQQVLEHWSLPVGPDLGIVLE
FLFKSKNLSFQGVAVALGPGNFSATRIGISFAQGLAMAKNVPLLGYSSLEGYLLSKDEKK
ALMLPGLKRGGVLTLSSEIPEEGLNEKRRGVGPGALLSYEEASDYCVAHGYYHVISPNPQ
LFASSFSDKITVEEVAPSVEQIRRHVISQFMFVEYDKQLSPDYRSYSCIF

CPn_0031   44708   44884
rs21-S21 Ribosomal Protein
CMPSVKVRVGEFVDRALRILKKKIDKEGILKAAKSHRFYDKPSVKKRAKSKAAAKYRSR

CPn_0032   44881   46098
dnaJ-Heat Shock Protein J
SLIGNVVFVGSVSGMDYYSILGISKTASAEEIKKAYRKLAVKYHPDKNPGDAAAEKRFKE
VSEAYEVLSDPQKRDSYDRFGHGDPFAGAGGFGGAGGMGNMEDALRTFMGAFGGEFGGGS
FFDGLFGGLGEAFGMRSDPAGAROGASKKVHINLTFEEAAHGVEKELVVSGYKSCETCSG
RSVHVHIPAGVDSGMRLKMEGYGDAGQGAPSGDLYVFIDVESHPVFERRGDDLILELPI
GFVDAALGHKKEIPTLLKTEGSCRLTVPEGIQSGTILKVRNQGFPNVHGKGRGDLLVRIS
VETPQNLSEEQKELLRTFASTEKAENFPKKRSFLDKIKGFFSDFTV

CPn_0033   46129   48171
pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha
& Beta Fusion
ERSMGVVQNQVISIRDVLKLVWELRFAEHKMLLLSRQSGSGGTFQLSCAGHELAGVLAG
KSLIPGKDWSFPYYRDQGFPIGLGCDLSEIFASFLARTTPNHSSARMMPYHYSHKKLRIC
CQSSVVGTQFLQAAGRAWAVKHSSADEVVYVSGGDGATSQGEFHEMLNFVALHQLPLITV
IQNNHWAISVPFEDQCGADLASLGRCHQGLAVYEVDGGNYTSLTETFSHAVDQARQHSVP
ALILIDVVRLSSHSNSDNQEKYRSALDLKLSMDKDPLILLEKEAINVFGLSPFEIEEIKA
EAQEEVRKSCEIAEALPFPSKGSTSHEVFSPYTETLIDYENSESAQNLRNSEPKVMRDAI
SEALVEEMTRDSGVIVFGEDVAGDKGGVFGVTRNLTRSFQPQRCFNSPLAEATIIGTAIG
MALDGIHKPVVEIQFADYIWPGINQLFSEASSIYYRSAGEWEVPLVIRAPSGGYIQGGPY
HSQSIEGFLAHCPGIKVAYPSNAADAKALLKAAIRDPNPVVFLEHKALYQRRIFSACPVF
SHDYVLPFGKAAIVHPGKDLTIVSWGMPLVLSLEVAQELASRGISIEVIDLRTMVPCDFA
TVLKSLEKTGRLLVIHEASEFCGFGSELVATMSEQGYAYLDAPIRRLGGLHAPVPYSKVL
ENEVLPHKESILQAAKSLAEF

CPn_0034   49496   48210
CT345 hypothetical protein
VNFLLPTTCRGILMAEISTPSLPDSSIVSQKTPPVPDPDSSPDHIPTIPTOAPFKPQRKK
ETPSSIVNAIAFAILAFLSCLGGVFAICLGCSLEITMPLFILTAVFIAFTLLYFIHYLEK
PKIPEPLPTPPPSPTLRAPTLTPEIPAPAPGIPLPPTLPKVDRTKLTCNPDIHYPSTYDP
KACFSLLKQLFSLDPETRPEDRKYSNKLASILLRSKEKSGFRFHCFKGHFSHDKILNKKS
GAVVISSHSSMDFSTTLGRAFAVTTCLQRSCWEKIKNNIPTPEKHLPIGSCVSGPWDVEE
GAQLYTSHLIVINPPTLETLIKEKMRRAITLKDFSMKEAFTNLVLAYLQCFDICIEHNLE
SVQLEVFGLNNLSADQEEFTTWESCCHLALLESVRILLASKEEYALSNVSVNSISQVPLQ
TACRALFLN

CPn_0035   51146   49569
CT339 hypothetical protein
ARTTLEEDAGSSLKPLPKTFPCATALYITHRRERKSEHQMWNRCQVFSSFFFRYPISSWL
IRLRASCECFQQRHPIFLCGLYWLAGITSRGHPECSALILIFLGMFLPRNPKQWLPLASA
WIISLMLTPAPFLHDGPISGTFVIHHAGGOGTYYGEALCIQTPCGKRAHHLSCQILSESR
LELKKVYELEGTLHHTSQIVFKSNACYKEIPRSRFYIMKEKCREGSCHFLNHRFPSSEVG
PFASSLLLCTPLPQNLRDLFROKGLSHLFAISGWHFSLCATTLWMLCALLPLKIKKILSF
IVLTSLACIFPMSLSVWRSWISVTLLCFSWCFCGSCSGLIRLGAGFILCGIFFSPPSPTF
VLSFLATLGILLFFPKIFSFLYTPWTQFLSPFWLYPIRYLAMTLAISLSAOLFIVLPIMQ
YFGSLPLEGLLYNLIVPFTILPIIVFLIATIILPCCSPITEALIQGFLSHPWLHNPNILK
TLSFAPVPPWMLTLAGLILFFIGILRTHVSPYASISATSYRFIETL

CPn_0036   50969   51795
CT338 hypothetical protein
AKSLWGGGERKKMFKPDNDSTFDVRSFFPFDVLCIEQLPKEMGWFVVGAKIFRLPRGWEL
MGLGKEDRIDFGLDFWGGVUGIEHKESPSICRFFGLLETIEVYIYRLEKEPYOLKMFVVF
KOFGRSGFGGEDFGLPDFLGSHGLRLPFLGDRHYEKFFSIHFGFGKWEDEGIFIMRGGLAKVGQK
LPLQLVVMNKMGAEDNKVGGGSGFFPFYGYEEPFAVOGFFPDPEIRRLGGGI4FYLLNEEGGLE
HIGGLETIELLGILGEGGYYPGFLGWLFNYLISGEEVYNE

CPn_0037   51702   52115
prsA-Phosphoribosyl Protein Hpr
KILGAYCGGLRALILLCGGRAWTIYIVPPCIMNEPTRTYLEGEKDTQDUIEELGANGIYKN
AAGGIHVPDAVIVIRLFIGEDIGVHIFTYAGKTIHAKSIMSIIHULAPGYGEILVTIRGGYEA

HR ILQK IODAFSSGFGEL

CPn_0038   52117   53831
CT318 hypothetical protein
MCTQSSTGNEEWR IAGTG IVSGMALGCKVFFLGTSPLHVRELTLPQEEVEHEIHRYYKALN
RSKIDIVALEQEVTKCCGLQEVSSILQAHLEIMKDPLLTEEVVNTIRKDRKNAEYVFSSV
MGKIEEGLTAVRGMPGVGDRVQDIHDISNRVIGHLCCGHKSSLGESDONLIIFSEELTPS
EVASANGAYIRGFVGLVGAATGHTAIVSRAKSIPYLANISEELWNIAKRYNCKLVLIDGY
...
RSIRWLLDYGVILEDQLQAIAKASLQGSIKVLIFGVSDVSEIIEVKKKWETIRTRFPKGH
KVSWGTHIEFPSAVWMIEEILPECDFLSIGTNDLVQYTLGISRESALPKHLNVTLPPAVI
RMIHHVLQAAKQNQVPVSICGEAAGQLSLTPLFIGLGVQELSVAMPVINRLRNHIALLEL
NCCLEITEALLQAKTCSEVEELLNRNNKITS

CPn_0039   54256   53963
CT319 hypothetical protein
ISMGSGYAKKKKEAKIMEQQFLEMEASLLEKRYEGQAGNGLVSVVINGKCDLISVKVQPT
CLDPEDPEVIEDLFRAAFKLAKEQMDQEMSLMRSTMPF

CPn_0040   55673   54318
dnaX-DNA Pol III Gamma and Tau
AFYTHSLGYTHTLQPYQASSRKYRPQIFREILGQSSVVAVLKNALVLFNRAAHAYLFSGIR
GTGKTTLARILAKALNCVHLSEDGEPCNQCFSCKEIASGSSLDVLEIDGASHRGIEDIRQ
INETVLFTPVKAKFKIYIIDEVHMLTKEAFNALLKTLEEPPQHVKFFFATTEIHKIPGTI
LSRCQKMHLQRIPEKTILEKLSLMAQDDHIEASQEALAPIARAAQGSLRDAESLYDYVIS
LFPKSLSPDTVAQALGFASQDSLRTLDNAILQRDYATALGIVTDFLNSGVAPVTFLHDLT
LFYRNLLLTNSTTSKFSSQYKTEQLLEIIDFLGESAKHLQNTIFEQTFLETVIIHIIRIY
QRPVLSELISSIKSRQFEGLRNIKEPTLTQQVSAPQPQPTYKEQSFLEKKNQPAAEGKII
SVEVKSSASIKSAAVDTLLQFAVVEFSGILRQ

CPn_0041   55888   57342
No robust homolog present in Genebank/EMBL as of 11/7/98
CKYLYHHSYPPPOHSVGSISSRYKLRVLAITFLVLGVLLLISGALFLTLGIPGLTAGVSF
GLGIGLSALGGVLVVSGLLCLLVKREVSKVCPEEIPAVQPEETPEGVPVTPFEKPALDEA
QKEQKTOKILDQLPOELDQLDRYIQEAFACLGPLKDLKYEDQGFLQDVKEEFQVFDFVQK
DMIAEFVELQQILCQEGRLLEFVINQTRYIGRDLFKREDSLYKLWEWLGYLPSGDVRGER
LKKSAREVVDRFMRTTCNIRKIAMTFDRHVYSVAKTAFEKAFGALETCVYESHRESYREA
FCEYEKAKLLGDEEKSAHAEQRFQDIKNRWEDVKDAFFWVKEDGKIEIDDAIGNSCKWSE
PYEEHRITRARWYKVAEHOLFNATMRVKDSLREHNEARVAFEKERSKENQRQVQKKKEKR
LRDLKELHDQELPRAQERLRELQALYPEIAVSVVEARREVASDLEKAHESIDKHYQSCVR
EQELY

CPn_0042   57346   58182
No robust homolog present in Genebank/EMBL as of 11/7/98
EEEEKQEAEFRENGTKIRSMEEVSEYLQQVENQLESCSKRLTKMETFALGVRLEAKEEIE
SIILSDVVNRFEVLCRDIEDMLSRVEEIERMLRMAELPLLPIKEALTKAFVQHVKASPLT
TKVEPYFKESPAYLTSEERLQSLNQTLQRAYKESQKVSGLESEVRACREQLKDQVRQFET
QGVSLIKEEILFVTSTFRTKFSYHSFRLHVPCMRLYEEYYDDIDLERTRARWMAMSERYR
DAFQAFQEMLKEGLVEEAQALRETEYWLYREERKSKKKH

CPn_0043   58432   60372
No robust homolog present in Genebank/EMBL as of 11/7/98
HHRFIMQVPLSPQLPPPPPDHSVGASFCLSKFRVLAITFLVLGVLLLISGALFLTLGISG
VSLGVGLGLSALGSVLVISGFLLLLERREVSGVGLEGIPTGIPVGPSAEPSSEEIQKKQK
AKQILDQLPQELDQLDTDIQHVLSCLGKLKDLKCKDRGLLKDAKEKLQVFDFVWKDMMHE
FVELQQVMDQESRYLEGLIHEVQSIAHKLFVDDVRNSHLGESCCGYLPSGDVRGERSLLKRF
AKEVVVARFMKVTRDIRKIAMAFNKNAYGAAKNAFDKAFGSLETCLYKSLTKSYRDTFCDY
KRAKILPDENNSARAEQRFREVKDHWEDLKETVFWVKEDGRIDIEVLTAVGGWPDRYPEH
LILEKRKDKVMSHQLWEATMRVKEAEVTYSVARVAFEKDGSGQNQKKFQEKTKERLRCLK
DLRDQECHRAQERLEKLTALYPEVSVSVVETEREBKFNLEKAYGNLEERYQSVVQDQEDY
WTEQKNREAEFRAKGTKVRSMEEVAEHLQILENLLEDCYKRLSKAETFALGVEREATEEI
EYTILSDAANRLKVLCEDIEDTLPRVEEIEMMLRMAERPLHPIKQAFTKAFVQYNRCKER
LAKVEPYYKESPAYVNSEERLQSLDQASQCIQRVPKGFKFRNGSMYI

CPn_0044   60278   60778
No robust homolog present in Genebank/EMBL as of 11/7/98
IAKSDCRVWIRLHSAYKESQKVSSLETEACTYREYLREQVQQFETQGVSLIKEELLFLSS
TLKSKLSYDPLIANIPCMKFYYCYYDDIDKARAQSRWLEKSERYRNAKRRFQEIVKKGLF
KEAKPLKKEEYRLLQEERSNKEKRLIYNKMAVARQRVQEFESMEIPE

CPn_0045   60961   62790
CT345 hypothetical protein
CKYTYHPPQLPPDHSVGATSWQPKLRILTITFLVLGVLLLISGALFLTLGVPGLAAGLSF
GLGIGLSALGGVLVVSGLLFLIRRGVSKVRPEEIPVTPSHEAQKILCQLPQELDQLDTS
IQEVVSCLGCKLKDLKYEDQGLLTEVQEKLRVFDFVRKDMVTEFLELQQVVAQEGQFLDYL
INQVQSISHKLFVPDVNIGAHLAELCGYLPSGDVRVERLKRSARQVVDRFMRVTCDTRKV
AMAFDENACGVAKNAFDKAFGALEECVYKSLTESYPEAFYEYKAIAVENAEDVEWLQDKN
KSARAEQRFREVKDRWEDLKETVFWVKENGCIDLEVLTAVGGWPDRGPEHLIPEKRRNKV
MSHKLWEATMRMKGAEGTYSVARVAFEKDGSRKNQKFQEKTKEWLRCLRDQECHRA
RERLAELEALYPEVSVSVVETERETKFKFLETAYGNLEERYQSVVRDQEDYWKEEENKEAE
FREKGTKVRSPEEVVEYLQILENLSEDCSKQLTIAEFVVLGVELEATAEFEYTILSDAAN
RLKVLCEDIEDILPRVEEIEIMLRIAELPFLPIKQAFTKAFLQYNSCKDKLAKVEPYCQE
SVDYKSGFRV

CPn_0046   62775   63263
No robust homolog present in Genebank/EMBL as of 11/7/98
ERFQSLNQDLQNVYQECQKATGLESEVSAYRDHLREGITEFETQGLVSLIKEELLFVSSTL
KSKLSYDPLIADIPCMKFYEEYDGIDKARVQSRWLEKSERYRKAKKGFQEMLKEGLFKE
DQALKKAEYRLLREKRMNKEKLLICNKIEAAQXRVQEFGPGDG

CPn_0047   63147   63652
No robust homolog present in Genebank/EMBL as of 11/7/98
FHFHLKVTIVGFFRFVLKGILTHYHFQKIRMTLTTGFVLHKCLRKDYELWFVYGGCPES
KVKIVFGGHEWL

CPn_0048   63687   65801
tyrlP Tri conserved hypothetical IM protein
MKELPHFGYNRLAIIKLGIGWVRYFLYTVGCGFIVAIFTFAWLKVLYVPEYKAGEISRIS
LPAFHDFGSGWGAIHKFYKRTAHIGEAFGKVYHLPLGFGGLLGKIPINADENTDYWFKKAAD
FLLGTHFVIGGPGRGTLKDLGIVPPLLGKEKKTLEIHIGGNKGNVIAQGFCHLKIFLIQEN

CPQPCFDAIHDILKIAHFEV   IEMSGCVKGELLGKRCIEKITYGTPILEKYQRIDDRG
AKILKQLRAQLLGVHTLFSCRGLWGAIFVVLLIGLWGYGALKALCPEMLKSPQRFHLYIA
ILTLGLLWCPGTEIEYAVWVGYLGYPRGLPFTAVLLGYFLGLPIAGFGCTFLALLYTLGS
DLWNNSWFLSINELCGWRIDVSLHRVSRLSSVFWAGMKLDGVAMCSELRFRILMTISRE
ALYACGIESFVYSLITAISVVALIPVFEASFGASTNFSLLTYLSPENALLKRLFKEAPGT
YQHSVLVGSLAEAAAQAIGADSLYCLVAAHYHDIGKLINFGFFSENQKILQQSGHSLSPL
ECAKMIMRHIPEGVVLAROAGLPESFIQVIEEHHGTSVIRSAYYSHMVENPSTGSFDEEL
FRYSGNKPSSKETTIIMIADSFEAASRSLKNASLPDLQRLIDQIIQGKLQDCQFSCSPIT
...

CPn_0049   66502   65817
No robust homolog present in Genebank/EMBL as of 11/7/98
LKEKRRNIVYLLVIYQEIFWLTMLHQPYYDKILTGNTIYIPGHTHKDSNKLFQKKSRAIW
VDEKPFSLDCFSNVFLIFVSLVPIAGLVRAYQIKKSLDRTTVQIGYSPSLSCEQKECVEA
FVNGYGLICISILGGLGILVPILILVVLSLLLLGILMLFSLSTYESIKNYISKHICWKSN
AT

CPn_0050   66849   66499
No robust homolog present in Genebank/EMBL as of 11/7/98
VSWFPILGIFLAMRYAKHQTNWNDENVKANLGYLPSTNCKNALCRMSSRLTSSIKTAGIL
GGCGILLPIFLLLLAILLISVLFQLIMLPFRLCCFALRQSVSSDTVTNLLLLNNTLA

CPn_0051   66797   67111
No robust homolog present in Genebank/EMBL as of 11/7/98
CFAYLIARNIPRMGNHETYIHPGVLPSSHAQDVSRSTVYPSRSFIMRRMLMGWNFNRVPS
KSSEQLMDGHRIPLIFFGKHHPTISILNVNRFSWLSIFYNGERGF

CPn_0052   68008   67304
hemC-Porphobilinogen Deaminase
KMLSVCYSDPCLSDFCQGKRPLRIASRNSNLAKAQVHECISLLRSWYPKLWFQLSTTETT
GDREKKIPLHLVENSYFFTDGVDALVHKGVCDLAIHSAKDLPETPSLFVVAITRCLHPAD
LLVYADHYVHEPLPLSPRLGSSSLRRSAVLKQLFPQGQILDIRGTIEERLDQLHRGHYDA
IVLAKAASLRLHLHHAYSIELPPPYHALQGSLAITAKDHAGKWKQLFTPIHCHSS

CPn_0053   69350   67986
sms-Sms Protein
IRMATKTKTQWTCNQCGATAPKWLGQCPGCHNWNSLVEEYVPQARSGTSSRSSTSAIALS
SIELENESRIFIDHAGWDRILGGGVVRGSLTLLGGDPGIGKSTLLLQTAERLASQKYKVL
YVCGEESVTGTSLRAKRLNISSPLIYLFPETNLDNIKQQIATLEPDLIIDSIQIIFNPT
LNSAPGSVAQVREVTYELMQIAKSAQITTFIIGHVTKSGEIAGPRVLEHLVDTVLYFEGN
SHANYRMIRSVKNRFGPTNELLILSMHADGLKEVSNPSGLFLQEKTGPTTGSMIIPIIEG
SGALLIELQALVSSSPFANPVRKTAGFDPNRFSLLLAVLEKRAQVKLFTMDVFLSITGGL
KIIEPAADLGALLAVASSLYNRLLPNNSIVIGEVGLGGEIRHVAHLERRIKEGKLMGFEG
AILPEGQISSLPKEIRENFRLQGVKTIKDAIRLLL

CPn_0054   70089   69313
rnc-Ribonuclease III
TLSFFPPIKIPNSKFKDGALLSMHHPPIDITAIEAKLNFTFTQPKLLEIALTHPSYKNESA
VQIEDSERLEFLGDAVLGLIVTEHLFLLFPSMDEGTLSTARASLVNAKACCRYTTMLGIG
DYLLIGKGKEKIQSERGRLSAYANLFESILGAVYLDGGLSPARKLTVPLLPPREEILPLMS
GNPKNLLQQFTQKQFRVLPVYQSTAVTDAQGNVSYQIQVLVNQEVWGEGNASSKKEAEKI
AAQQALDTYGNKNQNTMDV

CPn_0055   70096   70590
CT296 hypothetical protein
CFWICYLIRIRMRSALHLQHLRHFHNHGSILFENLLTIKDCFLLETKLQNFIAKASKTID
TVRWRENIFRSMPEIYTVVRKRRLDFFAAELVHRPKLSLVRDLWVFPGEEILEGEEDCHL
FLLLSGDRAGSGIFFTGPYPSDLYELEKGTTGLLLAFSSVGIPVI

CPn_0056   70917   72746
mrsA-Phosphomannomutase
EFLKLSLHRISLMKEVEQRIRSLYDAVTAENICRWLSNDCTQQDAKTILGWLDTDPAQLE
DLFGATLTFGTGGLRSLMGIGTNRINLFTIRRTTQGLVQVLRAHLPHFGDPMRVVVGCDT
RHNSIEFAQETAKVLAGNGCEVFLFQYPEPLALVSFTVRYERAIGGVMITASHNPPNYNG
YKVYMASGGQVLPPLDQEIVAACSAVNEILSVPSIDHPNIHLIGKEYEALYRDTLKQLQL
YPEANRISGRSLSISYSPLHGTGISLVPHVLKDWGFLSVHLVEKOAIGDGDFPTVQLPNP
EDPEALTLGIEQMLANDDDLFIATDPDADRVGVVCLEDGOPYRFNGNQMASLLADHILGA
WSKTRHLGEHDKLVKSLVTTEMLSAIAKHYHVDLINVGTGFKYIGEKIESWRNSTNKFVF
GAEESYGCLYGTHVEDKDAIIASALIAEAALQQKLQGKTLCDALLSLYETYGYFANKTES
VVFSAKTDEQEIRKKLSHLEEISSANFFSGKYQVEKFENYKQGIGFNLLSKDSYALTLPK
TSMLCYYFSGGGRVIIRPSGTEPKIKFYFEMSTHYPERVTDKEIQKQREAESFQHLDDFI
FDFKEKFSNL

CPn_0057   72913   73554
sodM-Superoxide Dismutase (Mn)
ILKRYVVMSFVPYSLPELPYDYDALEPVYISSEIMILHHQKHHQIYINNLNAALKRLDAAE
TQQNLNELIALEPALRFNGGGHINHSLFWETLAPIDQGGGQPPKHELLSLIERFWGTMDN
FLKKLIEVAAGVQGSGWAWLGFCPAKQELVLQATANQDPLEPLTGKLPLLGVDVWEHAYY
LQYKNVPMDVLKAFFQIINWCHIENRFSEIISSK

CPn_0058   73627   74562
accD-AcCoA Carboxylase/Transferase Beta
IRWLVRLFSYDKPKIKVQKIKADGFSGWLKCNHCHEMIHANELGQNYNCCPKCSYHYRIT
AIERVKLLADKDSWRPLYTDLKSQDPLEFIDTDTYANRLEKARKNTTESEGVIVGICTIG
LHPVALAVMDFNFMAQSMGAVVGEKLTPLIEEAIETRLPVIIVSASGGARMQESVFSLMQ
MVKTSAALAKLHEAGLPYISVLTNPTSGGVTASFAALGDIIIAEPKALICFAGPRVVAQV
IGEDLPEGAQKSEFLLEHGMIDKIVERKELKTTLQTLLDYFLAQEYTGCKSKAPRDLSKR
LKEIFLLTDDSE

CPn_0059   74562   75050
dut-dUTP Nucleot idohydrolase
IKHHTANCNDNIICNAILMTVFCELDGCGELPEYTTPGAAGADLRANIEEPIALLNYQRA
LIPTGIYAEIPEGYELQVRPRSGLALKHGITVLGPGTIGCDYRGEIRVILNRGDSTPFI
IEPKMPIAQVVLGIVVGATFVVKQESLAETARGGGFGHTCAS

CPn_0060   75004   75528
ptsN-PTS IIA Protein
PKLPEEVEVLVILGIAAKMPSYCQHQQLFSLFGLLGPRLVMFLGKIGRDEILQDLTPLVDA
AGLLEDKQAFFDALVRRENIMGTGIGMGVAIGIGKLESGGRIFFIAIGIIFGILWIWIDI
ALVRLVFLICGPENAQAEYLKLLSTLTLCLRRESRRQQILLGVNTIEEVMNVFVGW

CPn_0061   75501   76209
pcnN-PTL IIA Protein + HTH DNA-Binding Domain
RCHECICXDVKMDLKLDEVASLLDVCEHTVLQWLKEGAIPSYSMNNEYRFSREEIENWLL
HNQALMIQERCEDKEALKDLSLKYSLYKAIHRGGVLCDVVVHSKEEEALQYASKYIAQKFQ
LDESVLFEMLCHPEHLMCTGIGECIALPHAKDFLINAYYDIVVPMFLAEPIEYGALDGKP
VGILFFLFACQDKCHLNLVNKIVHLGHSLNARSFFKNYPNKDQLLAYVKEWESQTH

CPn_0062   76251   77690
EVVKKPQKGSERKQAKKEPRARKGYLVPSSRTLSARAJKMKNSSRKESSGCCNEISANST
PRSVKLRRNKRAEQKAAKQGFSAFSNLTLKSLLPKLPSKQKTSIHEREKATSRFVNESQL
SSARRKRYCTPSSAAPSLFLETEIVRAPVERTKELQDNEIHIPVVQVQTNPKEQNTKTTKQ
LASQASIQQSEGTEOSLRELAQGASLPVLVRSNPEVSVQRQKEELLKELVAERROCKRKS
VRQALEARSLTKKVARGGSVTSTLRYDPEKAAEIKSRRNCKVSPEAREQKYSSCKRDARA
NGKQDKTTPSEDASQEEQQTGAGLVRKTPKSQVASNAQNFYRNSKNTNIDSYLTANQYSC
SSEETDWPCSSCVSKRRTHNSISVCTMVVTVIAMIVGALIIANATESQTTSDPTPPTPTP

CPn_0063   78109   78267
No robust homolog present in Genebank/EMBL as of 11/7/98
PMYANCKHNCLCLYDFSRHRSPPGLPLTFTPPYSFTLGIFLGRCLSTSNIVLL

CPn_0064   78340   78576
No robust homolog present in Genebank/EMBL as of 11/7/98
LVMHTKIQCSAQYYRSRPAERAQTPPQPFLARDRADFWERHPRFSACCRVLLLVAWVVLAL
LFLFVMLLPLAAGSYLLAF

CPn_0065   78882   80651
CT288 hypothetical protein
YDYYKYNMFFKKNYMTDFPTHFKGPKLNPIKVNPNFFERNPKVARVLQITAVVLGIIALL
SGIVLIIGTPLGAPISHILCGCLLASGGALFVGGTIATILQARNSYKKAVNQKKLSEPLM
ERPELKALDYSLDLKEVWDLHHSVVKHLKKLDLNLSKTQREVLNQIKIDDEGPSLGECAA
MISENYDACLKMIAYREELLKEQTQYQETRFNQNLTHRNKVLLSILSRITTDNISKAGGVF
SLKFSTLSSRMSRIHTTTTVILALSAVVSVMVVAALIPGGILALPILLAVAISAGVIVTG
LSYLVRQILSNTKRNRQDFYKDFVKNVDIELLNQTVTLQRFLFEMLKGVLKEEEEVSLEG
QDWYTQYITNAPIEKRLIEEIRVTYKEIDAQTKKMKTDLEFLENEVRSGRLSVASPSEDP
SETPIFTQGKEFAKLRRQTSQNISTIYGPDNENIDPEFSLPWMPKKEEEIDHSLEPVTKL
EPGSREELLLVEGVNPTLRELNMRIALLQQQLSSVRKWRHPRGEHYGNVIYSDTELDRIQ
MLEGAFYNHLREAQEEITQSLGDLVDIQNRILGIIVEGDSDSRTEEEPQE

CPn_0066   80916   82655
No robust homolog present in Genebank/EMBL as of 11/7/98
GVYMANPTQSRPPSPEISIEEELEQELAGSSNTETISNTPPPSCAATAEEVSLFIEGGRR
NSEDEEEGPLGSCEVYDVVCITNQGDPEVRDHEVRVMYINGSGRTQHEGILDAMNICDLRG
EPVRFIHNSGYGLGSCFLGIRNRIPPRDNVISQAIQARWNEFFIFAENANRDYIVLFSGN
GGLYLQVALDNSIYSHHILCVGIGSSYYIQGNYRVHNYRVTGDWTTLLDRRGATAVNTTT
LPYADSAEGLFLPSVRCPSYQWALRCGEQCLIMDNNQQVGFRPQDSSSEIALVNLNQDH
STWTRLIEWIDRGDSQAVLELNPQPSHCRDIALTALYATTRISSLLQECLMISVTYAPEV
FVTYAIVTGYSIHTLRYFILLLTNRPGCRRHFRVLRLAALGLQSLGFLTVLLDHINVTRR
VNRRPPLISVIFCTASFATGSFIYVDLTRMFFTSLRSRLQLFVQRRLTGRGLPLRRVFVN
HLDSLRFSQNALITFHGGLFMPLIIGFFNQLVIQVPRVVIRPNTTAVYDLNQTSQEAWDS
GDVLAIGQTINFLLCMILLVINTFFFVRSVRRNLHRRPHR

CPn_0067   82920   84053
No robust homolog present in Genebank/EMBL as of 11/7/98
KGSGYSYRGPPMAVEGRVNSSQALNQDCQEVLANKQSKGLLRCRILSIVVAVITFIAGVV
LIALTLASILTSVPYLALGVFLLIVTLGCIIFALCSEKIKKVPPTPISHKEEIIAWFEER
KNIDMEKEKEDPEHFGRTATDIPMRSALDQFNHSCHHIHESPALTETYRSHQDVLLFKDW
CPVTLPDVTSEEEVLIRSVVGSYLLMEACVPKVSMLIDELHNKLKSPSERECLFIDKKTL
QRKASFLFTQKDLATFFLAYTRVNDGHLAPFRAGAKWILIHYVRLRRQHNQNDFFTPGHS
CYYARLAFNQTQRLYHQLFNVEKLRSIYANMDKDPLCHPWAFIPIYDLLKTEDHGDGFLE
QQEDREYPSRAAQDQFWG

CPn_0068   84909   84331
CT360 hypothetical protein
SFMIKKFFIYSLIFSCSFSAPLKGICNEDVSSQSRIEEDPEVLITQLNELIETPIEEGKE
IRNELQAISDGQKSSEEIEESCGTSDSEGLSEKTDKESSNEYVLDFFDSMVQRLEGISKM
CQSGQVAQIIDCFNREFDIRNRELELKNRELELREKDLEFKKSILDWNKEKVSRELAFQR
EQDIKQTLMLLKK

CPn_0069   85191   87086
No robust homolog present in Genebank/EMBL as of 11/7/98
LNFLYVYLLIFNLGIMTTPPPSRSSSPPPYDWIELQDLQNTNNNSSRATPPPPEVGGELP
PYFSASNFVVIERGAPSLPSPQQLLSLPEYSRQPPPGYFDETASITSRTSEEMFGTLVST
LCCPANSERDWDHEVNCIYIASTSDTQLEAVQQGMHITELRGEPVRVLYETGHLYAFAR
ENTCHSRLEVSHTVRAMTYFWDRFFSRHWNVGRRFLVFYQGNGGAYVQAALDSSMHTQDI
YVLGLSPTVYIRGNYHVQHYRVRGFWPSCLDSLAACAENTSVLPYGESSDGIFYPSLFSH
TFDNAIRYGERCLLVCSEGMGMLPETQQQTSPLTSLEGGHEVALVLNPQQNPEALSIASR
LMHEERGGRLESNYMPGRSSNPFMTSMYVLVRLNTLAQIYLMSPYYSFQSNDIVCLIFIS
GAAVETVGYIFLTVTDSTCGRRYLRVPRLVCTGLRNLALPTTLLELLILSYPRSVEGVPF
MVRFILGYMCTTRVVFFAWNLILHWPFRCLRHGIQLFVHRSIIGHTLGARITDLTLASMR
YAIVFPGIVVSCLLTALAHANTNILALDPYRLIESGDLRRPAFNDDEMQQADNPWDAYSI
GLVINTCIYMLILFANLIFMVYSVRRYHRSRR

CPn_0070   87399   87208
Nr robust homolog present in Genebank/EMBL as of 11/7/98
YKVGLFIHLKNQNFFSNQSRTYEQRFPKVSPHFESILPLQSVGFSSQGTLLISFRDTELKR
GLYI

CPn_0071   88066   87599
CT325 hypothetical protein
IKCLLRCILEFICPLQHARCLKKQHKIIEELFPEPFGFDHLYLKLMENSSSRDAFDKKRML
FEHLVVKXQCDLYLYEVYQQGILFFFTYTKALMCCGIASLFTEVYSGETPSTILTCKPIF
FQRLTCYLCFCRLXXIESLYHRMKQIAVQYLKFPCT

CPn_0072   88151   88057
CT324 hypothetical protein
MYHHTCHVKVKLILLYCLLFYFFHYPMCTPLCCCGISPSDQYVPQELFCDRLSSSR
CRCPUXHACDCPIVCPPIHSALVALTDLKLVPYNQHGFSWTTRLKNAVEKICLFLQRNWK
FILLYIIAWALIIVCHITVALTLTIWLCVCLGIGVVFGIFTATCLDKENKHRHVNSLWNL
INIKIIDDLPHTTRQILLATMIASIIALIYAVPQAVGLVIGFSICNQLSINTVYGARLGD

EATYAIDRKAHKKPIENIE   CHQIIKHLMINQKQLNALIEINRNNCTDPATANLLAS
LKLNLNQPMPYCFCMPECGVISGYLDLNRHGFCDIIARADCCIMTLGCTLQQIKKKEPDRI
IEGNH

CPn_0073   89353   89574
infA-Initiation Factor IF-1
SMAKKEDTLVLEGKIEELLPGMHFRVILENGMPVTAHLCGKMRMGNIRLLVGDRVTVEHS
AYDLTKARVVYRHR   89767

CPn_0074
tufA-Elongation Factor Tu
EDFEMSKETFQRNKPHINIGTIGHVDHGKTTLTAAITRALSGDGLASFRDYSSIDNTPEE
KARGITINASHVEYETPNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSATDGAMPQT
KEHILLARQVGVPYIVVFLNKVDMISQEDAEIIDLVEMELSELLEEKCYKGCPIIRGSAL
KALEGDANYIEKVRELHQAVDDNIPTPEREIDKPFLMPIEDVFSISGRGTVVTGRIERGI
VKVSDKVQLVGLGETKETIVTGVEMFRKELPEGRAGENVGLLLRGIGKNDVERGHVVCQP
NSVKPHTKFKSAVYVLQKEEGCRHKPFFSGYRPQFFFRTTDVTGVVTLPEGTEMVMPGDN
VELDVELIGTVALEEGMRFAIREGGRTIGAGTISKINA

CPn_0075   91087   91350
secE-preprotein translocase
SRSWFHKQQHNRKALSRKIGTVKKQAKFAGSFLDEIKKIEWVSKHDLKKYIKVVLISIFG
FGFAIYFVDLVLRKSITCLDGITTFLFG

CPn_0076   91334   91903
nusG-Transcriptional Antitermination
QPFCSVNCMYKWYVVQVFTAQEKKVKKALEDFKESSGMTDFIQEIILPIENVMEVKKGEH
KVVEKYIWPGYLLVKMHLTDESWLYVKSTAGIVEFLGGGVPVALSEDEVRSILTDIEEKK
SGVVQKHQFEVGSRVKINDGVFVNFIGMVSEVFHDKGRLSVMVSIFGRETRVDDLEFWQV
EEVAPGQESE

CPn_0077   91956   92435
rlII-L11 Ribosomal Protein
FFVSVPLFVEVSQCKVRFSMSVKKVIKIIKLQIPGGKANPAPPIGPALGAAGVNIMGFCK
EFNAATQDKPGDLLPVVITVYADKTFTFITKQPPVSSLIKKTLNLESGSKIPNRNKVGKL
TQAQVEAIAEQKMKDMDIVLLESAKRMVEGTARSMGIDVE

CPn_0078   92453   93160
rll-L1 Ribosomal Protein
SCRIMTKHGKRIRGILKNYDFSKSYSLREAIDILKQCPPVRFDQTVDVSIKLGIDPKKSD
QQIRGAVFLPNGTGKTLRILVFASGNKVKEAVEAGADFMGSDDLVEKIKSGWLEFDVAVA
TPDMMREVGKLGKVLGPRNLMPTPKTGTVTTDVAKAISELRKGKIEFKADRAGVCNVGVG
KLSFESSQIKENIEALSSALIKAKPPAAKGQYLVSFTISSTMGPGISIDTRELMAS

CPn_0079   93170   93688
rl10-L10 Ribosomal Protein
RGKMKQEKTLLLQEVEDKISAAQGFILLRYLRFTAAYSREFRNSLSGVSAEFEVLKKRIF
FKAIEAAGLEVDCSDTGHLGVVFSCGDPVSAAKQVLDFNKQHKDSLVFLAGRMDNASLS
GAEVEAVAKLPSLKELRQQVVGLFAAPMSQVVGIMNSVLSGVISCVDQKAGKN

CPn_0080   93720   94121
r17-L7/L12 Ribosomal Protein
VRVTKVTTESLETLVEKLSNLTVLELSQLKKLLEEKWDVTASAPVVAVAAGGGGEAPVAA
EPTEFAVTLEDVPADKKIGVLKVVREVTGLALKEAKEMTEGLPKTVKEKTSKSDAEDTVK
KLQDAGAKASFKGL

CPn_0081   94219   98016
rpoB-RNA Polymerase Beta
FREILSHONSRRTRMLKCPERVSVKKKEDIPDLPNLIEIQIKSYKQFLQIGKLAEERENI
GLEEVFREIFPIKSYNEATVLEYLSYNLGVPKYSPEECIRRGITYSVTLKVRFRLTDETG
IKEEEVYHGTIPLMTDKGTFIINGAERVVVSQVHRSPGINFEQEKHSKGNILFSFRIIPY
RGSWLEAIFDINDLIYIHIDRKKRRRKILAITFIRALGYSSDADIIEEFFTIGESSLRSE
KDFALLVGRILADNIIDEASSLVYGKAGEKLSTAMLKRMLDAGIASVKIAVDADENHPII
KMLAKDPTDSYEAALKDFYRRLRPGEPATLANARSTIMRLFFDPKRYNLGRVGRYKLNRK
LGFSIDDEALSQVTLRKEDVIGALKYLIRLKMGDEKACVDDIDHLANRRVRSVGELIQNQ
CRSGLARMEKIVRERMNLFDFSSDTLTPGKVVSAKGLASVLKDFFGRSQLSQFMDQTNPV
AELTHKRRLSALGPGGLNRERAGFEVRDVHASHYGRICPIETPEGPNIGLITSLSSFAKI
NEFGFIETPYRIVRDGIVTDEIEYMTADVEEECVIAQASASLDEYNMFTEPVCWVRYAGE
AFEADTSVTHMDVSPKQLVSIVTGLIPFLEHDDANRALMGSNMQRQAVPLLKTEAPVVG
TGLECRAAKDSGAIVVAEEDGVVDFVDGYKVVVAAKHNPTIKRTYHLKKFLRSNSGTCIN
QQPLCAVGDVITKGDVIADGPATDRGELALGKNVLVAFMPWYGYNFEDAIIISEKLIRED
AYTSIYIEEFELTARDTKLGKEEITRDIPNVSDEVLANLGEDGIIRIGAEVKPGDILVGK
ITPKSETELAPEERLLRAIFGEKAUDVKDASLTVPPIGLITSLASKSDDE
LVEEAVHLKDLQKGYKNQVATLKTEYREKLGALLLNEKAPAAIIHRRTAEIVVHEGLLFD
QETIERIEQEDLVDLLMPNCEMYEVEVLKGLLSEDYEATALQRLEINYKTEVHRMRNNRKL
GVIROVKVYVASKRKLQVGDKMAGRHGNKGVVSKIVPEADMPYLSNGETVQMILNPLGVP
SRMNLGQVLETHLGYAAKTAGIYVKTPVFEGFPEQRIWDMMIEQGLPEDGKSFLYDGKTG
ERFDNKVVIGYIYHLKLSHLIADKIHARSIGPYSLVTQQPLGGKAQMGQQRFGEMEVWAL
EAYGVAHMLQEILTVKSDDVSGRTRIYESIVKGENLLRSGTPESFNVLIKEMQGLGLGVR
PMVVDA

CPn_0082   97992   102221
rpoC-RNA Polymerase Beta'
CSSYGRRRLKNDVLEKIMFGENSRDIGVLSKEGLFDKLEIGIASDITIRDKWSCGEIKKP
ETINYRTFKPEKGCLFCEKIFGPTKDWECCCGKYKKIKHKGIVCDRCGVEVTLSKVRRER
MAHIELAVPIVHIWFFKTTPSRIGNVLGHTACDLERVTYYEEYVVIDPGKTDLTKKQLLN
DAQYREVVEKWGKDAFVAKMCGEAIYDLLKSEDLQSLLKDLKERLRKTKSCQARMKLAKR
LKIIEGFVSSVTRGVKTRGDLLMPNCEMYEVEVLKGLLSEDYEATALQRLEINYKTEK..
AILRLKTPEVIVRNEKRMLQEAVDALFDNGRHGHPVMCAGNRPLKSLSEMLKGKNGRFRQ
NLLGKPVDYSGRSVIIVGPELKFNCCGLPKEMALELFEPPIIKRLKDQGSVYTIRSAKKM
IQRGAPEVWDVLEEIIKGHPVLLHPAPTLHRLGIQAFEPVLIEIKAIRIHFLVCAAFNAD
FDTDWAVHVPLSVEAQLEAKVLMMAPDNIFLPCCGKIVAIPSKDMTIMLYLMADPTYF
PEFHKGKTKIFKDEIEVLRALNNYFIFDNVFYCGPRDETGRGIIIHEKIKVRIDQQIETT
PGRVLFHRIVPKELJFQNYSMPGYPIDELIL/IKKVGLEATVHFLDDLKDLGFIQATKA
AIGMGLKDVRIFDIKGHIILKDAYDFVAIVKFCYDDKIITEGERIEKTISINTEVSEQLSD
ALYVEIGKQTRSKHNPLFLHIDCYAAFINKSQLPGLGALRGLMAKVNAIIESPITSNFRR
GLTVLEYGISCHGARKGLADTAILKTADXXYITFPRLVDVAQDVIITEKIXUTLNIIIEICAI
QXDEEELLFLKDRIVGRTVAADVFGFDKCDKLLAQSRDVLNSVQAFAIDDWIIETIKIRS
TLTCHEPRNVCAKCVHLNLANIRLIGMKAVEIIAAQSIIGENTTQLTHHCTFHI/TSIAATS
CTPECITNSDCILVVHDLRVVIIIQEIIHNLVLIPFCALIVVAIDFGRTLNEYKKLUETKCIE
SLEVFFVELAVKILVADGTPVXXXPIGEVELIIIIFPIICDKDYFIKYFDLVFIICCTEKVV

HKNTGLVELIVKQHRGELJIDOIALYDDADLGEL   /AIPSGAIISVEEGQRVDPGMLLA
RLPRGAIKTKDITGGLPPVAELVEARKPEDAADIAKIDGVVDFKGIQKNKRILVVCDEXT
THEEEHLIPLTKHLIVQRGCDSVIKGCOOLTDCLVVPHEILEICCVRELQKYLVNEVOEVYR
LQGVDINDKHIEIIVROMLQKVRITDFGDTTLLFGEDVNKKEFYEENRRTEEDCGKPAQA
VPVLLGITKASLGTESFISAAGFQDTTRVLTDAACCSKTDYLLGFKENVIMGHMIPCGTG
FETHKRIKQYLEKEQEDLVFDFVSETECVC

CPn_0083   102296   103312
...
JELLNVAVVWGIRONGDDLQTLSFILDKIQVVNFALEIIKNIPGRISLEIDARLSFNVEAM
VQRAVFLSQLFEAMGGDKKRLLVKIPGTWEGIRAVEFLEAKGIACNVTLIFNLVQAILAAA
KAKATLISPFVGRIYDWWIAAYGDEGYSIDADPGVASVSNIYAYYKKFGIPTOIMAASFR
TKEQVLALAGCDLLTISPKLLDELKKSQHPVKKELDPAEAKKLDVQPIELTESFFRFLMN
EDAMATEKLAEGIRIFAGDTQILETAITEFIKQIAAEGA

CPn_0084   103356   103751
predicted ferredoxin
SEMKNKMDYKSQLVFSCPCCCKGNVCFSVFNLDVILTCNVCSSTYTFDSVIRNEIRQFVA
LCKRIHDANSILGNATVSVSVEDNOMDIPFQLLFSRFPVVLNLSLDGKKIAIRFLFDALN
TSILHQESDLIS

CPn_0085   104512   103766
CT311 hypothetical protein
FSMKFFILFILIVAQFPAFSAQPRTQVSASHSKQAKARRTSRIRSSAATNASVSRYKTRA
AARKKIGKFEKKPSLSPVQWVRYSGKNYSIQTPSLWQCIDCKTQLPEKLDVLLIGKGKGN
LTPTINIAQEITSKSSKEYIEEILAYHKANEMTLESGIFTQIQSPSGEFTIIKTEKNSSW
GRVFCLQATTVIDHTAYIFTSTATLDDYAELSFTFLKVVSSFQIRGGKEATSGDAILEKA
LEALQNENK

CPn_0086   104898   105527
atpE-ATP Synthase Subunit E
NIHANLNADGKLKQICDALRLDTLKPAEDEAAALLHNAKEQAKRIIQEAQEEARKILETA
EERAHQKIKQGEVALSQAGKRALEALKQAVENKIFRESLVEWLEHVTTDPEVSTKLIQAL
VQALEAQGVSGNLTAYIGKHVSPRAVNELLGKAVTTKLRKKSVVVGSFVGGVQLKVEEKN
WVLDLSSSALLEIFTRYLQKDFREMIFQGS

CPn_0087   105540   106376
CT309 hypothetical protein
SHEKIFSIFKVVVMTQYYFLSSFLPTQLPESVPLFSISDLDDLLYLNLSENDLCNYGLLK
RFFDFENFAFFWAGKPIPFSFGEVTOENVERHLSSOQWSDDNDFKDFLMNHKSSOD
RLNHFSDLFREFLSYHQTNSSKFLQDYFRFQQQLRVVLAGFRARVLNMDVSYVLRDEDSS
DPVVLEVLMQKDSPNYELPEEFSDLQGVLDDYGLLPHTLNRALALYQFHKLEGFCSDSYF
DGNVILARCATYMFAIRNSLASVEKGREIINHEKAIKW

CPn_0088   106352   108145
CT288 hypothetical protein
SYRKGNQMVTVSEQTAQGHVIEAYGNLLRVRFDGYVRQGEVAYVNVDNTWLKAEVIEVAD
QEVKVQVFEDTQGACRGALVTFSGHLLEAELGPGLLQGIFDGLQNRLEVLAEDSSFLQRG
KHVNAISDHNLWNYTPVASVGDTLRRGDLLGTVPEGRFTHKIMVPFSCFQEVTLIWVISE
GTYNAHTVVAKARDAQGKECAFTMVQRWPIKQAFIEGEKIPAHKIMDVGLRILDTQIPVL
KGGTFCTPGPFGAGKTVLQHHLSKYAAVDIVILCACGERAGEVVELVQEFPHLIDPHTGK
SLMHRTCIICNTSSHPVAARESSIYLGVTIAEYYRQMGLDILLLADSTSRWAQALREISG
RLEEIPGEEAFPAYLSSRIAAFYERGGAITTKDGSEGSLTICGAVSPAGGNFEEPVTQST
LAVVGAFCGLSKARADARRYPSIDPLISWSKYLNQVGQILEEKVSGWGGAVKKAAQFLEK
GSEIGKRMEVVGEEGVSMEDMEIYLKAELYDFCYLQQNAFDPVDCYCPFFERQIELFSLIS
RIFDAKFVFDSPDDARSFFLELQSKIKTLNGLKFLSEEYHESKEVIVRLLEKTMVQMA

CPn_0089   108111   109466
CT289 hypothetical protein
LDCWKKQWYKWRKDMQTIYTKITDIKGNLITVEAEGARLGELATITRSDGRSSYASVLRF
DLKKVTLQVFGGTSGLSTGDHVTFLGRPMEVTFGSSLLGRRLNGIGKPIDNEGECFGEPI
EIATPTFNPVCRIVPRSMVRTNIPMIDVFNCLVKSQKIPIFSSSGEHHNALLHRIAAQTD
ADIVIGGMGLTFVDYSFFVEESKRLGGFADKCVMFIHKAVDAPVECVLVPDMALACAEKF
AVEEKKNVLVLLTDMTAFADALKEISITMDQIPANRGYPGSLYSDLALRYEKAVEIADGG
SITLITVTTMPSDDITHPVPDNTGYITEGQFYLRNNRIDPFGSLSRLKQLVIGKVTREDH
GDLANALIRLYADSRKATERMHADHAFKLSNWDKKLLAFSELFETRLMSLEVNIPLEEALDI
GWKILAQSFTSEEVGIKAQLINKYWPKACLSK

CPn_0090   109439   110080
atpD-ATP Synthase Subunit D
VLAKSMSVQVKLTKNSFRLEKOKLARLQTYLPTLKLKKALLQAEVQNAVKDAAECDKDYV
QAYERIYAFAELFSIPLCTDCVEKSFEIQSIDNDFENIAGVEVPIVREVTLFPASYSLLG
TPIWLDTMLSASKELVVKKVMAEVSKERLKILEEELRAVSIRVNLFEKKLIPETTKILKK
IAVFLSDRSITDVGQVKMAKKKIELRKARGDECV

CPn_0091   110074   112053
atpI-ATP Synthase Subunit I
VRLNIHKYLFIGRNKADFFSASRELGVVEFISKKCFITTEQGHRFVECLKVFDHLEAEYS
LEALEFVKDESVSVEDIVSEVLTLNKEIKGLLETVKALRKEIVRVDFGAFSSSEIAELS
RKTGISLRFFYRTHKDNEDLEEDSPNVFYLSTAYNFDYYLVLGVVDLPRDRYTEIEAPRS
VNELQVDLANLOREIRNRSDRLCDLYAYRREVRLCNYDNEORLHQAKECCEDLFDCKV
FAVAGNVIVDRIKELQSLCNRYQIYMERVPVDPDETIPTYLENKGVGMVMGEDLVQIYDTP
AYSDKDPSTWVFFAFVLFFSMIVNDAGYCGLLFLMSSLLFSWKFRRKMKFSKHLSRMLKMT
AILGLGCICWGTTTTSFFGMSFSKTSVFREYSMTHVLALKKAEYYLQMRPKAYKELTNEY
PSLKAIRDPKAFLLATEIGSAGIESRYVVYDKFIDNILMELALFIGVVHLSLGMLRYLRY
RYSCIGWILFMVSAYLYVPIYLGTVSLIHYLFHVPYELGCGIGYYGMFCGIGLAVVLAHI
ORWWRGVEEIISVIQVFSDVLSYLRIYALGLAGAMGATFNQMGARLPMLLGSIVILLGH
GVILILGIMGIVIHGLRLNFIEWYHYSFDGCGRPLPRPLRKIVCSEDAEASGIHLDNNSIV

CPn_0092   112121   112573
atpK-ATP Synthase Subunit K
PYLKGAHEVSMIDMLVVSPALVLGLAMIGGAIGGMAGVASHAVMSRIDEFHGKLIGMGA
MRNNIVGFILMLLMQMAIKNGTLSPVCGIALGLSVGAALLVSRMQGKGVTGTQAYA
PSSIIVGKGYAAIGIVLSPSLFAVVFALLLL

CPn_0093   112440   113015
CT304 hypothetical protein
CKAIVVGAEFKIMLDLRQYMGVMQRLGLSNLFHCLLLPLRYYYKLVFGLTVLLAAIGV
ICIGLDIEDIGIFTEYVIPEYSAAQLGIIEQISCHDEVYGLQVVVTWSLPGRMRKCLPVT
LYLWVVGXKVEKLTYEVNQSAGYRVYCLKGLEYFELQSILVNRVALCGGNOEIVSRRH

CPn_0094   ...
valS-Valyl tRNA Synthetase
VYRVFLSRDHKFCGLRIMTTEDFPKAVNFCCTEPELVVFWEKNGMFKAEASSDKPPYSVIM
PPPNVTGVLHMGHALVNTLQDDVLVRYKRMGCFEVCVIPGTDHASIATQAVVERHLQASEG
KRRTDYSREDFLKHIWAWKEKSEKYVLSQLRCLGCTTODRKRFTMEPLANRAVKKAFKT
LFENGYIYRGYCLVNWDPVLQTALADDEVEYEEKDIWLYYIRYRMVGSQESIVVATTRPE
...
WIVGVYRSGAVIEPYLSKQWFVSVIEYAGAIGEPIELQDIKIFIKLFVKNYLSAVNHLRCW
CISROLWWGHRIPVWVHKICDDERVLCYCGESIPEEVACDFDSWYQDPDVLDTWFSSGLWP
LTCLGWPDENSPDLKKFYPTALLVTGHDILFFWVTRHVLLCSSHSGEKPFSEVFLHGLIF
GKSYKRYNDFGEWSYISGKEKLAYDMGEALPDGVVAKWEKLSKSKGNVIDPLEMIATYGT
DAVRLTLCSCANRGEQIDLDYRLFEEYKHFANKVWNGARFIFGHISDLQGKDLLAGIDED
SLGLEDFYILDGFNQLIHQLEEAYATYAFDKVATLAYEFFRNDLCSTYIEIIKPTLFGKQ
GNEASQSTKRTLLAVLLINVLGVLHPVAPFITESLFLRIQDTLGALPEGDGDAFTGHALR
MLRSRACMEAPYPKAFDVKIPQDLRESFTLAQRLVYTIRNIRGEMQLDPRLHLKAFVVCS
DTTEIQSCIPILQALGGLESIQLLDKEPEKGLYSFGVVDTIRLGIFVPEEHLLKEKGRLE
KERVRLERAVENLERLLGDESFCQKANPNLVVAKQEALKNNRIELQGILDKLASFA

CPn_0095   115956   118790
pknD-S/T Protein Kinase
ACIVCLDREDQRSLERYDIVRIIGKGGMGEVYLAYDPVCSRKVALKKIREDLAENPLLKR
RFLREARIAADLIHPGVVPVYTIYSEKDPVYYTMPYIEGYTLKTLLKSVWQKESLSKELA
EKTSVGAFLSIFHKICCTIEYVHSRGILHRDLKPDNILLGLFSEAVILDWQGAAVACGEEE
DLLDIDVSKEEVLSSRMTIPGRIVGTPDYHAPERLLGHPASKSTDIYALGVVLYQMLTLS
FPYRRKKGKKIVLDGQRIPSPQEVAPYREIPPFLSAVVMRMLAVDPQERYSSVTELKEDI
ESHLKGSPKWTLTTALPPKKSSSWKLNEPILLSKTRWLEVSPASWYSLAISNIESFSEM
RLEYTLSKKGLNEGFGILLPTSENALGGDFYQGYGFWLHIKERTLSVSLVKNSLEIQRCS
QDLESDKETFLIALEQHNHSLSLFVDGTTWLIHMNYLPSRSGRVAIIVRDMEDILEDIGI
FESSGSLRVSCLAVPDAFLAEKLYDRALVLYRRIAESFPGRKEGYEARFRAGITVLEKAS
TDNNEQEFALAIEEFSKLHDGVAAPLEYLGKALVYQRLQEYNEEIKSLLLALKRYSQHPE
IFRLKDHVVYRLHESFYKRDRLALVFMILVLEIAPQAITPQOEEKILVWLKDKSRATLFC
LLDPTVLELRSSKMELFLSYWSGFIPHLNSLFHRAWDQSDVRALIEIFYVACDLHKWQFL
SSCIDIFKESLEDQKATEEIVEFSFEDLGAFLFAIQSIFNKEDAEKIFVSNDQLSPILLV
YIFDLFANRALLESQGEAIFQALDLIRSKVPENFYHDYLRNHEIRAHLWCRNEKALSTIF
ENYTEKQLKDEQHELFVLYGCYLALIQGAEAAKQHFDVCREDRIFPASLLARNYNRLGLP
KDALSVQERRLLLRQKFLYFHCLGNHDERDLCQTMYHLLTEEFQL

CPn_0096   124347   118837
CT296 hypothetical protein
ETFLSILREFFMKSLPVYVSGIKVRNLKNVSIHFNSEEIVLLTGVSGSGKSSIAFDTLYA
AGRKRYISTLPTFFATTITTLPNPKVEEIHGLSPTIAIKQNHFSHYSHATVGSTTELFSH
LALLFTLEGQARDPKTKEVLDLYSKEKVLSTIMELSEGVQISILAPLLRKDIAAIHEYAQ
QGFTKVRCNGTIHPIYSFLTSGIPEDCSVDIVIDTLIKSENNIARLKVSLFTALEFGEGH
CSVLSDEELMTFSTKQQIDDVTYTPLTQOLFSPHALESRCSLCQGSGIFISIDNPLLIDE
NLSIKENCCSFAGNCSSYLYHTIYQALADALNFNLETPWKDLSPEIQNIFLRGKNNLVLP
VRLFDQTLGKKNLIYKVWRGVLNDIGDKVRYTTKPSRYLSKGMSAHSCSLCKGTGLGDYA
SVATWEGKTFTEFQQMSLNNWHVFFSKVKSPSLSIQEILQGLKQRLSFLIDLGLGYLTPN
RALATLSGGEQERTAIAKHLGGELFGITYILDEPSIGLHPQDTEKLIGVIKKLRDQGNTV
ILVEHEERMISLADRIIDIGPGAGIFGGEVLFNGKPEDFLMNSSSLTAKYLRQELTIPIP
ESREAPTSWLLLTEATIHNLKNLSIRLPLARLIGVTGVSGSGKSSLINNTLVPAIESFLK
QENPKNLHFEWGCIGRLIHITRDLPGRSQRSIPLTYIKAFDDINELFASQPRSLRQGLTK
AHFSFNQPOGACIQCCGLGTMTISDDDTPIPCSECOGKRYHSEVLEILYEGKQNIADILDM
TAYEAEKFFISHPKIHEKIHALCSLRLDYLPLGRPLSTLSGGEIQRLKLAHELLFASPKQ
TLYVLDEPTTGLHTHDIQALIEVLLSLTYLGHTVLVIEHNMHVVKVCDYVLELGPEGGDL
GGYLLASCTPKDLIQLNTPTAKALAPYIEGSLDIPVVKSEPPSSPKSCDILIKDAYQRNL
KHIDLALPRNSLIAIAGPGASGKHSLVFDILYASGNIAYAELFPPYIRQGLLKETPLPSV
GEVKGLSPVISVRKCSSSNRSYHTIASALGLSNGLEKLFAILGEPFSPLTEEKLSKTTPQ
TIIDSLLKSYKDDYVTITSPIPLGSDLEIFLQEKOKEGFIKLYSEGNLYDLDERLPLALI
EPAIVIQHTKVSPKNSSSLLSAISVAFSLSSEIWIYISQKKQRKLSYSLGWKDKKGRLYP
EITHQLLSSDHPEGRCLTCGGRGEILKLSLEEHKEKIAHYTPLEFFSLFFPKSYMKPVQK
LLKDENASQPLKLLTTKEFLNFCRGSSEFPGHNALLMEQLDTKSDSFLKLDDSNSALQVSPY
CKGSGLNDYANYVRINNTSLLDIYQEDATFLESFLNTIGTDDTRSIIQDLMNRLTFISKV
GLSYITLGQRQDTLSDGENYRLHLAKKISINLTNIVYLFEEPLSGLHPQDLPTIVQLLKE
LVANNNTVIATDRSCSLIPHADHAIFLGPGSPQGGFLMDSDTEVCPSVDLHANVPQTEV
CPKAPLSISKANHTRGSDRTLKVNLSIHHIQNLKVSAPLHALVAIGGVSGSGKTSLLLEG
FKKQAELLIAKGTTTFSDLVVIDSHPIASSQRSDISTYFDIAPSLRAFYASLTQAKALNI
SSTMFSTNTKCQOCSDCOGLGYOWIDRAFYALEKRPCPTCSGFRIQPLAQEVLYEGKHFG
ELLHTPIETVALRFPFIKKIQKPLKALLDIGLGYLPIGQKLSSLSVSEKTALKTAYFLYQ
TPETPTLFLIDELFSSLDPIKKOHLPEKLRSLINSGHSVIYIDHDVKLLKSADYLIEIGP
GSGKQGGKLLFSGSPKDIYASKDSLLKKYICNEELDS

CPn_0097   124549   126006
pyk-Pyruvate Kinase
DSMITRTKIICTIGPATNSPEMLAKLLDAGMNVARLNFSHGSHETHCQAIGFLKELREQK
RVPLAIMLDTKGPEIRLGNIPQPISVSQGQKLRLVSSDIDGSAEGGVSLYPKGIFPFVPE
GADVLIDDGYIHAVVVSSEADSLELEFMNSGLLKSHKSLSIRGVDVALPFMTEKDIADLK
FGVEQNMDVVAASFVRYGEDIETMRKCLADLCNPKMPIIAKIENRLGVENFSKIAKLADG
IMIARGDLGIELSVVEVPNLQKMMAKVSRETCHFCVTATQMLESMIRNVLFTRAEVSDIA
NAIYDGSSAVMLSGETASGAHPVAAVKIMRSVILETEKNLSHDSFLKLDDSNSALQVSPY
LSAIGLAGIQIAERADAKALIVYTESGGSSPMFLSKYRPKFPIIAVTPSTSVVYRLALEKG
VYPMLTQESDRAVWRHQACIYGIEQGILSNYDRILVLSRGACMEETNNLTLTIVNDILTG
SEFPET

CPn_0098   127494   126094
No robust homolog present in Genebank/EMBL as of 11/7/98
LVGKKFHQIKRTILEAPLYYLVSGIIALRHTPRSFLJIGIKGFCFLAFYIICDYRKTAL
TNLALAFPEKTFDERYKIAROCLQHILITLLEIIAIEOLVINIDKLITIVTISRNPKGFS
SEFVISHEDLEETFKNIQEKQILILFVIHQAMWELPFLYITKNYFGIAFAKAIFNQRLSIK
KIFALPEVFKSKIVPPKMSIQQGIEALFGIRLISIVSQALLMRXTYPLFUSPAFTTTS
FALLAYEYCGFFVIAVNVSRQAKGFEVISGAKLZANKSLIHYESVAILMIQWMSFLEKGIA
SQIFLANNIHKRWKRKIINVIKKKYFYSHILVFSIVSVISLFLFAIASCFSYTLHLAL
GNADULFELQFQFPEYSLIQLRNDQDIIALJSIVEFILDLIHNLAIHJJXHLFRKTYSSXAVY
IKHFLFKSLDILIPQAPLKNSLKIFYSIHLDDKEDVPNEKVPSPCDGLIVE

CPn_0099   127527   127846 12-7565
No robust homolog present in Genebank/EMBL as of 11/7/98
YYCASYYLKISRFAAKIIAPEIQIRLRCSIFTPDGFAATLLIRKVIFEACGTIVQIKMISIK
ETIAVPAKSPADTVATFALDGELSIRJJJTVLIAASKTFFFQSIEHIKFTLTKF

CPn_0100   129183   127982
CT011 hypothetical protein
RTQKKTFILLDLETMIKFLJOLFIRHWPRKVVSLGFAIIIWILVGOSVFITRTLTNVPVR
IVDLHPDQTVLGLQKGGFLNKKVSLTITGNKNTVGOLRPSNLEVVISAANHTESWIATID
KHNLVSVDHEINIRKDIHSVDANDIFVRLTQYTEDILLTITKPIGSPPKGYEYLDVWPK
YLNQKVSGPKEYINALKEOGLELTFNLNKISFEELERNRIAQGSHDEIIFPIPKEWKKIL
IPFFNTFMDLNDPOADFLRLLFLKRECIPLNLNLPVFLFFPVTFIQTMNPLEYSLDPVPP
...
TKTKETTKLYKKEW

CPn_0101   129986   129141
ybbP family hypothetical protein
PSTLCNFSOYTTOGPSKTMPFDITYYTTPLLEIILIWVMLNYLLKFFWGTRAMDVVFGLL
AFLFLFVLADKLHLPIIRRLMLHVVNIAAIVVFIIFQPEIRLALSRIRFHGKKFFIDTQE
QFVEQLAASIYOLSEROIGALVVLENKDSFDEYLSFSSVKINATFSEELLETIFEPSSPL
HDGAVILRGDILAYARVVLPLAHDTTQLSRSMGTRHRAALGASORSDALIITVSEENGSV
SLSRDGLLTRGVKIDRFKAVLRSILSPKEHKRKPLFSWIWKR

CPn_0102   130099   131466
cydA-Cytochrome Oxidase Subunit I
FYIQFWKFMDALILSRIQFGLFITFHYLFVPLSMGLSMMLVIMEGLYLVTKKQIYKQMTW
FWVGIFALTFVLGVVTGIMQIFSFGSNWANFSEYTGNIFGTLLGSEGVFAFFLESGFLGI
LLFGRHKVSKKMHFFSTCMVALGAHMSAFWIICANSWMQTPSGYEMVMHKGKLIPALTSF
WGVVFSPTTIDRFIHAVLGTWLSGVFLVISVSAYYLWKKRHHEFAKOGHKIGTICAVIVL
VLQLWSADVTARGVAKNQPAKLAAFEGIFKTSEYTPIWAFGYVMEKERVIGLTIRGGALS
FLVHRNIKTPVTGLDQIPRDEWPNVQAVFQLYHLMIMLWGVMVALTLISWSAYKGWRWAL
KPFFLVILTFSVLLPEICNECGWCAAEMGROPWVVQGLLKTKDAVSPIVQANQIVQSLVI
FSLVFIALLTLFITVLCKKIKHGPEEENDLTEFEVK

CPn_0103   131465   132511
cydB-Cytochrome Oxidase Subunit II
NRGIFMELSLTSLLPLAWYVILGVAVFAYSFGDGFDLGLGAVYLKAKEDKERRILLNSIG
PVWDGNEVWLVIIVGGLFAGFPACYATLLSIFYMPIWTLVLLYIFRGCSLEFRSKSESVS
WKIFWDIIFICSGTAISFFLGTIVGNLILGLPLSPDTSYASLSWILFFRPYAALCGAVVA
SAFAIHGSCFALHKTSDSLNARIAQOFPYILSSFLVFYVLFLGASLISIPKRFDAFPTYP
LLILLIALTSCCCVAAKTSVSKKRYGYAFIYSTLNLLSLILSAATLTFPNILLSTVDPQY
SYTIYNSAVETKTLKSLLIIVLIGLPFIITYTCYIYRVFRGKTNFPSIY

CPn_0104   133884   132676
CT017 hypothetical protein
EKSMRMLQISMLLLALGTAINSPAIYAADSQSVSFPEQLPSSFTGEIKGNHVRMRLAPHT
DGTIIREFSKGDLVAVIGESKDYYVISAPPGITGYVFRSFVLDNVVGEGEQVNVRLEPSTS
APVLVRLSRGTQIQPASQEPHGKWLEVVLPSQCVFYVAKNFVANKGPIELYTOREGQKKI
AMDLINSALNFAHIELEKSLNEIDLEAIYKKINLVQSEEFKDVPGIQGLIQKALEEIQDA
YLSKSLESQNTSIASSQCSTPKVSSSEVTTSLLSRHIRKQTALKTAPLTQGRENLEYSLF
RIWASMQQGNDHSEALTQEAFYRAEQKKKQVLAGVLEVYPHVVKNNPGDYLLKAQENTIA
FLYGTSINLEQWLGKRVTVECLPRPNNHFAFPAYYVVGIKEAS

CPn_0105   134883   134029
CT016 hypothetical protein
YVPFRKFSNQNPMLLIYCKKKEIHLQWPQTAKIRFTPKIAMKVKINDQLICIPPFISARW
SQIAFIESQEGENKDQGTLRLHLIDGKIISIPNLDQSIIDIAFQEHLLYLETSQSGKEDS
RDDDKLGVGVLMNVLQQITKGNDIQVLPKNLISPLFSGTNPIEAILQHTPEHKDHPDAPT
DVLEKMADVIRVLSGNNATLLPRPEPHCNCMHCQIGRVMNEEDTLAVSDKDLTFRTWDIM
QSGDKLYIVTNPLNPSDQFSVYLGPPIGCTCGEPNCEHIKAVLYT

CPn_0106   135073   136374
phoH-ATPase
EKVRTQMKKTHVIDTSVFIYDPEALFSFENTRIIIPFPVIEELEAFGKFRDESAKNASRA
LSNIRLLENAKTKVTDGVLLPSGSELRIEVAPLSNDDRRGKLLTLELLKIIAKREPHVF
VTKSLGRRVRAEALQIESRDYESKRFSFRSLYRGFRELQVSQEDIENFYKNGYLDLPLDV
VSSPNEYFFMSAGENHFALGRYYVSEGKIIALKAMDKSVWGIKPLNTEQRCALDLLLRDD
VKLVTLIGQAGSGKTILALAAAMHKVFDKETYNKVLVSRPIVPMGRDIGFLPGLEKDKLM
HWHQPIYDNMEVLFSINOMGNSSEALQALMDAKKLEMEALTYIRGRSLPKAFIIIDEAQN
LTPHEIKTIISRAGKGTKIVLTGDPTQIDSLYFDENSNGLTYLVGKFHHLALYGHMFMTR
TERSELAAAAATIL

CPn_0107   137321   136392
CT058 hypothetical protein_1
KKSPPPVTPKEIPTQPKPPIPQRPEVSPTPTDHIVPGSIEASPILGKKPSPDSMVSPLSL
FHKMLLENWTPVEEPFPWPPAEKNQKIFAWALNQSKLIFVSTSGNIAQPRLVTDSMSMMI
VNAANRTMSRDGACTNQVLSAAVSVDSWGLSQRPLNPEROGTPLNEGECRAGMWRNADGS
NHTGKQGKPHYLAQLLGPKAVDHHNKSQAAFDRCKNAYLNCFSLAQTLGVTFLQIPLISS
GIYAPPENRKKPNSEENKVRMRWIHAVKCALVAAMQEFGNEPGNTDRRMLIVLTDLKTPA
ITDPKKKGHL

CPn_0108   137887   137303
CT018
KNLFHYKAILMSIFNEEVFIISHRHTPLGQTSTALRNTPLVNPLHRTNLQRIASYIPIFS
TFIGIKTLKGISSLQYSMVLMTGNFSSVCKTLPCPEIYEELPKVRKEAWLEIFGIKALYY
LVLGVIKIIKLIVRYLCPCCRPPEPREPQNPLTPTPLDMGQQIDAIFSTPTSPTGFKDPF
LDDLLQEDKKKAPHL

CPn_0109   138646   141783
ileS-Isoleucyl-tRNA Synthetase
ROKMTADEVGKNSFAKKEEOVLKFWKDNQIFEKSLQNROGKTLYSFYDGPPFATGLPHYG
HLLACTIKDVVGRYATMDGYYVPRRFGWDCHGVPVEYEVEKSLSLTAPGAIEDFGIASFN
EECPKIVFRYVHEWEYYINRIGRWVDFSSTWKTMDASFMESVMWVFOSLYNVGLVYEGTK
VVPFTALGTPLGNFEACOQNYKEVDDPSLVVRMPLQNDGASLLVWTTTPWTLPGNMAIAV
HETLVTVRIODKKGEGQWILSQXCVSRWFINPEEFVILESFSGKDLVGRTYEPPFTFFQS
KREECAFKVLAASFVEESEGTGVVHMAPAFGEDDFLVCKENHVPLVCPVDAIFGFTEEIP
VVCCYIEHADKEIIKFLKKEGRIFYIGTVKIRYPFCWRTDTPLIYKAVNGHF/AVEKIK
DKMLHANGCUHWVPEIIQUAIRFGKWLEIIARDWAISRNRYWKTPIPIWKSADGEILVVGI
HELEELTITGCTDIHRIEIDDLNIVKDGKPFIRIPYVFDCWFDGSAMPYAQIHYPFENQK
ETEEAFFADFIAEGLDXYTRGWFYTLTVIGAILFDRPAFRNAIVNGIILAEG/IKMSKRLN
NYPESIKVVLGTVVAUALRLYLLIIGVVVKAEDLRFSDKGIEVVLKQILLPLTIF/LGFFNTY
AKLYGFEKIGDGIEPAYTEIDCWILGNLYSVVKFGMIQDYHILMFAVEPF/TFIDDLTN
WYIHHLHHHFWEAEDTPDRHGAAFGTLYEVLTVFGCKVIAPFVPFLAEDIYQFLFLEKEPES
VIIGCGFIGVVEMDKILPDLEKRMHIDIRELVGLGHIGLRKENKLKVRQPIANFCCCGSKDRLG

CLKTFEGLIAEEELNVKNVI   ADREIYYTOKENFRMLGKKVTGKMKEVCKALGELPNN
AIDKLIQEETWVLTIDDPEALGIDCLVTIARGIALFGVTLCCCQLREPLIVE
GIARELVNKINTHRRNOGLECCDRIALRIKTTEAVHRAFLDYENXECEFTTLIAYDETCD
SDFOGENWDINGHATOLEITVSGIDS

CPn_0110   141755   141827
lepB-Signal Peptidase I
LSYPSIFMKQHYSLNKSPHILRSTYKLLKSKKLAHSPADKKCLQELLEOLEEAIFEHDOE
TAVELAVONAFIVRVRRTQPVAFKIRLPLEPLAFAGLVVAFLLPOSXFELYEVPTIGMRPTI
KRYIKRKCMGKFGLFLYFVILTTVLLAGKFLEFTVDLIUNGNTHGFYSFDITTGIHTE
GQKTIIDFKQFNQSYGRLIFPTSMYGQFFDHKEWHQDEPNKLKDPHLSPVSYADLFGMG
NYAMVRILTEHQARTSHLLFNPGSPTKVYLEICHTANLSYPKPLLRHYEHQLSPAIQPMX
TLLPLRKEHLHLIRRNLTTSRFIVAQGCAYKYHQFKINTSGIAKAYAILLPKVPDGCYEY
SKGEAYQIGFGEIRYKLKSSHPLTOLNDKQVIELFNCGINFSSIYNPVNPLQAPLPNRYA
FFNQGNLYIMDSPVFIKNDPTLQKFVTSETEKOEGSSETOPYIAFVDKGLPPEDFKEFVE
FIHNFGIQVPKGHVLVLGGHTPMSADSREFGFVPMENLLGSPLCTFWPIGRMGRLTGVSA
PTTLSGYLVSGIALATGLSLIGYVYYQKRRRLFPKKEEKNHKK

CPn_0111   144761   143934
CT021 hypothetical protein
QLQNRYPIMPNDSSTYFERILQKYLMKKQGKTLFLFLFLSFLFSTAFSGLFASQTSSLRT
IQENIFLAKTGDTVLSRGSQRTFVLVKSTTPKTVWIEIIHSPCIAHKERPSLEQASWKT
VIHQLESPSQVFVVSLSSEGSQFFSLNTRTKSLEPVGKSTTVPAFLQIFDLPLSPAPANV
IKTKGKENKPWSPKVSFEGAPLTSISVNAWQGLWPKDRGPLSETGILMYFTQPDISVFPL
WVSIETPKGTSIVRAVDIGHGATSPYVVYSLPDSKTQ

CPn_0112   144743   145093
gatCB-(Pet112) Glu tRNA Gln Amidotransferase (B Subunit)
DSDFGVVANMKKNTHPEYRQVLFVDSSTGYKFVCGSTYQSEKTEVFEGKEYPVCYVSVSSS
SHPFFTGSKKFVDAEGRVDKFLKRYSNVRQPAQQPQPEEDALPAAKGKKKVVTKKKK

CPn_0113   145329   146405
pfrA-Peptide Chain Releasing factor (RF-1)
GFMKKKVAEYLNRLAEVEIKISNPEIFSNSKEYSALSKEHSYLLELKNAYDKILNLEKVL
ADDKQALAIEKDPEMVVMLEEGINENKVELEKLNKILESLLVPPDPDDDLNVIMELRAGT
GGEEAALFVGDCVRMYHLYASSKGWKYEVLSASESDLKGYKEYYVMGISGTGVKRLLQYEA
GTHRVQRVPETETQGRVHTSAITIAVLPEPSEEDTELLINEKDLKIDTFRASGAGGQHVN
VTDSAVRITHLPTGVVVTCQDERSQHKNKDKAMRILKARIRDAEMQKRHNEASANRSAQV
GSGDRSERIRTYNFSQNRVTDHRIGLTLYNLDKVMEGDLDPITTAMVSHAYHQLLEHGN

CPn_0114   146371   147261
hemK-A/G specific methylase
VMPTTSYSNMEIKKAIQEGTAYLDYYGVPLSDCEALYILMDLLEVSSRAKLFDLVGISET
MLMEYRKRLALRGORCPTAYLNGAVSFLGLRLRVDSRVLIPRTETELLAEYIINYLLSHS
EIQTFYDICCGSGCLGLAIKKSCPHVEVVLSDVCPQAVAVANENAKSNGLDVKILLGDLS
APYTRPADAFVCNPPYLSFNEIIHIDPEVRCYEPWKALVGGSTGLEFYQRIAQELPKIVT
STGVGWLEIGSSOQESIKNIFSKHGIYGRLHQDLSGRDRIFFLEMDGRDPVSSGAYS

CPn_0115   147279   148622
ffh-Signal Recognition Particle GTPase
MINSLSQKLSSIFSFLVSSRRINEENISESIREVRLALLDADVNYHVVKDFISKVKEKIL
GEEIWKHVSFGQQFIRCLHEELVAFLSDGREEFTIQKTPSIILLCGLQGAGKTTTAAKLA
DYVKIKNKKAKKVLVVPCDLKRFAAVDQLKILVAQTKAEFYQSQENKPINVVVKALAYAKE
NGHDFVILDTAGRLNIDNELMEELTAIQKVSQANERLFVHNVAMGODVTVQAFDQSLD
LTGVILSMTDGDARAGAVFSIKHVLGKPIKFECGCGERIQDLRSFDPQSMAERILGMGDTI
NFVKEHREYISEEEDAELGKKLVTAAFTYEDYYKQMKAFRRMGPLRKLLGMMPGFNNAKP
SQKEIEDSEQQMKRTEAIILSHTPEERKELVELDMSRMKRIASGCGLTLGDVNQFRKQMS
QSKKFFKGMSKGKMEQVRKKMSGGNQWR

CPn_0116   148592   148972
rs16-S16 Ribosomal Protein
EKNVRRKSVALKIRLROQGRRNHVVYRLVLADVESPRDGKYIELLGWYDPHSSINYQLKS
ERIFYWLERGAQLSSKAEALVKQGAPGVYSALLSKQEARKLVVRKKRRAYRQRRSTQREE
AAKDATK

CPn_0117   148983   150071
trmD-tRNA (guanine N-1)-Methyltransferase
TGMKIDILSLFPGYFDGPLTSILGRAIKORLLDVQLTNLRDFGLGKWKQVDDTPFSGGG
MLLHAEPVTSAIRSVRKENSKVIYLSPQGALLTAEKSRELAAASHLILLCGHYEGIDERA
IESEVDEEISIGDYVLTNGGIAALVLIDAVSRFIPGVLGNOESAERDSLENGLLEGPQYT
RPREFEGCKEVPEVLLQGDHKAISQWRLEQSERRTYERRPDLYLNYLYKRSIDHKFDEETT
TNRDHFKCDKISVVLEVNKLKRAKNFYCKVFGLDAMSCENKFCLPHEGKTIFWLREVQAE
KKNIVTLSLSLDCACEEDFCYLLRRWELFGGKLLEKQADEHAVWALAQDLDGHAWIFSWH
RMK

CPn_0118   150075   150464
rl19-L19 Ribosomal Protein
KKENFRWYIMVNLLKELEQEQCRNDLPEFHVCDTIRLATKISEGGKERVQVFQGTVMARR
GGGGGETVSLHRVAYGEGNEKSFLLNSPRIVSIEIVKRGKVARARLYYLRGKTGKAAKVK
EFVGPRSSKK

CPn_0119   150520   151164
rnhB-Ribonuclease HII
LMNTSISEIORFLSMIAFEKELVSEDFSVVAGIDEAGRGPLAGPVVASACILPKGKVFPG
VNDSKKLSPKQRAQVRDALNQDPEVCFVGIGVISVEPIDQVNILEATKEAHLQAISSLPIS
PDILLVDGLYLPHDIPCKKIIOGDAKSASIAAASILAKEHRDDLMLQLHRLYPEYGFDRH
KGYGTSLHVEAIRRYGPSDNHRKSFSPIKOMCAIV

CPn_0120   151125   151778
gmk-GMP Kinase
EELFCNKANVVCYCMNKILVTSPFGPDIIQKCCIKLFTISAPAVWVKTTLVRMLEQEFSSAF
AETISVTTRKPREGEVDIKIYHFVSHEEFQRLIDRQALLEWVFLFGECYGTSMLEIERIW
SLGKINAVAVDIQCALFIRSRMPSVGIFIAPPQEELERRLASRGSEEGSQORKERLEHSL
IELAAANQFUVVINDDLKVAYRVLKGGIFIAREIRHII

CPn_0121   151769   152008
CT011 hypothetical protein
EHINIKKDRFTNEKLNKLFNSPFSILVTYAIKQAKIYIAKGTANGENVAIETLVLLDREGI
QFEPTERIVVTASICTVERKKSHITNCPFKDISAYTVCDVK

CPn_0122   152062   153723
metG-Methionyl-tRNA Synthetase
RKVMPQKVLITSALPYANGPLHFGHIAGVYLPADVYARFRRLLGDDVLYICGGDEFGIAI
TLNADREGUYQEYVDMYHKLHKDTFEKLGFALDFFSRTTNPFHAELVODFYSQLKASGL
IENRISEGLYSEQEQRFLADRYVEGTCPRCGFDHARGDECQSCGADYEAIDLIGPKSKIS
VVELVKKETEHGYFLLDRMKDALLSFIQGCYLPDHVRKFVVDYIEHVRGRAITRDLSWGI
PVPDFPGKVFVVWFDAPIGYISGTMEWAASGGNPDEWKRFWLEDGVEYVQFISKDNLPFH
VVVFPAMELGQKLDYKKVDALVVGEFYLLEGROFSKSEGNYVDHDKFLGSYSLDKLRYVL
... ...
... ...
LFCACYCQKLLALISYPIIPESAVAIWEMIJPKSLENCNLDTMYARDLWKEEILDVINEE
FHLKSPRLLFTTVE

CPn_0123   155975   153774
recD-Exodeoxyribonuclease V (Alpha Subunit)
NSMEKICCYLEQILVENKDSGDITAYIKIPNKTTPILIKGKLPQPLELGSPIQIYGVVSH
SPSNTKYFQIHSYDSPLLYEYRGVFHYLTSKLIKGIGPKIAEKIIEKFQEKTCYVLDITP
ERLSEVSGISETRCVSICKQLCEQKILRKTLLFLQEYNIPIHYGVRIFKKYQEKSIEKIC
EDPFLLAREMEGIGFKTADFIAMKLGVPRNSESRLCAGIQHSLEELQEEGHTCYPIELLI
DVVAKLLNQDVFDTPITLEEIDTQILNMOKRKLLHIODISGTLHVWTRYLHLAEKTIVSD
LKRILFSSRRIRSIDGEKAIAWVEENLSIDLAEQQREAIKACFSEKLLIITGGPGTGKST
ITQAILKIFEQVTHKIILAAPTGKAAKRMTEITQKHSVTIHALLQYDFKTKSFRKNHDNP
IDCDLIIVDESGMMDTHLLHHFLKALPDYTTLVFIGDIHOLPSVGPGNILKDLITSNKMT
VIRLNKIFRQVHDSGIVTNAHRVNEGELPILYSETGRRDFLFFQKDDQEEALNHIIHLVT
KFVPOKYHIYPODIQVLAPHKKGTLGIYNLNKALKHALNPKKANLHGRFQSYAVGDKVMQ
IRNNYNKEVFNGDIGYVSTINFEDKAVVVRMEGKHVGYSFSELDDLVLAYATSVHKYQGS
ESPCIIIPIHTSHFMMLYRNLLYTAITRGKKLVILVGTKKAIAIATRNNRVQHRCTGLAE
VLKELDTKKNYADL

CPn_0124   156575   158068
No robust homolog present in Genebank/EMBL as of 11/7/98
IRSKQRTVAITLLVLGILLIASGIIFLAVAIPGLSSAVALGLGCGMTALGTVLLITGLVL
LIRSEKLALEQVEIKQARTRVNNELDQLSQYVFYTENVLDNLKRWSYRDLGFVRQAQEEV
TNLEQDIEEIFLTLRDIRNALDNEEFFMTHAKQCLAQVGESLFQDASIDEFINLAHLSEI
RQHLDINDPRWSMITKKVKGTVVRFIYVSTMYKQIKSNFEKSDFGOLRKMLLNNYKTIEE
VLYQSFQKGYNRAALLSEKTRIIHTSSLLHWEKDEDKHLNIKNECASRLENFKKFRTLFL
GLSEEDVIDFTGASGWDCSKLPRKEVPLDGGKKKLRFKRTFADEQVGDWDRTTSLEHMTP
QEEDPLDRLMDQVEQEATSVLKDQDRYWKEIETSEAKFRSLPREDDFEKQSQIDSYIRDL
DDHLSVWANQLSAAEDALIEVTDVQEHGNREMLKNIQQGLELIEDAVKATLPRVDFIQEL
LEKEELPLVAARMSLENS

CPn_0125   158072   158605
No robust homolog present in Genebank/EMBL as of 11/7/98
KISSCAEIMSEVKPLFLKNDSFDLATQRFQNLINMLQEQAEIYNEYEEXNARVQNEIKEQ
KDFVKRCIEDFEARGLGVLKEELASLTRDFHDKAKAETSMLIECPCIGFYYSIHQEEQRQ
RQERLQKMAERYRDCKQVLEAVQVEQKDMISSRVVVDDSYFEEEKEEQKVDNRKKEQD

CPn_0126   158806   161085
No robust homolog present in Genebank/EMBL as of 11/7/98
LLVFSYYCMGLFFFSGAISSCGLLVSLGVGLGLSVLGVLLLLLAGLLLFKIQSMLREVPK
APDLLDLEDASERLRVKASRSLASLPKEISQLESYIRSAANDLNTIKTWPHKDQRLVETV
SRKLERLAAAQNYMISELCEISEILEEEEHHLILAQESLEWIGKSLFSTFLDMESFLNLS
HLSEVRPYLAVNDPRLLEITEESWEVVSHFINVTSAFKKAQILFKNNEHSRMKKKLESVQ
ELLETFIYKSLKRSYRELGCLSEKMRIIHDNPLFPWVQDQQKYAHAKNEFGEIARCLEEF
EKTFFWLDEECAISYMDCWDFLNESIQNKKSRVDRDYISTKKIALKDRARTYAKVLLEEN
PTTEGKIDLQDAQRAFEROSQEFYTLEHTETKVRLEALQQCFSDLREATNVRQVRFTNSE
NANDLKESFEKIDKEVRYRQKEQRLYWETIDRNEQELREEIGESLRLQNRRKGYRAGYDA
GRLKGLLRQWKKNLRDVEAHLEDATMDFEHEVSKSELCSVRARLEVLEEELMDMSPKVAD
IEELLSYEERCILPIRENLERAYLQYNKCSEILSKAKFFFPEDEQLLVSEANLREVGAQL
KQVQGKCQERAQKFAIFEKHIQEQKSLIKEQVRSFDLAGVGFLKSELLSIACNLYIKAVV
KESIPVDVPCMQLYYSYYEDNEAVVRNRLLNMTERYQNFKRSLNSIQFNGDVLLRDPVYQ
PEGHETRLKERELQETTLSCKKLKVAQDRLSELESRLSRR

CPn_0127   162152   161130
ytfF-Cationic Amino Acid Transporter
ESFHFPSANOESRTRNVPLGIFHGLVACLYWGIVFVIPNFLGSFGDLDIVLTRYTIFGIF
SLIACAIKNPSVIKKTPLYIWRKSLLWTLLINPVYYFGITLGIRYVGSAITVVIASLAPT
AVLYHSNTKQKELPYSLLFAISSVIITGVILTHLSALNLPTAASPLYSILGVIAVILSTS
LWVTYVINQSLLEKHPNLTPDTWSYLIGISALIICLPMIIILDLCGITHVTHNLISHTP
GSERLLFLLLCSAMGIFSSAKALIAWNKASLNLSPALLGAILIFEPIFGLVLTYLYSQSL
PSLQEGIGIFLMLGGSLLCLVLFGRKVQKSLENSQVSSSNE

CPn_0128   162262   163053
bplI-Biotin Protein Ligase
EDRGRMLRNQVLVYCSEGVSPYYLRHTIRFLKYYSTQEGAFDILRVDGNFLIKNPFWEET
TRLLVFPGGADRPYHRVLHGLGTARIFQYVSEGGNFLGICAGAYFGSKMIYFYEPEGAPL
GGARDLGFFPGTAKGFAYRGNFSYVSPSGVRVSPQLFSDFGLGYAMFNGGCFFEGSEGYP
GVHIESRYDDLFCKPASIVSRIVSKGLAVLSGPHIEYLPHYCRMVKENVQKTREFLQRER
TTLDRYCONLVQRLRQPAFSKADC

CPn_0129   163747   163064
similarity to CT036
DEQYILSHIHMDPRIFVTSEPLQKTYQKLQEKHVVNLGIASQVSLTDLQNKTQYENNLIE
TTNEITYYFPVVHNPDILRSEWDPISNQLYLIFKKFFIHYHNLFSTALERNQILLIDSL
NTVGSSNPIARQMELLAFLCVFEQLDYNEDEYTIEPRDYFNRFVYKNSQTAPQIQSFGLLH
GYEEMGYASNNIRNVLTHSIVLCSPILYQLITEFDTTKIHADDFDCLI

CPn_0130   164251   163751
No robust homolog present in Genebank/EMBL as of 11/7/98
RSMVKCSSIIHENKKPAQLLPESKFAAITKLSLAILCSLFLGIAACILIALSGLLPNTLLI
IALSLSIIVLETIISLLITQCSKCVQKDEQKPKITFPKETPGLDPWLLNPLKNKIQSS
ETILLLDPTSINLKNELFFDSPEEWKKIFLKDPDFLIFYCALANWKILE

CPn_0131   164441   164580
No robust homolog present in Geneback/EMBL as of 11/7/98
FSPLKKERESEUAIFLIFFFTSAYVFDSIGFLFLELFMENAMSSSFVYNSPWIILRTSVAQ
FVFFKIIGKGIQVLLSTSVMLFIGLSVCAFIFFQYLIVFVLFIALIMLAISLVLFLLIRSV
RGSMVDKIMSEKSVALIQHENIPFLDVKRVVSLLPCSPYIKVRALWASSLILFEDPSQAA
VILLSSIWIFFSSIVMEALLLSIFQEKFSKYIDFVLPFLSIRFERVSILLVFLSAFTLDDLNEQ
SVHLSMINEEFLFFINKKAIGERSIQDLKHEFMSSLEPTGVPLDISSMSFQVSQAMFSVYRY
LAQFPAITSELSIGFHLLASFFCDVVHHTLASFENRPKDLADSDFLEAYKNVEWGEFISACEK

CPn_0132   166584   166561
No robust homolog present in Genebank/EMBL as of 11/7/98
SMIEFAFVPHTSVTADRSEDRMACRMNKLSTLAITSLCVLISSVCIHSGSLCISGTVGTY
AFVVGIIFSVLALVACVFFLYFFYFSSEEFKCASSQEFRFLPIPAVVSALRSYEYISQDA
INDVIKDTMOLSTLSSLLDPEAFFLEFPYFNSLIVNHSMKEADRLSREAFLILLGEITWK
DCETKILFWLKDPNITPDDFWKLLKDHFDLKDFKKRIATWIRKAYPEIRLPKKHCLDKSI
... ...
MEMMI ... ...

CPn_0133   167349   166564
CHLPS hypothetical protein
NSSAYMFKLLKNLFLIGCCIVGYFWMRKESIVEQWLSNRLHTQVTVGRVSIRTSGIKIRH
ICIHNPLASERFPYAAEIEYADVRFSSISMLLTKQLEISELIIHGANFTIFPYDSHGTKT
MWSLVWIKNFHPQKETPSNLWIDRAPVLIRRCLFLNTRLYGLRANHKDIPHLSVPSLEFHS
HTSSAKELPKLSEALPSLLYLALEESLYHLNLPGDIIKPLSQQAHKHFYSSYPQFQDRLN
DINTPGTPTEEIIGFIRGLFFH

CPn_0134   169131   167467
groEL-HSP-60
FADYRKLRRTTMAAKNIKYNEEARKKIHKGVKTLAEAVKVTLGPKGRHVVIDKSFGSPQV
TKDGVTVAKEIELEDKHENMGAQMVKEVASKTADKAGDGTTTATVLAEAIYSEGLRNVTA
GANPMDLKRGIDKAVKVVVDELKKISKPVQHHKEIAQVATISANNDSEIGNLIAEAMEKV
GKNGSITVEEAKGFETVLDVVEGMNFNRGYLSSYFSTNPETQECVLEDALILIYDKISG
IKDFLPVLQQVAESGRPLLIIAEEIEGEALATLVVNRLRAGFRVCAVKAPGFGDRRKAML
EDIAILTGGOLVSEELGMKLENTTLAMLGKAKKVIVTKEDTTIVEGLGNKPDIQARCDNI
KKQIEDSTSDYDKEKLQERLAKLSGGVAVIRVGAATEIEMKEKKDRVDDAQHATIAAVEE
GILPGGGTALVRCIPTLEAFLPMLANEDEAIGTRIILKALTAPLKQIASNAGKEGAIICQ
QVLARSANEGYDALRDAYTDMIDAGILDPTKVTRSALESAASIAGLLLTTEALIADIPEE
KSSSAPAMPSAGMDY

CPn_0135   169448   169143
groES-10KDa Chaperonin
MSDQATTLRIKPLGDRILVKREEEEATARGGIILPDTAKKKQDRAEVLVLGTGKRTDDGT
LLPFEVQVGDIILMDKYAGQEITIDDEEYVILQSSEIMAVLK

CPn_0136   171419   169569
pepF-Oligopeptidase
KGVPSLMTTELKTEALPTRTQVPRTQVPDKHCWDTTLMYANREEWKKDFDLCSSGKDRSPIWPEF
SPSHYQIDNPESLLELLSKKFSVERKLDQLYIYAHLIHDQDITNPEGESDYQSIVYLYTL
FSQEISWIOPALIALSEEKVAALLSSSVLAPYRFYLEKIFRLSPHTGTANEEKILASSFA
ALNVSNKAFSSLSDAEIPFGIAKDSNGEEHPLSHALASLYMQSPDQELRRTAYLAQFQRY
YDYRNTFANLLNGKVQAHLFEAKARNYPSCLEASLFQHNIPTTVYINLINETKKHTSLIN
RYFNLKKEALNLKEFHFYDVYAPISQTTSKNYSYEEGVDLVCKSLLPLGTHYVEILRNGL
LSNRWVDRYENKHKRSGAYSSGCYDSAPYILLNYTNTLYDVSVIAHEAGHSMMSYFSREA
QPYHDAQYPLFLAEIASTFNEMLLMEALSKSDQSKEDKIVIITKTLDTIFATLFRQTFFA
AFEYEIHSAAEQGTPLTEEFLSATYGNLQKEFYGGVVTSDSLSALEWARIPHFYYNFYVY
QYATGIIAALSFAEKILTQEPGALELYLKFLKSGRSDFPLNILKKSGLDMTTSAPLDKAF
AFITKKIDLLSSLLSED

CPn_0137   172263   171502
ybgI-ACR family
VCSMNVADLLSHLETLLSSKIFQDYGPNGLQVGDPQTPVKKIAVAVTADLETIKQAVAAE
ANVLIVHHGIFWKGMPYPITGMIHKRIQLLIEHNIOLIAYHLPLDAHPTLGNMWRVALDL
NWHDLKPFGSSLPYLGVQGSFSPIDIDSFIDLLSQYYQAPLKGSALCGPSRVSSAALISG
GAYRELSSAATSQVDCFITGNFDEPAWSTALESNINFLAFGHTATEKVGPKSLAEHLKSE
FPISTTFIDTANPF

CPn_0138   174094   172700
hemL-Glutamate-1-semialdehyde-2,1-aminomutase*
TNSRLFLAIKDQLLQNMWKLTKRNSMLNCSNQKHTVTFEEACQVFPGGVNSPVRACRSVG
VTPPIVSSAQGDIFLDTHGREFIDFCGGWGALIHGHSHPKIVKAIQKTALKGTSYGLTSE
EEILFATMLLSSLKLKEHKIRFVSSGTEATMTAVRLARGITNRSIIKFIGGYHGHADTL
LGGISTTEETIDNLTSLIHTPSPHSLLISLPYNNSQILHHVMEALGPQVAGIIFEPICAN
MGIVLPKAEFLDDIIELCKRFGSLSIMDEVVTGFRVAFQGAQDPQLRMIKGCGGGAIFREKILLRA
GLPAAALVGHRSILDHLMPEGTIFOAGTMSGNFLAMATGHAAIQLCOSEGFYDHLSQLEA
LFYSPIEEEIRSOGFPVSLVHQGTMFSLFFTESAPTNFDEAKNSDVEKFQTFYSEVFDNG
VYLSPSPPLEANFISSAHTEENLTYAQNIIIDSLIKIFDSSAQRFF

CPn_0139   174686   174093
yqgE
SPTKNKLRDIMKIPYARLEKGSLLVASPDINQGVFARSVILLCEHSLNGSFGLILNKTLG
FEISDDIFTFEKVSNHNIRFCMGQPLQANQMMLLHSCSEIPEQTLEICPSVYLGGDLPFL
QEIASSESGPEINLCFGYSGWQAGQLEKEFLSNDWFLAPGNKDYVFYSEPEDLWALVLKD
LGGKYASLSTVPDNLLLN

CPn_0140   175140   174673
yqdE
PRSNQQKIFCMSLEKELLEETPLVLLNFYKLVSFCNYAGMILGTEEKKFAIYGHVSMCQA
FQGADTEGHSPORPFAHDLLNFVFSGFDIQVLRVVINDYKDNVFYTRLFLEQKDREFLYV
VDVDARPSDSIPLALTHKIPILCVKSVFDAVVPYEE

CPn_0141   175817   175110
rpiA-Ribose-5-P Isomerase A
HSSSAVEKDLHLHEKKCLAHEAATQVTSGMILGLCSGSTAKEFIFALAHRIQTESLAVHA
IASSQNSTALAKQLAIPLLNPEKFSSLDLTVDGADEVDPQLRMIKCGGGAIFREKILLRA
AKRSIILVDESKLVPVLGKFRVPLEIGRFGRSAIIEEIRHLGYEGEWRLQDTGDLFITDS
SNYIYDIFSPNSYPNPEKDLLKLIQIHGVIEVGFVIEKVEVWGSSNSQLISKKYSV .

CPn_0142   176121   175816
No robust homolog present in Genebank/EMBL as of 11/7/98
SHSYVRKGTLEKFHFKILQLLSTKNSILHFCSHFEICRVSHDNAIQKIRHYPLKPIAEN
RINTLSFYDLKIDYPKDSSKRFPFLYSISPIPLHFLWEYFST

CPn_0143   177347   176214
yyxIG_US_1 hypothetical protein
RRTIMSITSLKRPLKSHFDCVCGFLRIEHLFKTFECLKESSISLDDLMQIEDIAIQDLIKK
QKAVILGFITDSEFRRATWHYDFHWSFIVSSJUHPATESVFFDSERAMIDDTVLTDKISVS
HHFVGHFKFVKALEDEFTTAKSTLPAIAGFLFSMIFMHSIEVTRKPFYIVTNSELIEDIVA
SSYRKVIFDLYDAKSRYIALINGTPCSISLVHGVWGGWIGIDEKFGIQDLLQQYILINNLVIAD

PPDDLV/RILJV/CRGN/HCKFFA:FGYDFIAKPLF. .V/OGYYLEFDHER5GDF5PLTFI
5GEKTV:LGLVTSKTPTLEIKDEVIARIHQAADYLPLERL5L5POCGFA5CEIGNKLTEE
EQWAKVALVKEI5EEVWK

CPn_0144   177242 180560
clpB-Clp Protease ATPase
KVLGVNFMEKFGDAV5EALEKAFELAK5SKHTY/TENHLLLALLENTE5LFYLVIKDIHG
NP5ILJITAVKDALGREPTV/5GEVDPKP5PGLCTLLRDAKQEAKTLGDEYI5GDHLLLAF
.IV.III.GL-I PT'II., ... II.. 'IITTI IV.II'.ILI I...II.I.ILI.GI
III. I.I. II. I.III III.IT-I/'YLI.IIP-VI.'II MII III ''ITTII V'I.IALPI/VII.IIPI.'I
KQLVVLDMGALIAGAKYRGEFEERLKSVLKDVEGDGEHIIFIDEVHTLVGAGATDGAMD
AANLLKPALARGTLHCIGATTLNEYQKYIEKDAALERRFQPIFVTEP5LEDAVFILRGLR
EKYEIFHGVRITEGALNAAVLL5YRYIPDRFLPDKAIDLIDEAA5LIRMQIG5LPLPIDE
KERELAALIVKQEAIKREQ5P5YQEEADAMQK5IDALREELA5LRLGWDEERKLI5GLKE
KKN5LE5MKF5EEEAERVADYNRVAELRY5LIPQLEEEIKQDEA5LNQRDNRLLQEEVDE
RLIAQVVANWTGIPVQKMLEGEAEKLLILEE5LEERVVQFPAV5AV5D5IRAARVGLND
PQRPLGVFLFLGPTGVGKTELAKALADLLFNKEAAHVRFDM5EYMEKH5I5KLIG55PGY
VGYEEGGG5L5EALRRRPY5VVLFDEIEKADKEVLNILLQVFDDGILTDGKKRKVNCKNAL
FIHT5NIG5PELADYC5KKG5ELTKEAIL5VV5PVLKRYL5PEFMNRIDEILPFVPLTKE
DIVKIVGIQMRRIAQRLKARRINL5WDD5VILFL5EQGYD5AFGARPLKRLIQQKVVILL
5KALLKGDIKPDT5IELTMAKEVLVFKKVETP5

CPn_0145   180717 182369
CT114 hypothetical protein
NCAA5FIWLNK55HRNLR5PMFK5FIVRYMFVGGLV5FLLPIPDLECANNVTKTYDKKA5
VI5RDLKLQEDCQKFWNLDPYKLE5LCAYQVLYHDDY55KRIRELFPQIQKDEVPIFATH
ILTLCKVDRGF5PEEI5LIQKL5YPGL5LA5LRG5TEIDPNTDLARALVV5EF5GDLGKN
RADYY5NCLDILALRIHAERQRYLDQ5PCVPGT5EFHKATIEAINTILFYEEAVRYP5KK
EHF5DEF5FL55VTDRKFGVCLGV55LYF5L5QRLDLPLEAVTPGHIYLRYQGGEVNIE
TTAGGRHLPTA5YCDCLDLEDLQVRTPEEMIGLTFMNQG5FALQKKKYKEAEEAYKKAQE
YLGDEELQELLGFVQILGGKKKEGK5LIGK5PRA5QKG5VAYDYLGKTAEAVALLEKCVEDIPNDL
PG5NYEEIA5YEEELKKAMK55HPCCEGQRRLA5VAFHLGKTAEAVALLEKCVEDIPNDL
5LHLRLCKILCDRHEYTKALKYFIIAERLMEDQGFLKKDNR5FALFYEVKKII5KVAPQK
ANTLLLME5ER

CPn_0146   182595 183095
No robust homolog present in Genebank/EMBL as of 11/7/98
IIVGI5M555EVVFQTVHGLGFGGL55K5VVPFKK5L5DAPRVVC5ILVLTLGLGALVCG
IAITCWCVPGVILMGGICAIVLGAI5LAL5LFLWGLF5NCCG5KRVLPGEGLLRDKLLD
GGF5RAAP5GMGLPGDG5PRA5TP5CLEELQAEIQAVTQAIDQM5DD

CPn_0147   183213 183671
No robust homolog present in Genebank/EMBL as of 11/7/98
HGGPMAVQ5IKEAVT5AAT5VGCVNC5REAIPAFNTEERAT5IAR5VIAAIIAVVAI5LL
GLGLVVLAGCCPLGMAAGAITMLLGVALLAWAILITLRLLNIPKAEIP5PGNNGEPNERN
5ATPPLEGGVAGEAGRGGG5PLTQLDLN5GAG5

CPn_0148   183822 185702
pknI-S/T Protein Kinase
GKWWRV55ME5EKDIGAKFLGDYRILYRKGQ5LW5EDLLAEHRFIKKRYLIRLLLPDLG5
5QPFMEAFHDVVVVKLAKLNHPGIL5IENV5E5EGRCFLVTQEQDIPIL5LTQYLK5IPRK
LTELEIVDIV5QLA5LLDYVH5EGLAQEEWNLD5VYIHILNGVRKVILPDLGFA5LIKER
ILDGFI5DEENRE5KIKERVLLHT5EGKQGREDTYAFGAITYYLLFGFLPQGIFPMP5KV
F5DFIYDWDFLI55CL5CFMEERAKELFPLIRKKTLGEELQNVVTNCIE55LREVPDPLE
55QNLPQAVLKVGETKV5HQQKE5AEHLEFVLVEAC5IDEAMDTAIE5E555GVEEGY5
LALQ5LLVREPVV5RYVEAEKEEPKPQPILTEMVLIEGGEF5RG5VEGQRDELPVHKVIL
H5FFLDVHPVTNEQFIRYLECCG5EQDKYYNELIRLRD5RIQRR5GRLVIEPGYAKHPVV
GVTWYGA5GYAEWIGKRLPTEAEWEIAA5GGVAALRYPCGEEIEK5RANFFTADTTVM5
YPPNPYGLYDMAGNVYEWCQDWYGYDFYEI5AQEPE5PQGPAQGVYRVLRGGCWK5LKDD
LRCAHRHRNNPGAVN5TYGFRCAKNIN

CPn_0149   185706 187700
dnlJ-DNA Ligase
ERFMKEEN5QAHYLALCRELEDHDY5YYVLHRPRI5DYEYDMKLRKLLEIER5HPEWKVL
W5P5TRLGDRP5GTF5VV5HKEPML5IAN5Y5KEEL5EFF5RVEK5LGT5PRYTVELKID
GIAVAIRYEDRVLVQAL5RGNGKQGEDIT5NIRTIR5LPLRLPEDAPEFIEVRGEVFF5Y
5TFQIINEKQQQLEKTIFANPRNAAGGTLKLL5PQEVAKRRKLEI5IYNLIAPGDND5HYE
NLQRCLEWGFPV5GKPRLC5TPEEVI5VLKTIETERA5LPMEIDGAVIKVD5LA5QRVLG
ATGKHYRWALAYKYAPEEAETLLEDILVQVGRTGVLTPVAKLTPVLL5G5LV5RA5LYNE
DEIHRKDIRIGDTVCVAKGGEVIPKVVRVCREKRPEG5EVWNMPEFCPVCH5HVVREEDR
V5VRCVNPECVAGAIEKIRFFVGRGALNIDHLGVKVITKLFELGLVHTCADLFQLTTEDL
MQIPGIRER5ARNILE5IEQAKHVDLDRFLVALGIPLIGIGVATVLAGHFETLDRVI5AT
FEELL5LEGIGEKVAHAIAEYF5D5THLNEIKKMQDLGVCI5PYHK5G5TCFGKAFVITG
TLEGM5RLDAETAIRNCGGKVG55V5KQTDYVVMGNNPG5KLEKARKLGV5ILDQEAFTN
LIHLE

CPn_0150   187759 192444
CT147 hypothetical protein
IIYKFFY5YNCPYFI5EFFVLLGVNMA55NN5TKGCGIP5WVNPNVQWNRA5QVGDQEA
N5LTPEAQT5R5WF5DRKHFLEVLDV5LEEMENNDLYKY5RYKTIILIATLVTVAITCIV
PI5MVFGIPMWVPCLILFGAGL5AFL5HRLQ5KCKEIHLRYRAYQIYRQQLL5QYPDLR
K5TLYKY5ITHVKPKKGFVGKLVENLRPDLHKNKDDGGAAAD5RLDFAGYGVKHYQTDAL
LGV5GVN5VAWQRLA5LIM5VKNDILNDVG5REPIDFAQR5ALVV5GKDIGGEIQPGGIL
DI5RDILAICGYCMNVGVEAKKAIDQYKKWYLN55TFIAWNPQLPAIAQ5YLLEQQRHLD
YAAKIFQDL5ALTTAHGTGOALEDL5LLCYYDQLIE5KGVGEKIIA5IHQKHLDLAMQD
:XCQEHLKKW5NLYHVF5ITIKEFTEGKLEQNEVV5RIQRLRGKLEK5KC5ILGNCRTNA
EYATK5EKKLADYLLQIGDREPFLTGMHKAIATGKAIQGKVEGVI5QHPEKQIMMLRC5I
EPLEGMLRREDWGAILOKNEDEVLALK5TMEAQLQGFKDLVGTWEGKYQEFKKNKL5KVL
V/DFTK:5Y5NLLNRLEVLHAE5CTDDLVLHVDRM5EDLKKTIEEIDGNLFQVTPEEL5LL
APE7Q:IHNELPLIVQEGNRLQEAICCEGV5QGLMLLIICLLMENDEKINKNIE55RKNLVA
TAP/QAR:IDARNICKQGLAPLIQRRNAC5LDNILQNM/LFNG5IRNIHALDTETLVAT55NM
F:MIIFTFDWNIYTNLLDVLEIQ5KPAPAPMENFDLP/:ALPEEVQDAVAEDV5GTHRLVHHQ
VLFRR:ADIKNM.:QLQK5INKWFMAKAIVLGIVA/LFCVL:AIFIQYNILCLLIL5CVG
LLLFQV:HL.IFDRI5K5KEFEKQVLETAQ5LIPATY5LPGEFNNKDLNRLAKLQDNLNLE
.5P5FWAKNIV:FILEJI:FFTKEK;IKDUTKEFRKQ5FIILNKRIKRRFKEGLI5QEAPVVRPT
II5DJIKNAEVFAHLIIRELEHLQKQKEEI5IRGDAL7/5EPMCL:LCEK5KYDNEKAHAAAMT
KRV5IKIANIDRIQKNNETYVRIQNFFRTLIQEKLGRDTVQEIDVVKEAKELHELAAIIYG
NT/:IK:LY5/DAKQKFKENVLIIAXGENLELEAVLIY/7TACQ:ILCHRIQMQA5FRERILLNP
I/IAIKINFAEICI/A:IREFMLKTLGL:VLTDFVRF5:D:FE5TV:TYN/ILKVREQLFDIEQRL
QALDITV:IFDYAAVQAALAAV/VRKIIE5LIV5TYGLV5A/JE:QT:;:KVTTLMRDLHAVEELV
FKY/VETV7RLNIG:IY:ILJRVIE:VLI5HLRDCD5:52K7II5DVVKKLFEILNNNV/J7NPNDPEC

QKYMQILLDAPV5LLYGAFK   :EFLLNIFTELNIAN5TKAAEEEAKRYVEEKGRGFETY
WEEAKQRLEAIAAELDDLRNQETLLECE:IPLANLK:GIF5DLNLREKV5VEKAALEEEIQ
GIQEQYAEMQGIEDL5LKQKFEDLQKKLEALEERLLQIGRRID55VDKQKELLGLLGREE
AA

CPn_0151   194179 192425
mhpA-Monooxygenase
CYENLFHYPRA5MADILVIGANPTGL:ILANML IQHGI5VKVIDHRA5PEDP5FLDCRKLP
.VIII.IL:FIIII?I' .. I W'II II IIII.V':I I.':IIIKAVYKPTLLEKFTC:ATPIIIIPFI.PTT:V:
IIF:HL:FGT:IPI ITILLII/L... I.I.... ...I. IP.. IILILT I.T-I'T'TIT 'YNI.I-:IEACN
NLDIRDLVK:JLRAARKINRKT/IFIRAUEGUFFEEDLRIHLLL/ITKIFLNFVFTNFCEKTK:
LCLPQGTH5I5PKLKCKLLVTTYNLVI5DENFHIKT5HHAFPPEHGNVLFL5GL5NTLLL5
YLNGINTNIHAAFNLAWKLLPVLKKAALKHLVITKEQEDGNILPYI5PTTEKRAKKLPF5
RFYTPALMY/FLKGCRKFNTTGEEYYYPPHQALKYR55DIIKM5PQDKEIHGPGPGMRAI
DARLENG5FLLDPLAK5KHLLIFFKDIPDLKEALQEEYGEWIEICNVKEPRILNLYHANP
N5LFIIRPDRYIGYRTHTFKLHELI5YLLRIFA5EKT5

CPn_0152   195274 194318
CT149 hypothetical protein
LIKMRKVAFLV5CLF5VAIGA5AAPVRVPGFPQIPEDLVQIKTEVCPKQEVCLAVTIKCD
DHNLIGVLHLPNTPTPEGGFPTVVLFHGFRGTKFGGLTGAYRKLGRKFAAVGIATLRVDH
AGCGD5EGVAEEVPIETYLRDAQTILETVQEHPDLNAYRLGI5GF5LGCHIAFELAKIYN
PRDLNIKAL5VWAPIADGGILLKELYENF5KHGEGDII5VGKDFGFGPPPIIVC5GDVDL
LIRIQDHVTAN5LPTKPYILHQQGIDDTLV5RTQQTLFKNTAPGRMTFI5YPNTGHNLAT
APDLDHILDQIV5HFQRTL

CPn_0153   195430 197892
leuS-Leucyl tRNA Synthetase
NMRYDPNLIEKKWQQFWKEHR5FQANEDEDKVKYYVLDHFPYP5GAGLHVGHLIGYTATD
IVARYKRARGF5VLHPMGWD5FGLPAEQYAIRTGTHPKVTTQKNIANFKKQL5AMGF5YD
EGREFAT5DPDYYHWTQKLFLFLYDQGLAYMADMAVNYCPELGTVL5NEEVNGF5IEGG
YPVERKMLRQWILKITAYADKLLEGLDALDWPENVKQLQKNWIGK5EGALVTFHLTQEG5
LEAFTTRLDTLLGV5FLVIAPEHPDLD5IV5EEQRDEVTAYVQE5LRK5ERDRI55VKTK
TGVFTGNYAKHPITGNLLPVWI5DYVVLGYGTGVVMGVPAHDERDREFAEHF5LPIHEVI
DDNGVCIH5NYNDFCLNGL5GGQEAKDYVINYLEMR5LGRAKTMYRLRDWLF5RORYWGEP
IPIIHFEDGTHRPLEDDELPLLPPNIDDYRPEGFGQGPLAKAQDWVHIYDEKTGRPGCRE
TYTMPQWAG5CWYYLRFCDAHN5QLPW5KEKE5YWMPVDLYIGGAEHAVLHLLY5RFWHR
VFYDAGLV5TPEPFKKLINQGLVLA55YRIPGKGYV5IEDVREENGTWI5TCGEIVEVRQ
EXM5K5KLNGVDPQVLIEEYGADALRMYAMF5GPLDKNKTW5NEGVQGCRRFLNRFYDLV
T55EVQDIEDRDGLVLAHKLVFRITEHIEKM5LNTIP55FMEFLNDF5KLPVY5KRAL5M
AVRVLEPIAPHI5EELWVILGNPPGIDQAAWPQIDE5YLVAQTVTFVVQVNGKLRGRLEV
AKEAPKEEVL5L5R5VVAKYLENAQIRKEIYVPNKLVNFVL

CPn_0154   197874 199202
gseA-KDO Transferase
T5EFCPMLRGVHRIFKCFYDVVLVCAFVIALPKLLYKMLVYGKYKK5LAVRFGLKKPHV
PGEGPLVWFHGA5VGEVRLLLPVLEKFCEEFPGWRCLVT5CTELGVQVA5QVFIPMGATV
5ILPLDF5IIIK5VVAKLRP5LVVF5EGDCWLNFIEEAKRIGATTLVINGRI5ID55KRF
KFLKRLGKVPF5PVDGFLLQDEVQKQRFL5LGIPEHKLQVTGNIKTYVAAQTALHLERET
WRDRLRLPTD5KLVILG5MHR5DAGKWLPVVQKLIKEGV5VLWVPRHVEKTKDVEE5LHR
LHIPYGLW5RGANF5YVPVVVVDEIGLLKQLYVAGDLAFVCGTFDPKIGGHNLLEPLQCE
VPLIFGPHIT5Q5ELAQRLLL5GAGLCLDEIEPIIDTV5FLLNNQEVREAYVQKGKVFVK
AETA5FDRTWRALK5YIPLYKN5

CPn_0155   199697 199488
No robust homolog present in Genebank/EMBL as of 11/7/98
N5L5FGVPFLEKLKI5LIPIEEMRHELFMKTHN555NGF5NQEKGIRTYFKR5DLLGYEDL
YFLRENINPN

CPn_0156   200147 199770
No robust homolog present in Genebank/EMBL as of 11/7/98
LGKQKLLARHMMHNIVVL5EEPGR5AFLGRTAFFPNKYPIACGGVGIP5TIGNLFTIWYC
FYFYRAATPQ5DHPDGCGFILLERLKELGAGFFYCDLRE5NTTGFTLFFEG5NKGVLKNH
LFIRDE

CPn_0157   200753 200298
No robust homolog present in Genebank/EMBL as of 11/7/98
F5FVTYKEALNIYQF5PGA5PNWQA5LMAQLN5YFCLGGETVTRII5LRP5GLILAKKE
KAVV5TAEKILKIL5FILFPLVLIALAIRYLLYNKFNKDLDRAVFFIPTEITTKAEELIIA
KNPALVKEAALTV5PLFY5LPKKYQLMKVETP

CPn_0158   201463 200894
No robust homolog present in Genebank/EMBL as of 11/7/98
PPKITL5INIDLLLEDLDTD5IPWPKLYL5EDFDFAYYPE5KAIIDTVAKLEKNNPGEEF
CLE5KKILARYLLEQLFKLETGLNFPT5TIDGGRE5FLIEF5HETKKPTWAFIYFYYYH
5NGPKLEKDFKQAGCEVHNRLLNLGLKYRPQAGAQNDGRNGGPYGPIGFLIVWEENYG5V
LKDHGFIKDN

CPn_0159   201811 201467
No robust homolog present in Genebank/EMBL as of 11/7/98
CCFGGETATRIF5HTP5GF5LATEEKY/QV5TAEKVIKILALIFFPIILIALAIRYFLHRK
FDRKCFVIPCDTPKELELILAANPQLVEKAAREVHPGFFALPTKYQ5MYIQT5KG

CPn_0160   203794 202127
pfkA-Fructose-6-P Phosphotransferase
TVELL5LNK5YFEIQRLRYRPEILTLLETIR5KHIQET5GPP5PPPELQKHIPNLCRIPE
V5IYTEQET55KPLKIGVLL5GGQAP7/5HNVVIGLFDALRVFNPKTRLFGFIKGPLGLTR
GLYKDLDI5VIYDYNMCKGFDML55GP5EKIKTEDOKKNILNTVKQLKLDGLLIIGGNN5N
TDTAMLAEYFLAHNCKT5VIGVPKTIDFDLKNCWIET5LGFHIT5CRTY5EMIGNLAKDAL
5AKKYHUIFIRLMCQQACYTTLECGLCTLPNIALI5ELIATRKI5LKQL5EDLALGLVRRY
K5CKGIYCTVLIPEGLIEHIFDTRKLIDELNVLIANCDG5IEKILGKLGPETLKTFHLFPK
DIANQLLIARDGHGNVRV:KIATEELLAVMVKKEIEKIKPHMEFINVGHFFTYEARAGFP
5NFICNY/GIALGI5ALFLVROKTY/7MIT INNIAQ:YTEWQKGATPIYKMMHLENRCGTE
TYV IKTD5VPPKGPAVQHILIQQ5DCGI/EDLYPFPGPLQYFGKEELIDQRPLTLIWENQT
H5PFQALY5F5GKR:L

CPn_0161   204658 204708
(predicted acyltransferase family)
HR:5T5RKQEFLLITI/VVLEKHEQ/TMF5IITLIJNFTTFCLLIFFLIIIYNPFYPIVILLHG
IA5IKT/:5KRIHVRLAUELTRU/IAALPVDLIJ5IGDLIE5ELMDF:ILFNYKQRIFEIIEYT
H5IJIIDQERLAIFR55L/X5TLAIJ/TLIFFNKIKALAVWAIPTI:XIELMAAPV//YNAPEVI

TM:QKGAITYACHTLNPDFYTQFLKIDIVKELM   NLPPILYMQGEQDLLVSINHRTL
FTEAFANQDKPITILTYPDVDHAFPFAESSALSDLTQWLKRELTSGE

CPn_0162   205870 204803
No robust homolog present in Genebank/EMBL as of 11/7/98
FVVTLYNIQSPFRIMKLYSISSDVDTPWIFQLMSKVDSYLFLCGNRIKVVSIVMQEPNLI
IGKVENVRISTIVKILKILSFLIFPLILIALALHYFLHAKYANHLLVSKILERAPQYVPI
IVIRSGDTASHYKLTTLVPVGOKNLQAMGSNPLEVEAALRTTKPSFFCVPAKYRQIIISSH
   ...............WITH...........ISKADF.....KILF.....
   ..............EIFEALL.HITFIPLTLH..TURYIYSHFTLHFTIWDVFFPQQ
PLDEDRGGGFEILEQLQELGVRFPICPSQGPDNPNFQGFQGIRIYWEDSYQPNKEV

CPn_0163   205831 206394
No robust homolog present in Genebank/EMBL as of 11/7/98
FEKAIVYCIKCKQIIKCISIIHTPTPATPLCTEGEIFPGPVDSAIQNDLERLLTVKKRPD
IIREYLRAGGSLVTTYPKEGORLRSPEQLRVLDDLVQSYPNHLHAIELDCGAIPODLIGA
TYIITFADFSTYILSLRSYQANSPSDDTWGIWFGSIDDPVQAVISFLKDHGFALPSTLAQ
DPLLCTNK

CPn_0164   206444 206998
No robust homolog present in Genebank/EMBL as of 11/7/98
LCFKCIYIKIIFSFLKQLMTRSTIESSDSLCSRSFSQKLSVQTLKNLCESRLMKITSLVI
AFLTLIVGGALIALACGGVLSFPLGLILGSVLVLFSSIYLVSCCKFFTLKEMTMTCSVKS
KINIWFEKQRNKDIEKALENPDLFGENKRNVGNRSARNQLEMILHETDGIILKRYMKGAK
MYFYL

CPn_0165   206983 207582
No robust homolog present in Genebank/EMBL as of 11/7/98
NVLLFMNWVPKTIDHVDPESEIDIRKVVSCYKLIKECOPEFRSLISELLGVIRCGLRLLK
RSKYQEQARTLPLFCLTRSYYODGYLTPLRAGPRDLINHYIHLRRRENPKHFFSP
KHPCYYARLAFNESVCVYRELFDIERLTKMYVEGDYSKEQEKNLQAILSFVKTLDEGKDF
LIEHKDTDLIGRGFTDVFCT

CPn_0166   207594 207962
No robust homolog present in Genebank/EMBL as of 11/7/98
NCLKQYNKSDSIMSESINRSIHLEASTPFFIKLTNLCESRLVKITSLVISLLALVGAGVT
LVVLFVAGILPLLPVLILEIILITVLVLLFCLVLEPYLIEKPSKIKELPKVDELSVVETD
STL

CPn_0167   208309 207977
No robust homolog present in Genebank/EMBL as of 11/7/98
NLWSHFPRGFFMLPFCPTILLAKPFLNSENYGLERLAATVDSYFDLGQSQIVFLSKQDQG
ITVEELSAKDRKFKPGSMNCTLYTEDPILPAHNSFSNCSDIQMRTPISPIH

CPn_0168   208716 208417
No robust homolog present in Genebank/EMBL as of 11/7/98
SYINLRRRENPEHFFNPGHPCYYARLAFNESVRIYRKLFNTAELKQMYGAGDYEQQNEDN
LKSILSFVQILDEKDGFDDFLATHKDTTFIGRGGADIFCS

CPn_0169   209537 208710
No robust homolog present in Genebank/EMBL as of 11/7/98
SFHIEFTIGENNMKNVGSECSQPLVMELNTQPLRNLCESRLVKITSFVIALLALVGGITL
TALAGAGILSFLPWLVLGIVLVVLCALFLLFSYKFCPIKELGVVYNTDSQIHQWFQKQRN
KDLEKATENPELFGENRAEDNNRSARSQVKETLRDCDGNVLKKIYERNLDVLLFMNWVPK
TMDDVDPVSEDSIRTVISCYKLIKACKPEFRSLISELLRAMQSGLGLLSRCSRYQERAKT
VSHKDAPLFCPTHSYYRDGYLTPLRAGPRYIINRAI

CPn_0170   211098 210025
No robust homolog present in Genebank/EMBL as of 11/7/98
NVRKNHIIRGEKYNTCTVIAFVLSMSYDTLFKNLEKEDSVHKICNEIFALVPRLNTIACT
EAIIKNLPKADIHVHLPGTITPQLAWILGVKNGFLKWSYNSWTNHRLLSPKNPHKQYSNI
FRNFQDICHEKDPDLSVLQYNILNYDFNSFDRVMATVQGHRFPPPGIQONEEDLLLIFNNY
LQQCLDDTIVVTEVQQNIRLAHVLYPSLPEKHARMKFYQILYRASQTFSKHGITLRFLNC
FNKTFAPQINTQEPAQEAVQWLQEVDSTFPGLFVGIQSAGSESAPGACPKRLASGYRNAY
DSGFGCEAHAGEGIETRTIFSSAKVNPEGLIEITRVTFSSLKRKQPSSLPIRVTCQLG

CPn_0171   212444 211149
*guaA-GMP Synthase
IIKLQSARRHLNTIFILDFGSQYTYVLAKQVRKLFVYCEVLPWNISVQCLKERAPLGIIL
SGGPHSVYENKAPHLDPEIYKLGIPILAICYGMQLMARDFGGTVSPGVGEFGYTPIHLYP
CELFKHIVDCESLDTEIRMSHRDHVTTIPEGFNVIASTSQCSISGIENTKQRLYGLQFHP
EVSDSTPTGNKILETFVQEICSAPTLWNPLYIQQDLVSKIQDTVIEVFDEVAQSLDVQWL
AQGTIYSDVIESSRSGHASEVIKSHHNVGGLPKNLKLKLVEPLRYLFKDEVRILGEALGL
SSYLLDPNRFFGPGLTIRVIGEILPEYLAILRRADLIFIEELRKAKLYDKISQAFALFLP
IKSVSVKGDCRSYGYTIALRAVESTDFMTGRWAYLPCDVLS3CSSRIINEIPEVSRVVYD
ISDKPPATIEWE

CPn_0172   213237 212440
*impD-Inosine 5'-monophosphase dehydrogenase (COOH-terminal
region only)
APIGAAIGIGPLGISRAHHLVEAGANVLVIDTAHAHSKGVFQTVLEIKSQFPQISLVVGN
LVTAEAAVSLAEIGVDAVKVGIGPGSICTTRIVSGVGYPQITAITNVAKALKNSAVTVIA
DGRIRYSGDVVKALAAGADCVMLGSLLAGTDEAPGDIVSIDEKLFKRYRGMGSLGAMKQG
GADRYGTQCQOKKLVPGGVGLVAYKGSVHDVLYQILGGIRSGHGYVGAETLKDLKTKAS
F/RITESGRAESHIHNIYKVQPTLNY

CPn_0173   214041 213715
No robust homolog present in Genebank/EMBL as of 11/7/98
TIFDLIYKIDSYKHQQGFMDFSVVPDRFVESTSPSPIEDIDAKTLVSNCCHYCSRCLFIF
LMLLSIIICFSVYGTSGETASLVFGILSLIVLVLLIIECRNNECCRRIS

CPn_0174   214215 214724
No robust homolog present in Genebank/EMBL as of 11/7/98
VIFIWF/EKIVILMIMTFICNSPSPALNPELSLIPPPTLVSSMTQTSLAYTIPAQGRRS
TLRIILLIFIIIGLATIICTFIVIFFLNGLNLLSTPSIICMXCLIIVGLLFLIMGLYFM
GGLDVILVLLLQVELSOAEEEREEEYIQEIEALRCAPRAECPTESPSTWL

CPn_0175   214856 215275
No robust homolog present in Genebank/EMBL as of 11/7/98
LLLACFGFLLRRPDMEQINKVIQDTTTVLYALNSFDPRLLLDTHRLCKQSPLEAENALGE
FIFILDTICFPLEKVAICILPCYHPKFYLSFIDRDDOGVHYEVLDGVFLKTVAACIIENS

FLTDGMSPELLSEVKEALK.   — -

CPn_0176   216271 216519
CT153 hypothetical protein.
NDDDPMDESDGEEASKDSAFSASFSYEFVKSSTRESKNTVTHSTASRTLYILRQDCSYDP
RALKVDDEFRYWVEKRLDAKNPDSLNAFVKEVGTHYVASVTYGGIGFQVLKMSYLQVEEL
EKEKISISVAAASSLLKSKTINATEKGYSSYQSESSAQTVFLGGTVLPDLQODKLDFKDW
SESIPNEPIPLAISVSSITDLIIPELFFSEDAQVLSQKKSALQQVILNYLESHKPKEEGP
.....XNLHINL...ALTYG...VVDYEALLIL..LWIYATFF.AIYKDRCTYT
LEKLNTTGDLFIRJSOEIRLKIINTJRVLATTJMLDLJRLFTIJSDJVFIITV

CPn_0177   217513 216608
No robust homolog present in Genebank/EMBL as of 11/7/98
DKREQTKSKFIFLSEESMKQPMSLIFSSVCLGLGLGSLSSCNQKPSWNYMNTSTSEEFF
VHGNKSVSQLPHYPSAFRTTQIFSEEHNDPYVVAKTDEESRKIWREIHKNLKIKGSYIPI
STYGSLMHPKSAALTLKTYRPHPIWINGYERSFNIDTGKYLKNGSRRRTSHDGPKNRAVL
NLIKSSGRRCNAIGLEMTEEDFVIARRREGVYSLYPVEVCSYPQGNPFVIAYAWIADESA
CSKEVLPVKGYYSLVWESVSSSDSLNAFGDSFAEDYLRSTFLANGTSILCVHESYKKVPP
QP

CPn_0178   218052 217789
No robust homolog present in Genebank/EMBL as of 11/7/98
VKEYLDFLVQRNVERDPQTKRHCTVSQKFGGESIDAKTTTGQLFHIAGKTEPGHGKLCLG
ESILKQLLALGIITGYENREREVWVYLD

CPn_0179   218550 218056
No robust homolog present in Genebank/EMBL as of 11/7/98
PKIWDTHFETRIEATSVPKFNRRLRKSFHKSGRSSRPSKACVANFFNFTLQAGRSGIIPG
KKAILLNVNDAKTPNYSCIFESIGFFNEQDLEAQHNQQAALVRKILKVVPHHFLKGLIAK
LPRSLKKDRKFMSSLIFTKLSYALDLSAPMHLEGKPNLSYEEKLD

CPn_0180   218963 218355
No robust homolog present in Genebank/EMBL as of 11/7/98
TSLHKILDCKYKPVFIQNTVASETYPSQILHAQREVRDAYFNQADCHPARANQILEAKKI
CLLDVYHTNHYSVFTFCVDNYPNLRFTFVSSKNNEMNGLSNPLDNVLVEAMVRRTHARNL
LAACKIRNIEVPRVVGLDLRSGILISKLELKQPQFQSLTEDFVNHSTNQEEARVHQKHVL
LISLLLCKQAVLESFQEKKRSS

CPn_0181   219175 218777
No robust homolog present in Genebank/EMBL as of 11/7/98
VHELFKIDGVYYFFKKFMKLFYNNYSLNSHHEKPSSLEKAVQALDSYFYWGGDTTDVLAR
DDISREIYCVRRLYIRFWIVSISQSLSRIPWRLKRILLRYCTLRGKYVMPILIKRIAILL
GLIRFSRLRKSVY

CPn_0182   220704 219334
accC-Biotin Carboxylase
RCIMKKVLIANRGEIAVRIIRACHDLGLSTVAVYSLADQEALHVLLADEAICIGEPQAAK
SYLKISNILAACEITGADAVHPGYGFLSENANFASICESCGLTFIGPSSESIAMMGDKIA
AKSLAKKIKCPVIPGSEGIIEDESEGLKIAEKIGFPIVIKAVAGGGGRGIRIVKEKDEFY
RAFSAARAEAEAGFNNPNVYIEKFIENPRHLEIQVIGDTHGNVHLGERDCTIQRRRQKL
IEETPSPILNAEIRVKVGKVAVDLARSAGYFSVGTVEFLLDKDKKFYFMEMNTRIQVEHT
ITEEVTGIDLVKEQIHVAMGNKLPWKQKNIEFSGHIIQCRINAEDPTNNFSPSFGRLDYY
LPPAGPSIRVDGACYSGYAIPPYYDSHIAKVIAKGKNREEAIAIMKRALKEFHIGGVQST
IPFHQFMLDNPKFLESNYDINYIDNLLAQGNSFFKEF

CPn_0183   221207 220695
accB-Biotin Carboxyl Carrier Protein
RRLGMDLKQIEKLMIAMGRNGMKRFAIKREGLELELERDTREGNRQEPVFYDSRLFSGFS
QERPIPTDPKKDTIKETTTENSETSTTTSSGDFISSPLVGTFYGSPAPDSPSFVKPGDIV
SEDTIVCIVEAMKVMNEVKAGMSGRVLEVLITNGDPVQFGSKLFRIAKDAS

CPn_0184   221814 221221
efp-Elongation Factor P
QWKIKFCCCEEKIMVLSSQLSVGMFISTKDGLYKVTSVSKVAGPKGESFIKVALQAADSD
VVIERNFKATQEVKEAQFETRTLEYLYLEDESYLFLDLGNYEKLFIPQEIMKDNFLFLKA
GVTVSAMVVDNVVFSVELPHFLELMVSKTDFPGDSLSLSGGVKKALLETGIEVMVPPFVE
IGDVIKIDTRTCEYIQRV

CPn_0185   222457 221765
rpe/araD-Ribulose-P Epimerase
AEVKKQESVLVGPSIMGADLTCLGVEAKKLEQAGSDFIHIDIMDGHFVPNLTFGPGIIAA
INRSTDLFLEVHAMIYNPFEFIESFVRSGADRIIVHFEASEDIKELLSYIKKCGVQAGLA
FSPDTSIEFLPSFLPFCDVVVLMSVYPGFTGQSFLPNTIEKIAFARHAIKTLGLKDSCLI
EVDGGIDQQSAPLCRDAGADILVTASYLFEADSLAMEDKILLLPGENYGVK

CPn_0186   222878 224068
*similarity to Cps IncA
PIKDKILMSSPVNNTPSAPNIPIPAPTTPGIPTTKPRSSFIEKVIIVAKYILFAIAATSG
ALGTILGLSGALTPGIGIALLVIFFVSHVLLGLILKDSISGGEERRLREEVSRFTSENQR
LTVITTTLETEVKDLKAAKDQLTLEIEAFRNENGNLKTTAEDLEEQVSKLSEQLEALERI
NQLIQANAGDAQEISSELKKLISGWDSKVVEQINTSIQALKVLLGQEWVQEAQTHVKAMQ
EQIQALQAEILGMHNQSTALQKSVENLLVQDQALTRVVGELLESENKLSQACSALRQEIE
KLAQHETSLQQRIDAMLAQEONLAEQVTALEKMKQEAQKAESEFIACVRDRTFGRRETPP
PTTPVVEGDESQEEDEGGTPPVSQPSSPVDRATGDGQ

CPn_0187   224218 225045
predicted methylase
VFLTYTRTLPMHSKFLSRRRKNSSHKEETGWDTIASSYHKIVQDKGHYYIIRETILFQLLP
SLTLGCSKSSVLDICCCQGFLEPALPKECRYLGIDITGPLIALAKKMRGVNGHQFKVADLS
KRLEFVEPTLFSHAVAILSLQNMEFPGFAIRNTATLLEPLQOFFIVLNHPCFRIPRASSW
HYDEHKKAISRHIDRYLGFHKIPIMAHNYQKDGPGTLGFHFPLGYWFKELGGHGFLVGGL
EWTGGKTGTGKRAKAENLGRKEFPLFLMLGCIKIK

CPn_0188   225090 226400
CT152 hypothetical protein
KFLHCGIMFRKLFPFGKKKTGGKQKLRNNGLLGAITQGIYVLLHHEAGKFAGVLGYGLL
TNVFILVFFLRLGQILFTNLMWFEWLLIKFLGYKKPGVAIVEAAVHATFGNIGLVLMGSF
FVFVWAILLHLLGLEDGLNKLFRTGWTGGLLYPLVGSYGYFFTVILVGHHFLFLVVYSWLYITQ
IMPIQYAKLFIGLSMTALVFILRFVPYLLLYILALFLYTAPLPPVAIQNTGALIIRTLFIG
GVWLVFQKAFFGLQVGIFNYGFTAGALVALPGFLLLLYIYTMIYLFYSXALFFIIQNRGKT

FIFLGDKILPGGYLQLITGY/ILALTTPQFNEGL   AQFIAKGSKVPIGEVSQCLDVL
EKECFLFYNNGYQPVFNFSELTIKDIADKLLHREIFKKFNPDLGITFIENGFONIFNQA
SKNKENLTLUEIARRIK

CPn_0189   226391   229825
CT111 homolog (Possible Transmembrane Protein)
ANQMKRRSWLKILGICLGSSIVLGFLIFLPOLLSTESRKYLVFSLIHKESGLSCSAEELK
LSWPGRQTAPKIKLTGEAKDEVFSAEKFELDGSLLRLLIYKKPKGITLGGWSLKINEPAS
....MAFFY..A..TPWDHLL....LAL.INLSAEATH
...............................VAFFY..A..TPWDHLL....LAL.INLSAEATH
TNDGKISHTASGEGNQIQMKLQGHIHKSTFYIVEGGSSFIELKPELASALCNQIIPLSTP
ITSKQIHATVSYAKIPLDITKWKHIEITSQAQLPEVAIHPKDPNLALOLRDTKLGIKKTE
KFSDIRYSSSTVLGGASPSHLNGLISIDNKKHLTKFRLQQAQLPHTYLRAIFPQPFVINV
PLDVAYYSLNIEGTYKNAHLEADAILDNPLLKLSCSMSGTWKNFLFKGQGTYHFNKKWQE
ILSPHFSYAEARFSGKAQITDTNLFFPKFSGKITARENELLIHAKFGSPNEPIKPETTSI
LIHGCFGCSLPLSLVSNHLAPFHLKKLTFSFHTDGGKFVTKGNLQNLQALIENPDYPDLNNTRI
LIPDLLLSLDESSTSPSSKDLKIQGSGEIFSLPLDSITKTYGKQVRLSPYFGSSGDLNFV
VNYNPKDQNKLTLLSNFKSEALLGELKLVMDFSMKLSSGTQGTLQWEVSPERYASFFKNA
SCSPTCLLHRTANVRLDISKLSCPEETKGLSCLTLLAAGGLEGSLEATPLIFYDNVSKET
FIINDFKGSLRANNLDAKIEYDLKGSCLAPRODSKTLAEFSLEGQVDHLFSPESREFKQT
ANWIHIPSSFIAGIIPMSPGLKAQISSLAGPRINVSIKNAFRFGEGPVDIMVDSENLQAQ
IPLILNEKSILLRENLTAHLSINEDVNKAFLQEFNPLLAGGAYSQYPVTLEIDKQNFYLP
IRPYSFEEFRIQSATLDMGKISIANTGTMYALFQFLDITDQKQFVESMFTPIFFSVQKGS
IICKRLDALIDRRIRLALWGKTDIAHDRLFMTLGIDPEVIKKYFHNTSLKTKNFFLIKIR
GSISSPEVDWSSAYARIALLKSYSLGNPFSSLADKLFSSLGDSTPPPTVHPFPWEKSNFD
SIENK

CPn_0190   229901   231274
No robust homolog present in Genebank/EMBL as of 11/7/98
LLGIKLMRKRHSFDSTSTKKEAVSKAIQKIIKIMETTDPSLNVETPNAEIESILQEIKEI
KQKLSKQAEDLGLLEKYCSQETLSNLENTNASLKLSIGSVIEELASLKQLVEESIEESLG
QQDQLIQSVLIEISDKFLSSIGETLSGNLDMNQNVIQGLLIKENPEKSEAASVGYVQTLL
EPLSKRIGETHKKVATHDVNISSLQFHMMSVAGGRFRGHIDMNGYRVLGLGEPKNGEDAV
SKDYLERYVSSQLTIDKVEDKPITKPNKGKLLYSQGTSPKLESPLPLGLLTSGISGFTWK
SASKSNDGSFPFSALRHKETESDTDCFQITSTTLSGNQAGTYTWSLSLKVLVPSIFQIEK
PEVQLSLVYSYEDWLPIDNIFNMSQPRTIPLALLGQTMLAGQKYDILELAAHQTNQTLMI
SPNCSRFSLQLKQTNQFENSPVDFYIVHAAHSCHWSGF

CPn_0191   232039   231314
glnQ-ABC Amino Acid Transporter ATPase
QHHFPVFLGYQKREGVMTIRVRNLAYSVNKKKILDGVTFSLERGHITLFVGKSGSGKTMI
LRALAGLVQPTQGDIWIEGEAPALVFQQPELFSHMTVLGNCTHPQIHIKGRSTEEAREKA
FELLHLLDIEEVAKNYPDQLSGGQKQRVAIVRSLCMDKHTLLFDEPTSALDPFATASFRH
LLETLRDQELTVGLTTHDMQFVHSCLDRIYLIDQGTVAGVYDKRDGELDSGHPLSKYIHS
AQ

CPn_0192   232643   231984
glnP-ABC Amino Acid Transporter Permease
EVGVDHWLAIARLLLRGCGYTLCVSGIGILCGSILGLLIGTVTSLYFPSKLTKLLANSYV
TVIRGTPLFIQILIIYFGLPEVLPIEPTPLVAGIIALSMNSAAYLAENIRGGINSLSIGQ
WESAMVLGYKKYQIFVYIIYPQVFKNILPSLTNEFVSLIKESSILMVVGVPELTKVTKDI
VSRELNPMEMYLICAGLYFLMTTSFSCISRLSEKRRSYDN

CPn_0193   233144   232686
*argR-Arginine Repressor
KLHGVFMKKKVTIDEALKEILRLEGAATQEELCAKLLAQGFATTQSSVSRWLRKIQAVKV
AGERGARYSLPSSTEKTTTRHLVLSIRHNASLIVIRTVPGSASWIAALLDQGLKDEILGT
LAGDDTIFVTPIDEGRLPLLMVSIANLLQVFLD

CPn_0194   233162   234241
gcp-O-Sialoglycoprotein Endopeptidase
EVPHTIKGNVFFSWFFMLTLGLESSCDETACAIVNEDKQILANIIASQDIHASYGGVVPE
LASRAHLHIFPQVINKALQQANLLIEDMDLIAVTQTPGLIGSLSVGVHFGKGIAIGAKKS
LIGVNHVEAHLYAAYMAAQNVQFPALGLVVSGAHTAAFFIENPTSYKLIGKTRDDAIGET
FDKVGRFLGLPYPAGPLIEKLALEGSEDSYPFSPAKVPNYDFSFSGLKTAVLYAIKGNNS
SPRSPAPEISLEKQRDIAASFQKAACTTIAQKLPTIIKEFSCRSILIGGGVAINEYFRSA
IQTACNLPVYFPPAKLCSDNAAMIAGLGGENFQKNSSIPEIRICARYQWESVSPFSLASP

CPn_0195   234172   235785
oppA-Oligopeptide Binding Protein
YSGNSYMRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRL
LSEISLWKHIYEGLVOENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAED
FIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSH
FLKLLALPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETK
TITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTF
NINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQ
AYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKE
FALLQADLSSGNFSLATGGWFADFADPMAFLTIFAYPSGVPPYAINHKDFLEILQNIEQE
QDHQKRSELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFRYAKEN

CPn_0196   235906   237519
oppA-Oligopeptide Binding Protein
KLKSYSKERSFMLRFFAVFISTLWLITSGCSPSQSSKGIFVVNMKEMPRSLDPGKTRLIA
GQTLMRHLYEGLVEEHSONGEIKPALAESYTISEDGTRYTFKIKNILWSNGDPLTAQDFV
SSWKEILKEDASSVYLYAFLPIKNARAIFDDTESPENLGVRALDKRHLEQLETPCAHFL
HFLTLPIFFPVHETLRNYSTSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHNKSRVKLH
KIIVQFISNANTAAILFKHHKKLDWQGPPWGEPIPPEISASLHQDDDLFSLPGASTTWLLF
NIQKKPWNNAKLRKALSLAIDKDMLTKVVYQGLAAEPTDHILHPRLYPGTYPERKRONERI
LEAQQLFEEALDELQMTREDLEKETLTFSTFSFSYGRICOMLREQWKKVLKFTIPIVGQE
FFTIQKFMLEJNY::LTVNQWTAAFIDFMSYLMIFANPGGISPYHLQDGHFQTLLIKITQE
HKKHLRHOLIIEALOYLEIICHILEPLGHPNLRIALHKNIKNFNLFVRRTSDFRFIEKL

CPn_0197   237512   238882
oppA-Oligopeptide Binding Protein
KNYHRKGDLKFICKFIKVCFKMFGRWTTLFLLFIGLTKGGGYGGKHKQGLIIPIHDDPV
AFGIHKQAKRAMDIGIAQLLFGGLTRETHREGGNDLELAIAGRYTV::EDFGGYTFFIKDSAL
WGDCTPIPGEDIRHAWEYAQENSPHIGIFQGLNFGTPGGNAITGHLDGFNPDFPKLLAFP
AFAIFKFGGGYTLVEYFPGHNIHLKKNPHGCYDYIICVSINSIKLLIIPDIYTAIH
LLNIGFVVAVVGGWIQITWELIIKQGGYHYYTYFVEGAFWIALNTKSPHLNDLQNRHIRLA
TTLDKFGGIEFALGFGGGQPAETLIIGIAPGPNQYKKQKPLTIQEKLVLTYPGDILRCQRIA
GILFKAWKAN:IDLILSILEYHLFVNKRKVQDYAIATGTVAVYYGANLIGEEDKLLQNF

EIIPIYYLSYDYLTQDFIEV.   A.IAVGLKYTYFI

CPn_0198   242145   240746
oppA-Oligopeptide Binding Protein
QIEYYIHKMHRLKPTLKGLIPNLLFLLLTLSSGCSKOKCEFLGKHLVIAHSHDLADLDPRN
AYLSRDASLAKALYEGLTPGTDQGIALALALAEGYTLSKDHKVYTFKLRPSVWSDGTPLTAY
DFEKSIKQLYFEEFSPGIHTLLJVIKNSSAIHNAQKGLETLGIQAKEDLTLVITLEQPFP
YFLTLIARPVFSPVHHTLPESYKKGTPPSTYISNGPFVLKKHEHQNYLILEKNPHYYDHE
.....PPLTLKYLPGGNGTLDFLTW...DWWGGAPLINFDGK:LVTGPGYSVSSTT
.....PPLTLKYLPGGNGTLDFLTW...DWWGGAPLINFDGK:LVTGPGYSVSSTT
KUTAKATFGEAKLTLFLAHLILTIGWGL:LALTI:AGEI:KLGRLTIGLAFIIRQGME
YHCFLKKRRQGDFFIATGGWIAEYVSPVAFLSILGNPRDLTQWRNSDYEKTLEKLYLPHA
YKENLKRAEHIIEESETPIIFLYHGKYIYAIHPKIQNTFGSLLGHTDLIQNIDILS

CPn_0199   241018   241983
oppB-Oligopeptide Permease
KCLIGLSLVFSYIKNRILFNLLSLWIVLTLTFLVMKTIPCDPFNDEGGNVLSEEVLQTLK
SRYGLDKPLYQQYTQYLHSIAKLDFGNSLVYKDRKVTNIISTAFPISAILGLGCSLFLSIG
GGIALGTIAALKKKKQRRYILGASILOISIPAFIFATLLQYVFAVKIPLLPIACWGSFTH
TILPTLALAVTPMAFIIQLTYSSVSAALNKDYVLLAYAKGLSPLKVVIKHILPYAIFPTI
SYSAFLTTTVITGTFAIENIFCIPGLGKWFICSIKQRDYPVALGLSVFYGTLFMLSSLLS
DLIQSIIDPQIRYAHGKEKKRK

CPn_0200   241996   242868
oppC-Oligopeptide Permease
EKKKHKLMENLSSAPSRSIWKSIIQNKMLVLGLTTLIILMLGALLLPWFYQDYEQTSLKD
ILVSPCSRFPFGTDTLGRCMFARTLRGLRLSLLIATIATLIDVCVGLLWATVAISGGKKI
DFLMMRTTEILFSLPRIPIIILLLVIFHHGLLPLILAMTITGWIPISRIYGQFLLLKNK
PFVLSAKAMHASTFHILKKHLLPNTLAPIISTLIFTIPNAIYTEAFISFLGLGIQPPQAS
LGTLVKEGINAIDYYPWLFFFPSLIHIALSISFNLIGEGAKTLCLEEGSHG

CPn_0201   242810   243715
oppD-Oligopeptide Transport ATPase
ASISSARGLKHYVSKRDLMDNYLLNIKDLTITSTNPKRTLIENLSLQLKENRNLALVGES
GSGKTTITKAILGFLPENCLIKTGSILFEDIDITKLSPKELHKIRGQKIATILQNAMGSL
TPSMRIGMQIIETLRQHHKMNKEEAYNKAMQLLTDVCIPNPKYSFSQYPFELSGGMRQRV
VIAIALASQPKLILADEPTTALDSMSQAQVLRILRNIQQQKQATILLVTHNLSLVKELCN
DICIIKDGKLIETGTVEEIFLSPKHPYTLKLLNAVSKIPIKKTSSPILKNKFQPLMSHQG
GL

CPn_0202   243682   244500
oppF-Oligopeptide Transport ATPase
VPTSNEYARWFHTTLLSIKDLSLTIRGKKILHNLNLIKGSYLTIVGPSGSGKSSLALT
ILDLLKPTTGTITFHMDPKIPRARKVQVIWQDIDSSLNPCMSIKGIISEPLNIIGTYSKA
EQNKEIYNVLDLVNLPKSVLHLKPYKLSGGQKQRIAIAKALVSKPELLICDEPLSSLDTL
NQSLILDLFQTIKKEYQNTLLFITHDMSAAYYIADTIAVMDQGSLVEHACREKIFSTPKH
TTTQDLLDAIPIFSLISTEMEPSEEYELQVASK

CPn_0203   244966   245802
No robust homolog present in Genebank/EMBL as of 11/7/98
IVPLPQKNNKETSCMNTYTFSPTLQKSFSLFLLEKLDSYFFFGGTRTQILVITPTNIRLA
AKKRGCKVSTIEKIIKILSFILLPLVIIAFILRYFLHKKFDKQFLCIPKVISNEDEALLG
SRPQAVEKAVREISPAFFSIPRKYQLIRIDTPKDDAPSILFPIGIEIILKDLCIDTLKQS
NLFLKREMDFLGHPEEKALFDSICSIEKDQEWMSLESKKLLITHFLKYLFVSGIEQLNPG
FNPENGRGYFSEISTAKIHFHQHGRYGPIRSSGPIMKEI

CPn_0204   245691   246002
No robust homolog present in Genebank/EMBL as of 11/7/98
PREWAWVFFRNKYSKDPFSSARSIWANPFFGTHHEGNIKIKGMGYQIFTRLKKLGISFSS
YNSINPNPYFFDEGCFVYWESQFKSALQDHGILQKQTETFYRNT

CPn_0205   246073   246327
No robust homolog present in Genebank/EMBL as of 11/7/98
IEDSIKGYGSASAFRNPPQLLLKFFLVCEELCILTVATHRALLETPLALSFFKELKTKYV
YRAKDILQLHNYKGFTILNTSPLCS

CPn_0206   246346   247161
CT203 hypothetical protein
IVDRRSPACYDSINSDAIGVSLLMDISHILEDLAYDEGILPREAIEAAIVKQMQITPYLL
HILHDATQRVPEIVNDGSYQGHLYAMYLLAQFRESRALPLIIKLFAFEDDTPHAIAGDVL
TEDLPRILASVCNDDSLIKELIETPKINPVVKAAAISGLVTLVGAGKIPRDKVIRYFAEL
LNYRLEKQPSFAWDNLIAGICTLYPGELFYPISKAFDGGLVDTSFISMEDVENIIHEETV
ESCITHTLCSSTELINDTLEEMEKWLEDFPIEP

CPn_0207   247209   248617
ybhI/sodiT1-Oxoglutarate/Malate Translocator
VNKKKRFLSLLFLTAVLLJIWFSPHPASINSNAWQLFAIFTTTIMGIIFQPVPMGAIAII
GISTLLLLTQTLTLEQGLSGFHNPIAWLVFLSFSIAKGIIKTGLGERIAYFFVSALGKSPL
GLSYGLVITDFFLAPAIFSVTAPAGGILYPVVTSLSDSFGSSAEKGTQDLIGSFLIKVAY
QSSVITSAMFLTAMAGNFLVAALAGHVGVSLSWVLWAYAAIIPGLPSLFLMPIILYKLYP
PKITCCEEAIRSAKLRLKEDGPLKKEEKTILMIFFLLV/LWTFGDLLGISATTAALIGLS
LLILTNILDWQKDVIANTTAWETFIWFGALIMHASFLKQLGFIPVLGDSAAALVSGLSWK
IGFPLLFLIYFYSHYLFASNTAHIGAMYPIFLAVSISLGTNPIFAALTLAFASNLFGGLT
HYGSGPAPLYFGSHLVTVQEWWPSGFALSIVNIVIWIGIGSLWWKALGLI

CPn_0208   249935   250602
pfkA-Fructose-6-P Phosphotransferase
SVAVILMGIPLYVDLDTIISSYSPPLPKEFQEAASLIAVPDTSHSKPVVPGVKTLFPQTYH
LPYLKFVQGENVVIITPLKVGVMFSXGPANGGHNVIQGLFNSLKDFHPDSSLVGFVNNGDG
LTHRIKGIDITEEFLGKFRNSIGFNCIGTGRKKIVTPEAKEACLKTAEALDLDGLVIIGGD
GGHITATAILAEYFAKRRPKTIIIGVPPTIDIGLQIHTLALIGEEIAEKNLPLKTIIHKICSVIA
DALGCKAHYHFIKLMGRSAIHIALEIALOTHHILTALIGEEIAEKNLPLKTIIHKICSVIA
DRAAMEKYYGVILIFPGII::ITSFIFEIIHLITEIEGLIEYEDKLIRLSPEIQRLLKSPPAPI
IEGILNDRRDAHGNVVV:K::F/DYLLIHLJGHILQQYFMIVGFNAIGHFLGYEGRSGLPTK
FIATYGGVGGGA::ILLARSHIGVFLETIIEGLAGGPPHPVIPLRAIFVVKMFTVKQQADGTLQ
FKIFKYLVDIGGTAFRRSKGLFYIWALADGYFIIGIGIFTFIMHGGNFPPLTLLLGHN
FWGPHYGRGIEIPPFTY

CPn_0209   251069   251272
No robust homolog present in Genebank/EMBL as of 11/7/98
HGGHRIIRLKMETYGRGGTSILAFYITGLYIHRKLJGYPGFGFIPKPRVIAGTIVAGHLAIAYRGNI

HLGMT/KLLPVLSFPRSLLRTTSLWYRP

CPn_0210   252459   251440
No robust homolog present in Genebank/EMBL as of 11/7/98
YQKLWEREREYFKTIREKEHATISTMLVELEALKREFAHLKDQKPTSDCEITSLYQCLDH
LEFVLLGLGGSKFLKATEDEDVLFESQKAIDAWHALLTKARDVLGLGDIGAIYQTIEFLG
AYLGKVNRRAFCIASEIHFLKTAIRDLNAYYLLDFRWPLCKIEEFVDWINDCVEIAKRKL
CTFEKETKELHEGLLREEHAMEKCSIODLORKLSDIIIELHDVSLFCFSKTPSQEEYQKD
....MFKENT... .....

CPn_0211   252765   252463
No robust homolog present in Genebank/EMBL as of 11/7/98
ECVMSYPDISNVQASSIQSALLHKTSDQIQQKRCFKQSTFVILAVSLVIIGSLFLLAGVA
ILTVFSHGVLSLVFGVLGIVLGLLLLAGGVGLLVEEAKSLL

CPn_0212   254081   252888
No robust homolog present in Genebank/EMBL as of 11/7/98
ELSYGVVVSIYSEILSFSELTSCKHSLFPPFGPIETASIRIHHVFNVVIVCLIILGTLFVC
LGMVFLGVFSTYLLGMSSMILGLLLISIGLALLKFKERYGLEPKELPGVEGGFDKKLPSE
IIOMQDQIADLARELDLEQKKDTLIRGFSARLDVLEGSKTEKKQILKIGVPRNLSEIQER
AOEQNSILEQCKEALLFRRKSAQEIFKKLYDRKAAFWRSYREDLWCYSEIHVSKKALSNL
YIGDVFEGTAPHFLMEAYAMCRTAKNLRNYVKVCVEDMRVNEEKKRAKQLSVSELLCCCT
EISTDLENETHLFTSDSEDVLEEYQIHCIRVTMLHALWAIYNDEVVSRKPIDTLDRVRAR
MAVEDCIETFSEELQMCVVHTKTLELEIAQLYVDILLEA

CPn_0213   254345   254190
No robust homolog present in Genebank/EMBL as of 11/7/98
ILVVFSRVIFSNTNQIGIPRLELILPLWKKENDPFCFLFSRVEGTFIILNIK

CPn_0214   255768   254446
No robust homolog present in Genebank/EMBL as of 11/7/98
FLGLKEDYERPTYCNIPPAPHPQRVDSKGCIASHVSTVVVVALFILGIFFLSGSLAFLVH
TSCGVLLGAALPILCIGLVLLAVALIVFLCHKHKTRQDLDYYDQDLDSLVIHKKEIPNDI
SELRVTFEKLQNLFQFHTKDFSDLSQELQGKFINCMEKWLTLEDEVTKFLIVRDRFLETR
RNFTTFGEQVKGIQSNIFDLHEEKSSLYLELYRLRKDLQVLLNFFLLPPGILKVDYDEIE
AIKGLFIRLTSRLDKLDVKAQERKKFINEMSREFYEVEKAFDIVDRATKKLMDRAKKESP
ARLFMGRTESLLEMKKNEEALKNQGLDPENLSHPELFSPYQQLLILNYLNSEIVLHHYEF
LISGTVTSGLTLEECENRMRAASTGLNALLVRKLQFRGAIKSAYFEKLTEIEKELRSLQD
VIKSLELELIHKIKDIVTEET

CPn_0215   257039   255759
No robust homolog present in Genebank/EMBL as of 11/7/98
LTSSKKQVMSSAIARDCFPSPSPQPSSTLGVHPPKYKSLILSVSLIVLGVLLLCVGMLLL
VNAIFSFSVLTVGLGGAGVFLGSLLLILGLIFFVSYHRKLSEATRSLEQKITLEYQPWAD
LRKELNEVQEWSNFLLDEWEDFKEVVAQHKSQFATFEGDLLLFGREVKYETIWKELDGR
DVALLTELKNIWGPLEFLRKKGDRLQCEIDKLRKEVMKVGKSGLKLACELTKFKSALKDV
KIEQECYRDKRKVEKLEVFPEGYRRELLEVLKTRLSVEKEIQLFEEVVSAFEEKLASLHR
TVFSEEELQEALDKAKAELLDIQVRKSVVEDLSCEPTLIQYHLLRLYEVQCRIVEQFLTQ
TFSSEQEKVLEEYEALKARIRKTLRVKLDQVRANVAFVASTTDLLSESESLDGNDSVFED
AHDDFLD

CPn_0216   257623   257174
No robust homolog present in Genebank/EMBL as of 11/7/98
NKARTHNPVTFDRIQVDFIPEDTSLRINSYIVAGGLLILGVVLSILSVICLDIGLVGLSA
GAAPTLGLGCLIFALFLFSFSLILLLSQEKRVPDVLSLYLEKEVPQYETPLYKEDLESER
DMSAISERLGIIEEKLRIAEKFRYSDSVFV

CPn_0217   257881   258579
ypdP
PKCCLKGFLSVNELIFGFQTFSVVVLGVFFASRGKAWLTGWLSLLSSIMNVFVLKQIHL
WGFEVTSADVYVIGLLTCLNYAREHYEKNDINDAMLCSWVISIAFLVLTQLHLFLIPSPN
DSSQEHFLALFSSTPRIVVASLVTLIFVQIVDIKLFTFLQRVFSKKYFAMRSTISLLFSQ
LIDTIIFSFLGLYGLVSNLCDVMIFAMLVKGIVITLAIPTLTVTKAVLDRRSS

CPn_0218   259064   258582
No robust homolog present in Genebank/EMBL as of 11/7/98
IFLSKKVFFESYEDFANVASSWPKSLRALVQGRYFVDSELKETPYRIHDFKKTPIHHRLY
RSLPIISTICGIIRLIEAHSGPIHPRDKMKYRFEVLQAVIEILGLGVLILVFDIIGCFLA
FLVAIILSLLLYCNSTFTCVQNLSFTERMLEGIGEAVNFLA

CPn_0219   259348   260472
tgt-Queuine tRNA Ribosyl Transferase
GSSLALKFHLIHQSKKSQARVGQIETSHGVIDTFAFVPVATHGALKGVIDHSDIPLLFCN
TYHLLLHPGPEAVAKLGGLHQFMGROAPIITDSGGFQIFSLAYGSVAEEIKSCGKKKGMS
SLVKITDEGAWFKSYRDGRKLFLSPELSVQAQKDLGADIIIPLDELLPFHTDQEYFLTSC
SRTYVWEKRSLEYHRKDPRHQSMYGVFHGGLDPEQRPIVGRFVEDEPFDGSAIGGSLGRN
LQEMSEVVKITTSFLSKERPVHLLGIGDLPSIYAMVGFCIDSFDSSYPTKAARHGLILSK
AGPIKIGQQKYSQDSSTIDPSCSCLTCLSGISRAYLPHLFKVREPNAAIWASIHNLHHMQ
QVMKEIREAILKDEI

CPn_0220   260660   261238
No robust homolog present in Genebank/EMBL as of 11/7/98
FYSFLKKKGIFYMSKESIRSYSEISTPTPIFRETPSKEGVAYKLQLRSPAKDCILRNRVS
LKGALLRSIPFYCSFLGAKRIHSAWSAKDAPCTTRVYHYLVGGLELLGLGVVVLACKVLA
TALKFLFSKASSKIKQMKWREKARNLAAKDTVCSIKEFCSVDLTSCFTRCFRLRNRVVEE
GASENQTVREIIV

CPn_0221   261621   262064
No robust homolog present in Genebank/EMBL as of 11/7/98
DALRYKYEICIQMVNRYKSGAEFSADHYYDDHLVPMVYKRNLRGLAPVENEVCLFEEHNL
LESVVAGIDIMSSLLCLCRLHSVWSTQDPFKDSKISIIFHTALGCILETLGLGIIVLLIKIT
ITILLILFTHLLLLYFMYCAAYSDFHPI

CPn_0222   262474   262842
*weak similarity to Bacteriophage CHP1 (ID44)
GEKFLKIWEKLRELNAFELTQPEEYRNRWVLMHYLYCRFYRTQHAKVWIYRCVHEASLYE
KHIFCTLIYDDKHLPGYGGLVKIJILQLFLKRLRKMISPHKIRYFFANCAYGTKLQRPHYHL
EEI

CPn_0223   262950   263111

No robust homolog p. .at in Genebank/EMBL as of 11/7/98
ITMLIGRYGGDDQFTEATKNYYFIIKLGFVRDNLEGLTNPISEIVSETSSSIKDSVLRSL
FILGSILGCARLYITLATHDPLDETOEKIWHTIFGALGLGLGHLLLFKLIFWILHCIF
HLVIGFCX . . .. . .

CPn_0224   263402   263674
No robust homolog present in Genebank/EMBL as of 11/7/98
YTFFKNPKKNKKMKFNSIIFLENTKHYFDIFREGFVRDRHGLMEASDWLLSTEITIIRSIL
....W....... ....

CPn_0225   263646   264541
No robust homolog present in Genebank/EMBL as of 11/7/98
NSFTIKFLLMTKNAINSQTTTPQPNLTDAEPIASRAQCKSIAVIISLFALGHLLLCLGII
LISIPIPGLAAQVALGLGIVSLILGIALANIGFLCLLLRCKQVPQKPDTLPSESSKQPSE
GSTPTALPWQAGEFLEKVQVSATPILLPKNKDEELSAKVMKEGAEAASSIKQAVLESTEK
LIDARKQEESRREARKKIVAEEAEASRKRIQQQMAADQEALRKRKEEVAKRK

CPn_0226   264545   264967
No robust homolog present in Genebank/EMBL as of 11/7/98
AIFNRKRMPYYANTLEFIQGTQSLCPLFKYGFVRHHYKGQLEIEDASHDWDFLEPPSTWK
RTLLAAIPILGSVIGLGRLFSIWSIREPQDSQEYKSIFWHTLCAVLEILGLGIVALILKI
LATFIMAMPGLKRVATFLFYS

CPn_0227   265467   265009
dsbB-Disulfide bond Oxidoreductase
KERFNIFVSCKLLKEIMMINFIRSYALYFAWAISCAGTLISIFYSYILNVEPCILCYYQR
ICLFPLTVILGISAYREDSSIKLYILPQAVLGLGISIYQVFLQEIPGMQLDICGRVSCST
KIFLFSYVTIPMASVVAFGAIVCLLVLTKKYRG

CPn_0228   266242   265412
dsbG-Disulfide Bond Chaperone
VKDRADFLNLKEKFSCSILKKENAFEFYVFCSIKQLTNSSLRGPLNKKILVLCTAMFFIV
CFGFLIHKKHTILPPKAHIPTNAKHFPTIGNPYAPINITVFEEPSCSACAEFTTEVFPLL
KKHYIDTGEISFTLIPVCFIRGSKPAAQALLCIYHHDPRQADIDAYHEYFHRILTYPKEE
GSHWATPEVLTKLAEGLKINSGRSVNPKGLEQCIASGQYNEQIKKNNLYGSQVLGGQLAT
PTAVVGDYLIEDPTFHEIERAIQHIRQLQAVEGDHDD

CPn_0229   266163   267560
CT178 hypothetical protein
NSKAFSFLRIEQENFSFKFKKSALSFTYNTANLTKSTFTFILLLLLRKKDQGLRFMDKET
LENIYRHFRYRFLKLNILPAFLGLLLLCSPNTLNYTQVDVIFSDRLCSCLLIFLAIASLT
KRSLLWLGAPLGIWVTLFACVAGRSPTIFANDTLIGFAILAVVCISPTRPEALEVGPTLP
EGFSYNPSAGGRRAAVLFLSLLGWLEARYLTASSLGITSSQSSNFLLLYSSIMTVYSLLV
VLSLAGSERRWHTRPKIVIATALALTGVIILTLLPIILHQLRYDCWLCLCLTIEPALAVV
FAYDETRATLRYISQFLGDKRALTRASFFGSEYYKHTLSWEERTVLPLRKAYKQAFEGIS
FPINQLLAILVATVFVKVNSSMGLPTFPRNFLNICCWFIIVLFILAFAESLRHLRWHNLI
FSAAILFSPVLFHIPVESPMFLPIIVTGLILIILSIGKRRRTKRKL

CPn_0230   268277   267576
CT179 hypothetical protein
RFKKALIYMSSQPLVTTSSSLSRYVVLTGEEKVACYKKAFNHIWHGAPAIILAAALLMFC
IFGFVLGSILLGAPLEGASILYDVTLPWLLPSILVFVLLVLPLNIYAYSHHKQVLALHER
ITQSNYKEIYDHCEKEKRTPNKKALSLYIESQVLVPEYSKRFSSMILGKTLKIIPKKDSP
ESLKHDELIQKALERAKENIYMNKNQREKRDEREAKKEAKNASKTNPLWEGLGT

CPn_0231   268996   268253
tauB-ABC Transport ATPase (Nitrate/Fe)
PQAFVSIQDRGFSMLQAHRLCYSCDNQVILKDASFQASPGTITIILGSSGVGKTTLFRLL
AGFLPLQEGELLWNGSPLNRKDVAYMQQKEALLPWRTALKNMTLSTELGINTSHNALSNE
RLEEIIHNFDLGQLLDRYPDELSGGQRORIALAAQCLSLKPILLLDEPFSSLDVLLKEQL
YQDIVALAKKENKTVLLVTHDFHDVSCLGDVLYVIKNKTLTPVPLDPSMRPLNNGLCFIK
DLKKHLYT

CPn_0232   270134   269232
*similarity to 5'-Methylthioadenosine/S-Adenosylhomocysteine
Nucleosidase
KKFLMRRFLFLILSSLPLVAFSADNFTILEEKQSPLSRVSIIFALPGVTPVSFDGNCPIP
WFSHSKKTLECQRIYYSCDSFGKYFVVSALWPNKVSSAVVACNMILKHRVDLILIIGSCY
SRSQDSRFGSVLVSKGYINYDADVRPFFERFEIPDIKKSVFATSEVHREAILRGGEEFIS
THKQEIEELLKTHGYLKSTTKTEHTLMEGLVATGESFAMSRNYFLSLQKLYPEIHGFDSV
SGAVSQVCYEYSIPCLGVNILLPHPLESRSNEDWKHLQSEASKIYMDTLLKSVLKELCSS
H

CPn_0233   270439   270248
No robust homolog present in Genebank/EMBL as of 11/7/98
EKARTMFLGKVLLFLLRISRRSYVQEIGIFFHLETPDLKIVLCAFVSTFIVVEMDVSLKN
KGQS

CPn_0234   271246   270548
CT181 hypothetical protein
FIMLQSCKKALLSIVVSILAFHPIPGMGVEAKSGFLGKVKGWFSKKEIQEEARILPVKDS
LSWKRYDYTSSSGFSVEFPGEPDHSGQIVEVPQSEITIRYDTYVTETHPDNTVYVVSVWE
YPEKVDISRPELNLQEGFSCFMHQALPESQVLFMOARQIQGHKALEFWIVCEDVYFRGMLI
SVNHTLYQVFMVYKNKNPQALDKEYEAFSQSFKITKIREPRTIPSSVKKKVSL

CPn_0235   271395   272177
kdsB-deoxyoctulonosic Acid Synthetase
VFVRYLLMKPEESECLCIGVLPARWNGGRYPGKPLAKIHGKSLIQRTYENASQSSLLDKI
VVATDDQHIIDHVTDFGGYAVMTGPTGGHGTERTGEVARKYFPKAEIIVNIQGDEPCLNS
EVVDALVQKLRSSPEAELVTPVALTTDFEEILTEKKVKCVFDGEGRALYFSRSCPIPFILK
KATPVYLHIGVYAFKREALFRYLQHGGTPLSDAEDLEQLRFLEIIGGKIHVCIVDAKSPSV
DYPEDIAKVEQYITHLGNAYF

CPn_0236   272138   271766
pyrG-CTP Synthetase
GKFTYHMPFKVIFLTCYVVGGLGKGLTAACLALILERQRLHVAMLKLDPYLNVDGTHNP
FKHGEIYVTDDGVETDLDLGHYHRFGGGAALGHHGGSATGYGIYARVIKRERFDYLGSTVQ
VIHHITHEIIQVILDAAKEIGGDVLIVEICFFIGDIEGLFFLEAIRQFRYDHGEDCLNIH
MTVVPYLQAADEVKKKPTQHGGGGILPIIDIAILCRGEYFLTQEVKKKIIGLFCNVPNR
GIVVIKYVQHRDAYKKIFEALTHAALPIYHIAAEIFGIDAEGDEHLTMELGGYDAGLVPGXFG

VRGWEGK IAAAKFCREQG IPYFGICLGMGVLVVE1   JLNLDQANGLEHDPNTPHP IVY
VMEXODPLVATYGTMRLGAY PCLLKPCGKAHKAYNESSLIQERHRHRYE VNPDY IOSLED
HGLRIVGTCPPQGLCE I IEVGDHPWM IGVQFHPEFVSKL ISPHPLF IAF IEAALVYSKDA
JHV

CPn_0237   273741   274214
yqgF Family
TILRMQAMGKPSGCKAYLG IDYGKKR IGLAYAAEPLLLTLP IGNIEAGKNLKLSAEALHK
[illegible line]
[illegible line]

CPn_0238   274210   275838
zwf-Glucose-6-P Dehyrogenase
PCNHQKLRDFNFRNFLLFVIFASAGTKKEIKMTNVVQETIGGLNSPRTCPPC ILVIFGAT
GOLTARKLLPALYHLTKEGRLSDQFVCVGFARREKSNELFRQEMXQAVIQFSPSELDIKV
WEDFQQRLFYHRSEFDNNMGYTSLKDSLEDLDKTYGTRGNRLFYLSTPPQYFSRIIENLN
KHKLFYKNQDQGKPWSRVI IEKPFGRDLDSAKQLQOC INENLNENSVYHIDHYLGKETVQ
NILTTRFANTIFESCWNSOYIDHVQISLSETIGIGSRGNFFEKSGMLRDHVQNHMMQLLC
LLTMEPPTTFDADEIRKEKIKILQRISPFSEGSS IVRGOYGPGTVQGVSVLGYREEENVD
KDSRVETYVALKTVINNPRWLGVPFYLRAGKRLAKKSTDISIIFKKSPYNLFAAEECSRC
PIENDLL:IRIQPDEGVALKFNCKVPGTNNIVRPVXMDFRYDSYFQTTTPEAYERLLCDC
IIGDRTLFTGGDEVMASWKLFTPVLEEWDQDSSPSFFNYPAGSSGPKEADAL IERDGRSW
RPL

CPn_0239   275863   276672
devB-Glucose-6-P Dehyrogenase (DevB family)
KSISMTNIGIETMATLINFNDTNKLLLTKQPSLFIDLASKDWIASANQAIKQRGAFYVAL
SGGKTPLEIYKDIVINKDKLIDPSKIFLFWGDERLAPITSSESNYGQAMSILRDLNIPDE
QIFRMETENPDGAKKYQELIENKIPDASFDMIMLGLGEDGHTLSLFSNTSALEEENDLVV
FNSVPHLETERMTLTFPCVHKGKHVVVYVQGENKKPILKSVFFSEGREEKLYPIERVGRD
RSPLFWIISPESYDIADFDNISSIYKMDIL

CPn_0240   277861   276698
No robust homolog present in Genebank/EMBL as of 11/7/98
LVYFMVFKSPSSESVVKANSVVRSNFCYFLENKFVSPSESTEVMFSEIMKGRVPDIESLFD
RPTDMMMTGFKAAQNLGNLFNSFGILIMCFSQCKSCQTPEKETSAIVLGATLLFFVVALI
LGPTLGALVYCAYKVYTLGKMIYSLNKAKAKVLRHPAQNVFHRAAGVATIRSSEEAVKAC
KLYKSAMIGSLVVSLIASLALIALTAGIVLVLFFVARGAAPVITAAMMGCCAAGGGALLI
SLLGLWIAIVRKAKHQEACVGHLTNVVLHTAVSEALLHDPSHFQTNALARDLFLTDCLSH
YGHLFSNEEVAQLVQGGAPGGGRPSQHYGGSSDYQNRRGGNGNFGGSHFGGGGGFAGSH
FGAGYPTAPTMPSAPPPFPPPPAYDTIYG

CPn_0241   279372   278203
No robust homolog present in Genebank/EMBL as of 11/7/98
IFLVKFMSAMISLSSSHEASIASNTQVRDVLVSLAMDEFVEHNTEILPIKVFLARGTLSS
TAIIDDLKDVVETEGEHHFQVYSNISLKHIYQRFFEKIFGIGCCPLLLVTDSHHTDPCGA
LITGIFAAVLFTVLAIVFGPTLGILCYSAYKIYQLTKKISSLSRTHTEVINSVQKSDPFI
HRSGAVAAAASQSTIKACKVFRQSTLIFFVVLGLIITISLAALIVGLVFALFFLDPGAPA
VMTAAMIGCCAAGGTGILLSVIGFLLASVYSVQKSQEGVHHMHTALLRCIVSNTIIOMPY
LPITPGTKKVLTQSIRRYQQFFSDDEYRDIESEVPLNRQTTPPPSYETLFHEEGSDGSSN
VIPRESPPAYSTIDSSNSPFPSSSPPPYYR

CPn_0242   279975   279487
No robust homolog present in Genebank/EMBL as of 11/7/98
KSLKYCSLYQFSQKPTVILMACSIFFRMSQGDYDDDEPLSKKTACLVVDTMLYPVIAVVCA
VVSVVLLILKVLFLLLSFPFKLCSASSALPGERVSLGSHFKCLYGGGLPYLLACLLIVFV
IGTAIHGFIISHRTSEDARLSSAIVFMQAPILQLAGMSGLIKP

CPn_0243   280609   280133
No robust homolog present in Genebank/EMBL as of 11/7/98
INYNYLVFLLKFVKGRIIHACSIGYHLCNANEPDRFVASKVALVADILLYPFMAVICAVV
FAVLMVVKLLFLAIKFLVNTCIAACKSRPLPSCKENFQCLFGPKDKPGPSDWLGCLVLIP
IIGTLIYSTIITVQSDTNRLRYFIISPAYQVGSTAIINW

CPn_0244   280906   281556
adk-Adenylate Kinase
GAFEVTKGSVFIIMGPPGSGKGTQSQYLANRIGLPHISTGDLLRAIIREGTPNGLKAKAY
LDKGAFVPSDFVWEILKEKLQSQACSKGCIIDGFPRTLDQAHLLSFLMDVHSNYTVIFL
EISEDEILKRVCSRFLCPSCSRIYNTSQGHTECPDCHVPLIRRSDDTPEIIKERLTKYQE
RTAPVIAYYDSLGKLCRVSSENKEDLVFEDILKCIYK

CPn_0245   281627   282499
ydhO-Polysaccharide Hydrolase-Invasin Repeat Family
TCQKEIMKHYLSFSPSADFFSKQGAIETQVLFGERVLVKGSTCYAYSQLFHNELLWKPYP
GHSFRSTLVPCTPEFHIHPNVSVVSVDAFLDPWGIPLPFGTLLHVNSQNTVIFPKDILNH
MNTIWGSGTPQCDPRHLRRLNYNFFAELLIKDADLLLHFPYVWGGRSVHESLEKSPVDCS
GFINILYQAQGYNVPRNAADQYADCHWISSFENLPSGGLIFLYPKEEKRISHVMLKQDSS
TLIHASGGGKKVEYFILEQDGKFLDSTYLFFRNNQRGRAFFGIPRKRKAFL

CPn_0246   282955   282551
rs9-S9 Ribosomal Protein
VVAKSTIQESVATGRRKOAVSSVRLRPGSGKIDVNGYSFEDYFPLEIQRTTILSPLKKIT
EDOSQYDLIIRVSGGGIQCGOVIATRLGLARALLKENEENRQDLKSCGFLTRDPRKKERKK
YGHKKARKSFQFSKR

CPn_0247   283430   282969
rl13-L13 Ribosomal Protein
D:YI IMEKRKDTKTTIVKSSETTKSWYVVDAAGKTLGRLSSEVAKILRGKHKVTYTPHVA
M:D:VIVINAEKVRLTYAKKCQKIYRYYTGY ISGMREIPFENMMARKPNY IIEHAIKGMM
HKTHLGKKQLK:LRIVKGDSYETFESOKPILLDI

LEVMKFEFSVALKYLIPGRG   AIVSLFTVGIISLVVWLJIVFISVIHGLEQRWIEDL
SQLHSPITILPSDTYYSSYYYQTDKHSSLJRYYTKTLGEKIAGPQVDVYDPESDYLLPET
FPLKDCDLGGOQKDRVKMTLESLGPYLQSQHGKVLEEEDGVGYLDLKTSLELQKPQRRNL
THFLTYPSKLSYEDKVLRYDETDYTSAELMPFNRSPSGWEQDFHNLEELYRGASIILPST
YKDSGYKVGDTGVFSTYSIENEKETQYTVHVIGFYNPGLSPLGGRTVFIDPDLARSIRSQ
SEGLGMSNGFHLFFPNTKRIVFVKKQIENILTSLGVDDYWEISSLHDYDYFQPILDQLQS
DQVLFLFVCILILIVACSNIVTMSMLLVNNKKKEIGILKAMGTSSRSLKIIFACCGAFSG
ACGVVIGTIFAIITLKNLQFIVKALNYLQGRETFNTAFFGQNLPNSVHPQAIYFLGLGTL
[illegible line]

CPn_0250   285002   285742
rl33-L33 Ribosomal Protein
KDSSHASKNREIIKLKSSESSDHYWTVKNKRKTTGRLELKKYDRKLRRHVIFKEAR

CPn_0251   286036   287559
*conserved hypothetical protein
SPDSCLPWMSPFKKIVNRLLCYISFQKESRTLPI::IREPRMTTKSLGSFNSVISKNKIHF
ISLGCSRNLVDSEVMLGILLKAGYESTNEIEDADYLILNTCAFLKSARDEAKDYLDHLID
VKKENAKIIVTGCMTSNHKDELKPWMSHIHYLLGSGDVENILSAIESRESGEKISAKSYI
EMGEVPRQLSTPKHYAYLKVAEGCRKRCAFCIIPSIKGKLRSKPLDQILKEFRILVNKSV
KEIILIAQDLGDYGKDLSTDRSSQLESLLHELLKEPGDYWLRMLYLYPDEVSDGIIDLMQ
SNPKLLPYVDIPLQHINDRILKQMRRTTSREQILGFLEKLRAKVPQVYIRSSVIVGFPGE
TQEEFQELADFIGEGWIDNLGIFLYSQEANTPAAELPDQIPEKVKESRLKILSOIQKRNV
DKHNQKLIGEKIEAVIDNYHPETNLLLTARFYGQAPEVDPCIIVNEAKLVSHFGERCFIE
ITGTAGYDLVGRVVKKSQNQALLKTSKA

CPn_0252   288112   287576
CT144 hypothetical protein (frame-shift with 0253?)
ATSTVCALWILQTYQSHDDAASCSFRRACRFGRYWLGGVNVPWNKFNQTSTQSTVINSAI
YIDSSQTWMMRFQASASIPRLFRISIFMTKHGDWIDNGTGCGELLLVAYEANQNPLFPDIR
IELAMSTCSGTSYYRARPMQWLCSTYYAVRPGYFVLENRSYSFRVQSFSWNIATLPFVN

CPn_0253   288474   287950
CT144 hypothetical protein (frame-shift with 0253?)
FCGGRLMSSSIPTTQKITISIPTFVRFNIESINLTDEQKKTALTIGGNIATENTQVLGNF
VDADGGLICQNDLSVGGNINITPQTFNTMVFSGRVNLSNSPFSYQDSLGNKRQDYANINT
EQPQQYVPYGYYKLTRVHMHQRAALSGGHVGSGDIGWGESMYLGISSIKRQHKVQ

CPn_0254   289268   288459
CT143 hypothetical protein
IPMKTLGVKDONLFIDQATLSVERNVRIENNLETRDLKVLDTTTSPCEFIVKGNVSAEGS
QLNATTLSDGFNIYSKTDVSQTPVCNNISDPQSARDALTFSYYRKTGCQAANLYTTYPGN
GYYVAPNTTIETHVAAITSKSVSRNATPDFSRYADIEPVVKLKQVGIYQVTMQLTRWSGQ
HDGDNSATLILNFVSGNNKTLLCTSDTRGGYSSDRTSVAVTAIFSVTELVSSPPYDYPWI
NLESTIWWNLMSLSTCVIWFPFPSNFVEVD

CPn_0255   290183   289329
CT142 hypothetical protein
TLLKVIMKNNINNNECYFKLDSTVQGDLLAANLKTFDTQAQGISSTETFSVQGNATFKDQ
VSATGLTSGTTYNLNAQNFTSSQISIDFKNNRLSNCALPKEDCDPVPANYVRSPEYFFCS
KPLIGDFDFNSGESYLPLTGSEYTLYQSRNVNSIFRFIGWKQSTRELTVGGNTAIQFLAA
GTYIVSFTVGKRWNNGWNGWGGAIYINNGLGQVQCESTIYSGGGYATIGTLGTSIYRASVD
VAPNPNDPNASDRYRAGIFYLSNGGSSAGIGNYSFSLLYYPDDRG

CPn_0256   291282   290398
CT144 hypothetical protein
FCGGRLMSNPTPKTKISIPTFVRFNIQSINLTEDQKKTTFTVGGKVTTENTVVRGDLTCT
DGGLTCQSDLTIQKDINIRPTSTNSHVFDGRLNLSNSPLSYKNSQGQDITDYEKMSSGKP
QEYVPFGYYKRTQIMMAQRAAHSSGYVGGGSVPSGSYVPWNKFDQTSTQKTSGTEIYIDP
NDSTKLVFEVNNKVPKLFRISVIMAKHGSWLDNGTGADILLAANEYEQGGGRINVTDLAH
TTSRGSSYETRPLQVVCVTYYAQNNGYFTFQNRAGGGLRVSFFSWNIVALPYVE

CPn_0257   292136   291267
CT143 hypothetical protein
GVVMKRRNLQKILPNASTPSTNVAENTGIKDQNLFLDQATLNVDGNVDIENFLETRDLKV
ADTITSPCEFTVGGGLSAESSQFKATTLSKGLEITSEDQDGRVPKFTNVSDPQSPRDALT
YNYYRNTGCQALNLYTYYSSSQPTTVGKPIETVCQNPNPETYRISASAKIYDAVTRFPYI
QFKAPGIYOVTIQIRRESGOHSGLDNPNLYLNLMIGNNKTLLCASDTRGYSGGHRTSIAV
TGTFTLTEIVATPPHDYPWLFLETTIGLDIKSMSTCVIWFPFQANFAEVD

CPn_0258   292534   292133
CT142 hypothetical protein (frame-shift with 0259?)
CFSFCRLGSKFEKITLGGNTAIOLLAAGTYILTFTIGKRWGWNNGWGGSIRLFEGKYTGD
GTMLCGSTVYSGGGYSTIGYLSTAVYRDHSDIDPDPNNPSDKYHNNFLFVRNGDHSAVIG
NYSFTLLYFAGDKV

CPn_0259   293031   292441
CT142 hypothetical protein (frame-shift with 0259?)
IYFVFKRKTYNYFIEMTTTNNQDNNECYFKLDSTVGDLLASNIQTFDKQAKGISSTETF
SVQGNATFKEKVSATGLTSASTYKLNATGPAPSSITIDMKNNRLSNPALPKNPCDPVPAN
YVRSPQYFFCAKPIEGTFMFDGSSRYLPITGDGSNYTLYQSSKAGDVFRFVDWDQNSKKL
HLGGTQPYNFLLQEPIS

CPn_0260   294090   293548
secA-Protein Translocase Subunit
AYLDFSKRSCVEEDHVSKKINRNDLCPCGSNKKYKQCCLKKEEQTARYTTECKFKFSAEV
LSASEQGEACDNCTKLFQRLSQSLTSEQKAAVGKFHQITKNKEVMSKKALKKAQAKEEKL
VTEKLQOHNFEILNTGENLAPPMESTATLNQDTNFVCEDFIPTOEDFRISENSQKPPVEE
D

CPn_0261   294272   295011
yrbO-PP-Loop Superfamily ATPase
YSFNRPFIVFMGTLLLNPFWMKAVKRIESLVRKALYTHTMLANHKKIVVALSGGKDSLTL
LLMLKAIGGRGFPGLDLHAVNIGYKVGGAEVNRPYLTHIGDQICIDPFRTIPGSYAPETP
EGYIKGGQARRRLLFQAAKEIGASAIAFHHRDDLVQTALLHLLHKAKFACMLPVLDMVIIF
GVTILRPLIFTPEFWIRKFAKEIFIFARVTVRGIVVGIIGGFAEQGILKLLEEVFPLAHINIA
LAIQEHGGKKIQKI

CPn_0262   295055   295111
surE-SurE-like Acid Phosphatase
LLFNINKEVKVYLVLHNKRLKIILTNDAVIPTAKGMESCLVCALLFANIGDIYLAAFQAFQS

IK.MAI.LNOV/CASPYAYPQPVKEAWAVGGSPT.   ILGLRTLFESVSPDLVISGINCG
INICKNAWYIXIT IGAAKQALVDGIPSMALSQDNHISFFQQDKAPEILKALVIYLLSQPFP
ILTGLNINFPTIPGGGSWEIMRLVPPIDEFFYEEPQYLGSVNKNQYYVCKISGVRIGEHP
IEEELACMLENHIGVSPIFSONGPIGLMTLEEFQKTQENFNASLLSSELTTKIF

CPn_0263   296174   297136
yrtU hypothetical protein
ITALSRRKLRVRPPILAKYAFRGFRMSHGPRPTKFSFPLYFSKTLSWFILGGFLAACGVQ
I. I. I. I. I. I. I. I. I. ILAGMIDI.RPADLIF.L.FIFI.SLANIDLI. COPITYITOMLTAY
I. I. I. I. WI.MIDIFVAYCHAIMITTTVI. I IALI. RPVI. ILI. PIPIZIDTOTTEIUI
IINKKKGYTVCAGAITFIFALSGIVYKNWHTAFVSFLTYGIATKVMDMVILGLEDT
KSVTIITSSPRKLGHILMETLGIGLTYIHAEGGYSGEPRNLLYVVVERLQLSQLKEIVHR
EDPSAFIAIENLHEVINGRRT

CPn_0264   297730   297155
ubiD-Phenylacrylate Decarboxylase
MKRYVVGISGASGVILAVKLIKELVNAKHQVEVIISPSGRKTLYYELGCQSFDALFSEEN
LEYIHTHSIQAIESSLASGSCPVEATIIIPCSMTTVAAISIGLADNLLRRVADVALKERR
PLILVPRETPLHTIHLENLLKLSKSGATIFPPMPMWYFKPQSVEDLENALVGKILAYLNI
PSDLTKQWSNPE

CPn_0265   298632   297730
ubiA-Benzoate Octaphenyltransferase
XIIIVRLNYFLNLVNFKYSIFSILFLSASTVFALSINEISQNLSFKEGFKISVFGAIAFV
FARTTGIVVNQCIDRFIDKKNTRTSKRVLPANLVSLNFAWVLSLFCSFLFLFLCKILRIF
SLGIASLTLMIVYPYMKRVTFFCHWGLGLVYTVAILMNFCAFAESGLSMRLCFLALLWGG
SVGMVIAANDIIYAIEDTEFDREEGLRSVPAHYGEKKAVEIAKVNLWVSYLAYIFSGFVG
SLDKEFYFTAIIPLVVILKVVRMYSNYSKKDQEGESKFFLANIAIALSFLVSMTLFWSLS
R

CPn_0266   299181   299876
No robust homolog present in Genebank/EMBL as of 11/7/98
IMALDEINNQNNPSQQIASSTSQTSKINQDRKTFACTVTLLVVATLMILSGIVVLLFTIGS
LGLSVPLSGILGTFAVTVGAVLFITGLTILVRKSLGIEQKNEDLNFLKIKTPTPPARPLM
SKFSVTCSTTSIVLGMALLIGAVVSVFFLTGYLQLGLCAGLVGLGTALFVAGLARMSPRS
LADQEGSGSADSQSNIVGIGEPKAAQEQKWYKMAVVRGEDGIPTAIRLTPEK

CPn_0267   300122   300910
No robust homolog present in Genebank/EMBL as of 11/7/98
VSIMSLNKTNALLNQPEPAVCLNAWDPKYINQDRKTFACTVTLLVIATLMILTTGVIVLL
AMGSPGLSVLVSTIIGTSVTTLGTALFIIGLVKLIKKSLAWIQYQKYFQEVVKQKYEPFS
IPKNDNVHKLTSCLPSPLDIESPSPEASTPVSKLRIACSGVAIVLGVTLLIGAVVSVFFC
TGYLQLALCVGFACLGTALFVGGLAGLRTHSLIAQGIMYLYLTYYLSSALEERNETVKDQ
RNEINTYLTEECRQQKREKALLE

CPn_0268   300914   301318
No robust homolog present in Genebank/EMBL as of 11/7/98
KQWALSLMSQCQSSSTSTWEWMKSFVPNWKNPTPPPLSPIPSEDEFILAYEPFVLPKTDPE
NAQANPGTSTPNVENGIDDLNPLLGQPNEQNNANNPGTSGSNPTSLPAPERLPETEENS
QEEEQGSQNNEDLIG

CPn_0269   302468   301476
Dipeptidase
VAFRCVMTIDMHCDLLSHPHFCRKDPAVRCSPEQLLSGGVRQQVCAIFVPHSRGEPNCDK
QNSLFFSLPNQYPDIGLLSYEEEENGSSSQKKSLSLIRSIENASALGDDTAPLGTLLAKL
IHLTKQGPLAYLGIVWKGDNRFGGGTEAPKRLSNDGKVLLDIMYELGVPIDLSHCSDKLA
EDILDYTADKLPNLAVIASHSNFRSVLDHRRNLVDAHAKEIVRRKGVIGLNLVRSYVGDS
LGDLEKHVLHAENLGILSSIVLGSDFFYANEDENFFFNECSSAEAHPVLNQLIHRIFSKG
KAESILSSRAEKFLKQVIVEQVNPKITDVKL

CPn_0270   303343   302468
ywlC-SuaS Superfamily-related Protein
SIFGVIVPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGFVLSLYASEAEERLYALKDR
EPSKAFALYVNSIEDIENISGYPLSPTAKKLAQLFPGAITLVVKHRNPRFPKETLAFRIV
DHSVVREIVDHCGTLIGTSANLSEFPSALTAQEIFADFADHDLCIFDGPCSHGLESTVVA
SDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTVKNQEQLVSFLSGSLDF
KGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPELFPFLSPYYIE

CPn_0271   303628   304362
Lysophospholipase esterase
KLMTDYSFFRRKIGNIEAIECPGNPQDPIIILCHGYGSLADNLTFFPSICSFSKLRPTWI
FPNGILPLENDFRGSRACFPLNVLLLQELSRLYANGVGNLQEKYDELFDVDLETPKEALE
ELILNLNRPYNEIIIGGFSQGAILATHLVVLTSQNPYAGALIFAGARLFNQGWEEGLKQCA
QVPFLQSHGYEDEILPYHLGAHLNDLLLTKLNGQFVSFHGGHEIPSVVFQKMQVTVPNWI
DPARG

CPn_0272   305272   304340
dnaX-DNA Pol III Gamma and Tau
FNRQSDATYATWVMHLEEENQGWEALLRKVVYHQEVPPAILLHGFTLPVLQDKAEQLASEI
LLSSSPGSEHKVSQKIHPDIYQFFPEGKGRLHSIDLPRGIKKQIYISPFEANYKIYIIHE
ADRMTLAAISAFLKVFEEPPKHAVIILTTAKVQRLPKTIISRSLSIFIERGEKILCSKET
FSYLFRYAQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEVLLELYRDRYTLNLGLKAS
ALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQLVSLQYKEKEL
VSVSPGQDLSN

CPn_0273   305853   305227
rdk-Thymidylate Kinase
IIVFTIIEGGEGCGKSSLAKALGDOLVAQDRKVLLTREPGGCLIGERLRDLILEPPHLE
LSRCCELFLFLCGPAQHIQEVIIPALRDGYIVICERFHDGTIIVIQGIAEGLGADFVADLC
IKVVGPTPFLPNFVLLLDIPADIGLQRKHRQKVFDKFEKKPLSYHNRIREGFLGLASADP
IPYLVLDAPEILACLIDKVMLHTQLGLCT

CPn_0274   308368   305852
gyrA-DNA Gyrase Subunit A
KGTIIHEIIKDEIIVPKNLEEEMKESYLRYCMSVIISPALPDIRXGLKPIGQRRVLYAMKQL
SLIICAFHRKCAKICIGTSGDYHPIKIESVIYPTLVPMAQNWAMRYPLVDGGVINFGSIDGD
IIVAMRYTEARLTHICAMYLMEDLDKDTVDIVPNYDETKHEPVVFPSKFPNLLCNGGSGIA
VIMATHIPHHNUIELIEATLLLLLANPQASVDEILQVMPGPDFPTVGIICGSEGIRSAYTT
GRGKIKVPARLHVEFNEDKIHRESIIITEMPYNVNKIIPLIEQIANLVNEKTLAGISDVRDE
ILVIAIPIVVLEIKKGFGSIEIIINRLYKFTDVQVTFGAHMLALDKNLPRTMSIHRMISAWI
RHHRPEVIPPRTRYELNKAETRAHVLEGYLKALIICLDALVKTIREGGNKEHAKERIIESFG

FTEPOALAILELRLYGLTII.   IQKEYFELLNKIAYYKQVLSDEGLYKDIIRNELQDL
LKHHKVARRTTIEFSACDIRDIEDIITNEGVIITIGGDDYVKRMPVKVFKEQRRGGHCVT
GFDMKKGAGFLKWYGAFTKDYLLLFTNFGQCYWLKVWQLPEGERRAKGKPIIWFLGGIR
PGEELAAILNIKNFDRAGFLFLATKRGVVKKVSLDRFSNPRKKGTRATEIDEGELIAAC
HIVSDEEKVMLFTHLGMAVRFPHEKVRPMGRTARGVRGVSLKNEEDKVVSCQIVTENQSV
LIVCDQGFGKPSLVEDFPRETHRGGVGVRSILINERNGNVLGAIPVTDHDSILLMSSGGQA
IRINMQDVRVMGRSTYT/RLVHLKEGCALVSMEKLGSSNENDDEVLSGSEEECSDTVSLR

TIIII.'''   IIIIIIIII.   IIIIIIIII
FMDPKENYICAGAITYICGGLAVRERPHMYIGDTGITGLHHLVTEVVUIGIDEAMAJTCS
RIDVRILEDGGIVIVDNGRGIPIEVHERESAKQGREVSALEVVLTVLHAGGKFDKDSYKV
SGGLHGVGVSCVNALSEKLVATVFKDKKCYQMEFSRGIPVTPLQYVSVSDRQGTEIVFYP
DPKIFSTCTFDRSILMKRLRELAFLNRGITIVFEDDRDVSFDKVTFFYEGGIQSFVSYLN
QNKESLFSEPIYICGTRVGDDGEIEFEAALQWNSGYSELVYSANNIPTRQGGTHLTGFS
TALTRVINTYIKAHNLAKNNKLALTGEDIREGLTAVISVKVPNPQFEGGTKQKLGNSDVS
SVAQQVVGEALTIFFEENPQIARMIVDKVFVAAQAREEAAKKARELTLRKSALDSARLPGK
LIDCLEKDPEKCEMYIVEGDSAGGSAKQGRDRRFQAILPIRGKILNVEKARLQKIFQNQE
IGTIIAALGCGIGADNFNLSKLRYRRIIIMTDADVDGSHIRTLLLTFFYRHMTALIENEC
VYIAQPPLYKVSKKKDFRYILSEKEMDSYLLMLGTNESSILFKSTERELRGEALESPINV
ILDVESFINTLEKKAIPFSEFLEMYKEGIGYPLYYLAPATGMQGGRYLYSDEEKEEALAQ
EETHKFKIIELYKVAVFVDIONQLKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLE
EVINYLKNLGRKGIEIQRYKGLGEMNADQLWDTTHNPEQRTLIHVSLKDAVEADHIFTHL
MGEEVPPRREFIESHALSIRINNLDI

CPn_0276   311140   310793
CT191 hypothetical protein
DMFLKRKKRGGSQVQNKRTASPIKHAKHYLHNYLQELQKIMAARPHDAIDAWNQVFRDKY
KGMSQAIGFRDHILLVKVYNSSLYALLKQTPQNDLIMSLYQVASHVQIREIQFLLG

CPn_0277   312003   311404
No robust homolog present in Genebank/EMBL as of 11/7/98
NISIFYPKYFIEGKEVLIKNLPPLIFYGVILMIINVRAPAFGITSVQQFSTNFQAAIPIL
NIVIGCSRISSTYAEDIEEVAQEKLEKSTHSKSSTSVNLWAHRVRGVVEILGGGIVILAL
EITALVLQVVIIKLIKCLIDVLCVCLFGLGVCVVAIIGAIAFCVVVVVKYLGFCSQGEELE
PIEVRTLISPDKPYPTVVYV

CPn_0278   312884   312060
*conserved outer membrane lipoprotein
RDSMKKKLSLLVGLIFVSQVDVSKKLGDHILLSKVSFSVYPGEVFGIVGHSGSGKTTLLRC
PVDDYRIPNRLLLDKQVDANYFQHQAFLDDECERYDCKGELVVIAKVHLEPQAIYSKKHS
SLERLKSQKKLTIAIPVDRTNAQRALHLLEECGLIVCKGPANLAMTAKDVCGKENRSINI
LEVSAPLLVGSLPDVDAAVIPGNFAIAANLSPKKDSLCLEDLSVSKYTNLVVIRSEDVGS
PKMIKLQKLFQSPSVQHFFDTKYHGNILTMTQDNG

CPn_0279   313546   312875
* Possible ABC Transporter Permease Protein
KKIMQSDLIQILLKETVNTLYHVSTAFFFSCAIGGMLGLGLFCTSPKSLNPKKSLYATIS
MILSFLTAIPFAILIVILFPITRWIVGTSLGPTASIVPLTIGAIPFVVTIVVDAFRNSAL
NYLESAVALGIPKRNILFGILLPESYPQLIFSLKSLVVHLISCSTLAGFVGGGGLGQLLL
QYGYYRFEWSVTTSVLVITLVLIESVRILGDFWGRRVLKYRGIL

CPn_0280   314593   313550
dppF-Dipeptide Transporter ATPase
IKGEAWLVSEQHSPIISVQDVSKKLGDHILLSKVSFSVYPGEVFGIVGHSGSGKTTLLRC
LDFLDMPTSGSISVAGFDNSLPTQKFSRRNFSKKVAYISQNYGLFSSKTVFENIAYPLRI
HHSEMSKSEVEEQVYDTLNFLNLYHRHDAYPGNLSGGQKQKVAIARAIVCQPEVVLCDEI
TSALDPKSTENIIERLLQLAQERGITLVLVSHEIDVVKKICSHVLVMHQGAVEELGTTEE
LFLNSENSITNELFHEDINIAALSSCYFAEDREEVLRLNFSKELAIQGIISKVIQTGLVS
INILSGNINLFRKSPMGFLIIVLEGEVEQRKKAKELLIELGVVIKEFY

CPn_0281   315033   316103
*dhnA-Predicted 1,6-Fructose Biphosphate Aldolase (dehydrin
family)*
ISLRRHTLMLNIHDILGNDDENLLSYQCKHITKDKLTLPSHDFVDKVFGLSDRNNRVLRS
LQTMFSKRLANSGYLSILPVDQGIEHSAGASFAINPIYFDPENIVKLAIESGCSAVAST
YGTLSLLSRKYAHKIPFMLKLNHNELLSYPTKYHQIFFTQVEAAYSMGAVAVGATVYFGS
ETSNEEIVAVSNAFAKARSLGLATVLWCYLRNPAFVANGVDYHTAADLTGQAADHLGATLG
ADIVKQKLPTCQGGFKAINFGKTDERVYSELSSNHPIDLCRYQVLNSYCGKVGLINSGGP
SGKNDFTEAAARTAVINKRAGGMGLILGRKAFORPLSEGIQLLNLVQDIYLDPNITIA

CPn_0282   316084   317529
xasA/gadC-Amino Acid Transporter
ILILQSLNFSKKVFMHSHSKPTKPLGTFTVGHLSLAVVISLRNLPLTAKHGLSTLFFYGL
AVICFMIPYALISAELASFKPQGIYIWARDALGKWWGFFAIWMQWFHNMTWYPAVLAFIA
STIVYKINPELAHNKVYIATVILAGFWILTFFNFLGITSSALFSSICVIIGTLIPGVILV
SLALFWIFSGNPIAISLSWGNLLPNFSNVSSLVLLAGHLLALCGLEANANLASDMVNPRK
NYPKAVFIGAIATLTILVLGSLSIAIVIPKEEISLVSGL/KTFTLFFDKYNLSWHTGIVV
VMTIAGSLGELNAWMFAGTKGLFISTONDCLPRLFKKVISKNVPTNLMLFQGIVVYIFTL
LFLCLDSADLVYWILTALSVQHYLAMYICLFLCAGPILRIKEPRAQRLYSVPGKFLGICTM
SILGILSCAFALWVSFLPPRELAQISEGSKIGYTTFLLLAFSLNCLIPFGIYFTHKRLSK
KS

CPn_0283   318581   317532
No robust homolog present in Genebank/EMBL as of 11/7/98
GRRLSTFQDLIKNAVAKIISFRKSPPNPVKLLIKFAKKDLVNSSIAPLVEVLLEILEAPG
EEILEVLFSLDPMWLKSMLDPKKHSTLGIEISSETAETIESCSLGLISINLLLSGLCLRS
SHDRCQAVKIIQQFCFQFSSEEVONFVEQRNILTPFLIHHLFECGDEVALLNQLGLRLDLIV
PNALYPEPDPSCWQIINSEDCAKDAEDQQEDFNKTKEACYEGLKKLVVLPALGITSIFQLL
RARRFKQGAEILMAIDRKKMKQNPFIFLEALLEIGEEFCIGVGKYLKLLMPIHLWDKLLIA
IYLGYFQDGLICQIEIETFCRRANLNPEAFQAAIQQGFLLGFLFPKMLLD

CPn_0284   319054   318551
No robust homolog present in Genebank/EMBL as of 11/7/98
FLLMRIIPAFQVPVIPEIYVNNTIIYCILGLKIIILRPIITYLIILAILAIATLMIVLYPVXIIS
VIIFVI/IMLIFLIVNINTLVAYLFYQQGGIEKTVVFGITIIPIVFFIIDEDLNILILIREEDII
VIIAIDELLKNFPAIDFRPKMLPYIRIFLDEVIRIFNESFEEDIHTIIKIII

CPn_0285   319661   319061
No robust homolog present in Genebank/EMBL as of 11/7/98
KELFHLFFFTANKEFTACHHLIVIPFIYICFICIICIPITIICILCAILIVLILLAVVFAIMATIIVL

AAPLGLLVWCCAASVCSMMAIVSLMCLYKCCKP,   SNEEKIDPTKDLEIKDPESLKPV
PVECQSLPKERKTVSFKAKIPSIVEDDFKPYVIQSTFYHQNKVYSKPIAERMQSLEKEIT
TLIVDFPRALEESSKSGSLLRGVISEIKNLFLPRFLSRKVKYGLTACLPRLGSIVEEYA
SSDLLILLLTKPEPLNMVTQQLIAHLNSLKTEKRKLTPHMQKLVLSINFWFYGWSLEEKC
IEKIVAYDPNLLTDELKAHLEACNIVQFLLSFQSSEMQREFRALFPSDAQELPSAKDGSN
YVPAINSSEYMYDFKDLSVLKKSLSERLAFCEKIPSPSSWNFTSSVASHYKDFSLLFTFF
SNQQSVILQNPFLLIELLHENPKCQTFLKGLLEKAMPHSNWAALFRPMLMGMLCSGIARK
KELKIIAEHLTVPFKEITTQAIASGKILDLLLQHLFDF

      :   322149   320650
mgtE-Mg++ Transporter (CBS Domain)
SCRESKGKIMVGEQNRNEEKLDTAFSSGNLMDSRTSHLDDELSFKLEKAFTCLSTDIHSH
DLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCITAKVAFIINTDSASRWAIFRRLSD
SEVCALIEQMPPDEAVWVLDDIPDRRYRRILELIDSKKALKIRDLQKHGRNTAGRLMTNE
FFAFLMETTVKDVSACIRSNPGIDLTRLVFVLDFKGELQGVVTDRSLIINPPEMSLKQIM
NQIEHKVLPDATREEVVDLVERYKIAALPVVDEENFLIGAITYEDVVEAIEDIADETIAR
MAGTTEDVGYQTCHVVQRFLLRAPWLLVTLFAGLISASVMAYFQKISPALLALIIFFIPL
INGMSGNVGVQCSTILVRSMATQTLSFGRRRETIFKEMSIGLLTGVVLGILCGLVVYLMG
FLGLNIFSGGGIQLGVTVATGVLGASLTATTLGVLSPFFFAKLGVDPALASGPIVTALND
IMSMIIFFLIAGGINFLFFN

CPn_0287   324230   322089
No robust homolog present in Genebank/EMBL as of 11/7/98
RRCMIRSPLPFISSKRALNMLGLQDEFSCPEDVVDFLFSEIELLAQQDEPSEGYLALSRS
LLMMTHNHPKVVKRVIFYGVSYGLKHKSMSIFIDVLTYIDFLFEKLGISASDRLSLCSAR
TCINFELYSQTGEMXFLSEVVDNFRLIEQLLKMHPQLKNRLGWEHFRIGAKQEEVSLVAS
ASVYQAVGRSFIELYHKHLELSDLACGMKCLALALDLSPNNAHIHADYAKGLVVLGTRQG
KSLLIERGMEHFSKAIFLSFSRDGDTLAYQNYRYSYALASVKLFDLTYKKEHFDQAMNIL
YQTVQAFPNLSGLWMVWGELLIRSGWLNSNMKYIEVGLEKLASLQKKTNDPIALSGLLAT
GIAILGLYLEEPNLFKDSRHRLISAMRTFPGNSALVHALGVVQLCSALYFNEDSHFASAI
SCFQSCLEWDLDATGMWQKLFDAYFSWGIKKKSARLLRKAVDVASRLCSLRPEAFLFWSD
RGLALKCLAEATIDEAYKEIFLSESLLHYQRAWDLSGRLEILELWGQSHYLLAELQQSLF
HYDEAYTLLTKVDLTLSSSRVKLILAAVLLGKGRLLQDTDPAEEAREILEPLVEVYLEDE
NFLLLLGKVYLFLFWKNKNVCLGKLARTYLEKATSLGCPEAYYTLGKFYAVIKDVNKAWG
MVIRSAQYGVRITEAKWLNDPYLANLREIHAFREVVENQKGRLWLGNKTEMKRN

CPn_0288   325785   324571
CT288 hypothetical protein
ISITIREFLFFGFECRAKFYNVIMSCFNLTSTNESLRPISPKASFPKQGWQSYFRSALRK
HRSDTLSVSVCKVNKYDANLFVRLTVIALAVVGVLILFSIMLASIQGTLVITSWPLVTAA
ILIPTILLTGGMYILHRLGKKVDVISGVCIPPFSRRCWVPISSSHTLEKFDEKHVSACSY
LDISTLSADGSGIAAVYQCPPLLFRAFPCFGIPCAMPFVALLRMIYNLIRFLYPYFIIF
RMIYEHFFCKHLPEDDRFIYKDVAREMGRSLAAFLKAPFYASACHIGAFYSLLDPLAGRV
LMGSVERDWNDNVILARSVSLANEAHSLFRFEGGGGRKGLGQHAFYLMLCCQPQSVFLFD
KGEIVSGAHPSIQLPERRGLDTSGRYPHISVIPDSGNDSAKNFIV

CPn_0289   325797   326996
CT289 hypothetical protein
NFNRLMKKQRSHYKKKNNLLLLLSILVGLGLGSVQSPWIVYSAECIANTFLKFLRLLSIPL
VFCALGSTITSIQNFNTMVTLGKRILYTTLLTTVIAASIGLLLFFLLRPQMITQDALATT
TKCNPLGYLDVLSDTLPENIFKPFLQGNVISAACLAVLLGTASLFLQEKEKHFVNQFFNS
FFSIFLNLARGGLKLLPIAMLGFSVILFKELKDQSNVKVWIEALTONAWDTGAGWGLLLVYA
GFASKKTGVVSNGALTAICNNLVSLIMGIIIFSTCASLDILGTTQLQDGAGASSIGITFI
YLPELFTRLPGGIYLTTLFSSIFFLAFSMAALSSMISMLFLLSQTLAEFGIKPYISETLA
TIIAFVLGIPSALSLTFFSNQDTVWGVALIVNGLIFIYAALVYGFPKLKKEVINAAPGDL
RLNKAFDYIIKYLLPIEGILLLGWYFYEGLFPENGQWWNPISLYSLGSLVLQWSLGLIIL
WKFNKQLYLRFSRYNHEIL

CPn_0290   327027   328523
Na-dependent Transporter
RSALTMNKKHASFSSRLGFIFSMIGIAVGAGNIWRFPRVAAQNGGGAFLILWLCFLFLWS
IPLIIIELSIGKLTKKAPIGALIKTAGKKFAWAGGFITLVTTCILAYYSTIVGWGLSYFY
YAVSGKIHLGNDFAKLWTSHYQSSIPLWAHLTSLGLAYLVIRKGIVHGIEKCNKILIPAF
FLCTIALLLRAVTLPGAVOGIKOLFSCDKSCFSNYKVWIEALTONAWDTGAGWGLLLVYA
GFASKKTGVVSNGALTAICNNLVSLIMGIIIFSTCASLDILGTTQLQDGAGASSIGITFI
YLPELFTRLPGGIYLTTLFSSIFFLAFSMAALSSMISMLFLLSQTLAEFGIKPYISETLA
TIIAFVLGIPSALSLTFFSNQDTVWGVALIVNGLIFIYAALVYGFPKLKKEVINAAPGDL
RLNKAFDYIIKYLLPIEGILLLGWYFYEGLFPENGQWWNPISLYSLGSLVLQWSLGLIIL
WKFNKQLYLRFSRYNHEIL

CPn_0291   328658   329194
incB-Inclusion Membrane Protein B
EKHMSAPIPTPOELSDQITCLNVQYQQVSELARENKGDIEGLKTLTAALTADAGIQPSAD
EIYSLQTAAALILSASEKPGSGPSGSTEGSVTVQSPCKFKKVLAVVLTIIALIAIAVLIA
CIIAACGGFPLLLSALNLYTIGACVSLPIIASTSVALICLCTFVANSLIKPVITVRTTR

CPn_0292   329201   329836
incC-Inclusion Membrane Protein C
VKNTKISDFMTSPIPFQSSGDASFLAEQPQQLPSTSESQLVTQLLTMMKHTQALSETVLQ
QQRDRLPTASIILQVGGAPTGGAGAFQPGPADDHHHPIPPPVVPAQIETEITTIRSELQ
LMRSTLCQSTKGARTGVLVVTAILMTISLLAIIIIILAVLGFTGVLPQVALLMQGETNLI
WAMVSGSIICFIALIGTLGLILTNKNTPLPAS

CPn_0293   329940   332723
CT293 hypothetical protein
VWSMQRVLRLLFNLHHGEEKRAFLFFLLGLVWGIGCYGTLSLAEGLFIEKLGSAELPKIY
LGSSLILCVLSSLILYNLFKKHISATALFLIPVSLSILCNFYLILSSIFAIDPPRSPLFF
YRTVIWSLTILSYTSFWGFVDQFFNLQDGKRHFCIFNAIIFLCDAIGSGIIASLVHTIGI
QGILILFTAALVLTFPIVFYVSKSLKSLSDDHDLFIDTGHPPPLSKALKLCFYDKYTFYL
LCFYFLMQLLAIATEFNYLKIFEIOFASKEEFELVAHIGKCSLWISLGNMCFALFAYSRI
VKRLGVNNIILFAPLFLSLFLFWTFKTTLSIAVLAMVVREGVTYALDDNNLQLLIYGVP
NKIRKJIRIVVESFIEPIGMLVWSLICFLSSGQYVFCLIISLIATILVCLVRITYAKAIL
KNLSAQALQLTRSMQDWIKGMTVKQKRQVELFLLAHLKHPSERHQTFAFQHLLNLASRSV
LPSLLAHMNKLSLPNKLKTIEMVKSSLWAKDFLTLELLKRWTSIFPHPAIASAIHLYFAE
HDLLHITHIAEDLVDTVGDRLLAAILTVRROEAYGPYRDLAKRLKELLNSDQPEDIVMG
LTILFLEKNPONFPILLDFLNTKNEDILIVTCKALHITHVRANHKFYCPELLKPLRQCSHN
DEAJQYLLKTIIIALDLHFVKDLLMTTHQLKNTTQRKYAEAMIGKLRDKEVAPAFLQVLTDE
THHNRCKLAAKALCKLUNWLLKKHAYKIVKSKASKALFYSYHCHYIQKKFYPTYNLGLLA
NTLIERNYYAHVNFMLSLLGILGSSMEHSGVLIRALTSKNQKIKAQALESLEKHTDSHLFSL
LEPFYKQICMKYSSEKYYFKCGVIPLTLKELLNMMENSPHSLNKLTAQQLKEELSYCDPDF
QSVRTIYNQEHEDFRTEESETLISFLSI

CPn_0294   333077   333502

IRNFFKNLIDRAFLLKKTIIHTSLDMOLLLTIADKTETIIFKIYGNVFHICQPGFSFYII
VECYITISKEKLESPLNLKRLDCFGEEGLFNNKPAEYNALSANTQARMLVLGKGQIMIVE
ECPSVALSFLELYAKGIKFREB   ...

CPn_0295   333866   333627
acpP-Acyl Carrier Protein
AMSLEDDVIAIIVEGLGVDPKEVNENSSFIEDLNADGLDLTELIMTLEEKFAFEISEEDA
...

CPn_0296   334792   334422
CT296 hypothetical protein
KIPIRGMICMDITLVGGSRGIGLGIVKLFLENCGADVEIWGLNEERGQAVIESL
TGLGGEVSFARVDVSHNGGVKDCVQKFLDKHNKIDILVNNAGITRDNLLMRMSEDDWQSV
ISTNLTSLYYTCSSVIRHMIKARSGSIINVASIVAKIGSAGOTNYAAAKAGIIAFTKSLA
KEVAARNIRVNCLAPGFIETDMTSVLNDNLKAEWLKSIPLGRAGTPEDVARVALFLASQL
SSYMTAQTLVVDGGLTY

CPn_0297   335724   334774
fabD-Malonyl Acyl Carrier Transcyclase
SRSNKDDNFMKKRYAFLFPGOGSQYVGMGODLYMEYPEVRELFDFANERLGFSLTSIMFE
GPEDLLMETVHSQLAIYLHSMAVVKVLSQRSSIQPSLVSGLSLGEYTALVASDRISVLDG
LELVRKRGOLNNEACNQSPGAMAALLGLPSEVIEENITSLGQGIWIANYNAPKQLVVAGI
AEKVDQAIELFRDLGCKKAVRLKVSGAFHTPLMQVAQDGLAPDIYALCMKDSSLPLVSHV
VGKSLVNTEEMRECLAROMTSPTLWYQSCYHIESEVDEFLELGPKVLAGLNRSIGISKP
ITSLGTFAQIEKFLSEV

CPn_0298   336742   335717
fabH-Oxoacyl Carrier Protein Synthase III
YTSFFLYMWFSVNKNKKAAIWATGSYLPEKVLSNADLEKMVDTSDEWIVTRTGIKERRIA
GPQEYTSLMGAIAEKKAIANAGLSKDQIDCIIFSTAAPDYIFPSSGALAGLYHQEIEDVPT
FDCQAACTGYLYGLSVAKAYVESGTYNHVLLIAADKLSSFVDYTDRNTCVLFGDGGAACV
IGESRPGSLEINRLSLGADGKLGELLSLPAGGSRCPASKETLQSGKHFIAMEGKEVFKHA
VRRMETAAKHSIALAGIQEEDIDWFVPHQANERIIDALAKRFEIDESRVFKSVHKYGNTA
ASSVGIALDELVHTESIKLDDYLLLVAFGGGLSWGAVVLKQV

CPn_0299   336726   337415
recR-Recombination Protein
RKKLVYYSESLYSNLNLGPRPECKNKIHITMTRYPDYLSKLIFFLRKLPGIGFKTAEKLA
FELISWDSEQLKILGNAFHNVASERSHCPLCFTLKESKEADCHFCREERDNQSLCIVASP
KDVFFLERSKVFKGRYHVLGSLLSPITGKHIENERLSILKSRIETLCPKEIILAIDATLE
GDATALFLKQELQHFSVNISRLALGLPIGLSFDYVDSGTLARAFSGRHSY

CPn_0300   337768   340152
yaeT-Omp85 Analog
GRLLGMLIMRNKVILQISILALIQTPLTLFSTEKVKEGHVVVDSITIITEGENASNKHPL
PKLKTRSGALFSQLDFDEDLRILAKEYDSVEPKVEFSEGKTNIALHLIAKPSIRNIHISG
NQVVPEHKILKTLQIYRNDLFEREKFLKGLDDLRTYYLKRGYFASSVDYSLEHNQEKGHI
DVLIKINEGPCGKIKQLTFSGISRSEKSDIQEFIQTKQHSTTTSWFQDVNPLCTPYTVDDD
SLAITNYLHNNGYADAIVNSHYDLDDKGNILLYMDIDRGSRYTLGHVHIQGFEVLPKRLI
ERQSQVGPNDLYCPDKIWDGAHKIKQTYAKYGYINTNVDVLFIPHATRPIYDVTYEVSEG
SPYKVGLIKITGNTHTKSDVILHETSLFPGDTFNRLKLEDTEQRLRNTGYFQSVSVYTVR
SQLDPMGNADQYRDIFVEVKETTTGNLGLFLGFSSLDNLFGGIELSESNFDLFGARNIFS
KGFRCLRGGGEHLFLKANFGDKVTDYTLKWTKPHFLNTPWILGIELDKSINRALSKDYAV
QTYGGNVSTTYILNEHLKYGLFYRGSQTSLHEKRKFLLGPNIDSNKGFVSAAGVNLNYDS
VDSPRTPTTGIRGGVTFEVSGLGGTYHFTKLSLNSSIYRKLTRKGILKIKGEAQFIKPYS
NTTAEGVPVSERFFLGGETTVRGYKSFIIGPKYSATEPQGGLSSLLISEEFQYPLIRQPN
ISAFVFLDSGFVGLQEYKISLKDLRSSAGFGLRFDVMNNVPVMLGFGWPFRPTETLNGEK
IDVSQRFFFALGGMF

CPn_0301   340163   340762
(OmpH-Like Outer Membrane Protein)
IKDLSKEIFVVFRKGFWYPFSIPKLVQVIMKKLLFSTFLLVLGSTSAAHANLGYVNLKRC
LEESDLGKKKETEELEAMKQQFVKNAEKIEEELTSIYNKLQDEDYMESLSDSASEELRKKF
EDLSGEYNAYOSQYYQSINQSNVKRIQKLIQEVKIAAESVRSKEKLEAILNEEAVLAIAP
GTDKTTEIIAILNESFKKQN

CPn_0302   340766   341866
lpxD-UDP Glucosamine N-Acyltransferase
SKFKEFSMSEAPVYTLKQLAELLQVEVQGNIETPISGVEDISQAQPHHIAFLDNEKYSSF
LKNTKAGAIILSRSQAMQHAHLKKNFLITNESPSLTFQKCIELFIEPVTSGFPGIHPTAV
IHPTARIEKNVTIEPYVVISQHAHIGSDTYIGACSVIGAHSVLGANCLIHPKVVIRERVL
MGNRVVVVQPGAVLGSCGFGYITNAFGHHKPLKHLGYVIVGDDVEIGANTTIDRGRFKNTV
IHEGTKIDNQVQVAHHVEIGKHSIIVAQAGIAGSTKIGEHVIIGGQTGITGHISIADHVI
MIAQTGVTKSITSPGIYGGAPARPYQETHRLIAKIRNLPKTEERLSKLEKQVRDLSTPSL
AEIPSEI

CPn_0303   342982   341921
CT303 hypothetical protein
REQKGLHHMDVSRKINRHTQFYVDSIDGVIKNFDHKPSEDKSRDHEELEEKLLTITKRIV
ASAQEFQNRKTDSKNYYLKKTQWLPFKNEELEQTKELFAMLTSMDKKIAQLFFYSPGCSS
DWVEFTEVICHLNDSIGLGGVLLCCGLFEQQCEHVVTVNKKLDLPLLLGTTVVNSLRYYL
TYRNISLLNCOSMSELGKELGDVLKQHGVAFTLFKEIVDIDLLNYVKLIQGLKRSGNIQ
ARIYDNOVPTLPSVSSSPIALRYSLANTIRGLALHVDFSSLKFISPSILSNTEHTAKALN
SGGECFIFSNLDEFNLGMKIVMQLLRTCKISPEILNKNIMKILMIKRRVRSLYI

CPn_0304   344091   344158
pdhA/odpA-Pyruvate Dehydrogenase Alpha
DQKPLPKRLFYKKVMDTSAPYNIACOYTEKCTVFRILDLYCGAACIKFLKQMVLIREFEA
RGEEAYLEGLVIIFYHIYAQQEAVATAAIANTYLDPWVFSSYRCHIALAILLNIPLQEIAA
ELLGKETYICALIRCGSMMMAYGPNFFKYIFTIIVI7JIPLAAIAAFTIKYOFQKNRVSLCFIG
IFGAVAIIVFHETLNFVIIJIQLFLMLIFFNNWCHYTSLNRAVAKQPIAEIQCSSYDIRAV
TVNIFOLFNIILLIFREAYRYMVUTEIIVEVGTIIHFRCHILIDINLYHCKEFMCLFKK
DFIVIAPIWLIRLFVITEEEFQHIRQFCKTAVLFAFINAKLIDDHYVTTLFETVYA

CPn_0305   344142   345157
pdhB/odpB-Pyruvate Dehydrogenase Beta
HKECMPFHKTLRIEGALRFAIDEEMCHDPNVIIEGEMVDYGFAAVKVTPGLLDKWIPKRV
LDAPITFAAFSKTIGIMAALGLPPTIEFMSWDPCVALQGIICHAAKMIHMNMTKIKFCVPI
VFRNITFAAAQVISQIISIHVTANIIGHLTIAPGHPYDAKGLLKSATRNNNIVILFLEN
ELEYNLYGEVITEEYLVPIGKAHRVQFFRIDCTIITYGMVSITKEACILAKKRWMSLSIEI

```
IDLRTIKPLDIGTILSSVRKTSRCIVIEEGHYF,     SEIIALITEHVFDSLDAPPLRVC
QKETPMPYSK[LEQATLPNVNRILDTIEKVMR
```

CPn_0306   345136   346431
pdhC-Dihydrolipoamide Acetyltransferase
```
GKFVISLLKMPKLSPTMEVGTIVKWHKKSNDQVSFGDVIVEISTDKAILEHTANEDGWIR
EILRHEGEKIVIGTPIAVLSTEANEPFNLEELLPKTEPSNLEASPKGSSEEVSPATTPQA
ASATFTAVTFKPEPPLSGPLVFKHVGTTNNLGPLARQLAKEKNIDVSSIQGSGPGGRIVK
KXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
VAIPDGIITPIIRCADRKNLJHISAEIKSLALKARNQSLQDTEYKCSJFIVSNLGHTGIT
EFTAIVNPPQAAILAVGSVTEQALVLDGEITIGSTCNLTLSVDHRVIDGYPAAMFHKRLQ
KILEAPAVLLLN
```

CPn_0307   348998   346515
glgP-Glycogen Phosphorylase
```
NGCIVEDFSSFDKNKVSVDSMKRAILDRLYLSVVQSPESASPRDIFTAVAKTVMEWLAKG
WLKTQNGYYKNDVKRVYYLSMEFLLGRSLKSNLLNLGILDLVRKALKTLNYDFDHLVEME
SDAGLGNGGLGRLAACYLDSMATLAVPAYGYGIRYDYGIFDQRIVNGYQEEAPDEWLRYG
NPWEICRGEYLYPVRFYGRVIHYTDSRGKQVADLVDTQEVLAMAYDIPIPGYGNDTVNSL
RLWQAQSPRGFEFSYFNHGNYIQAIEDIALIENISRVLYPNDSITEGQELRLKQEYFLVS
ATIQDIIRRYTKTHICLDNLADKVVVQLNDTHPALGIAEMMHILVDREELPWDKAWEMTT
VIFNYTNHTILPEALERWPLDLFSKLLPRHLEIIYEINSRWLEKVGSRYPKNDDKRRSLS
·IVEEGYQKRINMANLAVVGSAKVNGVSSFHSQLIKDTLFKEFYEFFPEKFINVTNGVTPR
RWIALCNPRLSKLLNETIGDRYIIDLSHLSLIRSFAEDSGFRDHWKGVKLRNKQDLTSRI
YNEVGEIVDPNSLFDCHIKRIHEYKRQLMNILRVIYVYNDLKENPNQDVVPTTVIFSGKA
APGYVMAKLIIKLINSVADVVNQDSRVNDKLKVLFLPNYRVSMAEHIIPGTDLSEQISTA
GMEASGTGNMKFALNGALTIGTMDGANIEMAEHIGKENMFIFGLLEEQIVQLRREYCPQT
ICDKNPKIRQVLDLLEQGFFNSNDKDLFKPIVHRLLHEGDPFFVLADLESYIAAHENVNK
LFKEPDSWTKISIYNTAGMGFFSSDRAIQDYARDIWHVPTKSCSGEGN
```

CPn_0308   349213   349596
No robust homolog present in Genebank/EMBL as of 11/7/98
```
FFTQENMAVTAQTPQTTQPOPSVSHKATHRYCSWVFFKPILVSLGLLLASLTTLGLVIA
SGVTLSLGIGIVLAIQIVLAGIALVLAFNHIRQFKQARTAELNSHXHISAPAAATVQKQK
LEDRYSSK
```

CPn_0309   350977   349595
CT309 hypothetical protein
```
FMRAWEEFLLLQEKEIGTNTVDKWLRSLKVLCFDACNLYLEAQDSFQITWFEEHIRHKVK
SGLVNNNKPIRVHVTSVDKAAPFYKEKQMQQEKTAYFTMHYGSVNPEMTFSNFLVTPEN
DLPFRVLQEFTKSPDENGGVTFNPIYLFGPEGSGKTHLMQSAISVLRESGGKILYVSSDL
FTEHLVSAIRSGEMQKFRSFYRNIDALFIEDIEVFSGKSATQEEFFHTFNSLHSEGKLIV
VSSSYAPVDLVAVEDRLISRFEWGVAIPIHPLVQGLRSFLMRQVERLSIRIQETALDFL
IYALSSNVKTLLHALNLLAKRVMYKKLSHQLLYEDDVKTLLKDVLEAAGSVRLTPLKIIR
NVAQYYGVSQESILGRSQSREYVLPRQVAMYFCRQKLSLSYVRIGDVFSRDHSTVISSIR
LIEQKIEENSHDIHMAIQDISKNLNSLHKSLEFFPSEEMII
```

CPn_0310   353472   351049
60IM-60kDa Inner Membrane Protein
```
YFDLLSLIFRVYQMNKRTLLFVSLIGIAFVGCQIFFGYNEFRSCKNLAEKQRKISEQTLA
AVESVGLSVASWDTDVNGEEHKNNYAVRVGDKLFLLHNGEAAQSVYSSGESWSFVDHKCG
FDNIHLALYRQQGSSFNPTNTGKVFLPTNHEGLPVLVVEFRNNKEPLVFLGEYAQGRISN
KDSTIFGTALVFWRSGSDYIPLGLVDSREEKLVSLDLRITRAVIFGNDQDSAKSSDTANH
YVLFNDYMQIIVSSEESGSIEGINLPFASTNNKSIVNEIGFDRDLASEKSPEALFPGLSSK
LPDGQQAKNSIGGYYPLLRRGLLSDSKKLLPLEYHALNVVSGRELATPVALRYRVLSYTP
HSIQLESLDRSVQKVYKLPENPEEKPYVFETAITLTKETEDVWVTSGVPEVEINSNASAP
TIKYRVIKKNKGSLDKVKLPKVKEPLAIRRGVYPQWILNSNGYFGIILTPLSEIASGYGS
LYISGSTAPTRLSAISPKNQLYPVSKYPGYETLLPLPKDAGTHRFLVYAGPLAEPTLAVL
DKTITQEKGENPEYLDSISFRGVFAFITAPFAALLFIIMKFFKLVTGSWGISIILLTVFL
KLLLYPLNAWSIRSMRRMQILSFYIQQIQQKYKNEPKRAQMEIMGLYKTNKVNPITGCLP
LLIQLPFLIAMFDLLKSSFLLRGASFIPGWIDNLTAPDVLFSWQTSIWFIGNEFHLLPIL
LGIVMFLQQKVTSLHKKGPVTDQQKQQQVMGNMMAILFTAMFYNFPSGLNIYWLSSMILG
VVQQWITNKILDSKHLKNEVVLNNKKHR
```

CPn_0311   354453   353575
CT311 hypothetical protein
```
DMRAEMAVIYWDRSKIVWSFEPWSLRLTWYGVFFTVGIFLACLSARYLALSYYGLKDHLS
FSKSQLRVALENFFIYSILFIVPGARLAYVIFYGWSFYLQHPEEIIQIWHGGLSSHGGVL
GFLLWAAIFSWIYKKKISKLTFLFLTDLCGSVFGIAAFFIRLGNFWNQEIVGTPTSLPWG
VVFSDPMQGVQGVPVHPVQLYEGISYLVVSGILYFLSYKRYLHLGKGYVTSIACISVAFI
RFFAEYVKSHQGKVLAEDCLLTIGQILSIPLFLFGVALLIICSLKARRHRSHI
```

CPn_0312   354518   354976
CT101 hypothetical protein
```
CTHARNIKYFLILFPGILWISAGHKLLLKATAIALDPLSSFFTYCLLSMVSWGLASLKHR
YLLSKTIRKQLSLSSEFFSQKITWIAYIKQTFISRRFLIMVIMIAFSLVLRRYISNPOAL
FVIRATVGYALIKTAIAYFSKLQNALMENPEGN
```

CPn_0313   354957   355355
acpS-Acyl-carrier Protein Synthase
```
WKILKEISANSMEIIHIGTDIIEISRIREAIATHGNRLLNRIFTEAECKYCLEKTDPIPS
FAGRFAGKEAVAKALGTGIGSVVAWKDIEVFKVSHGPEVLLPSHVYAKIGISKVILSISH
CKEYATATAIALA
```

CPn_0314   356285   355353
trxB-Thioredoxin Reductase
```
MIHSRLIIIGSGPSGYTAAIYASRALLHPLLFEGFFSGISCGOLMTTTEVENFPGFPEGI
LGPKLMNNMKEQAVRFGTKTLAQDIISVDFSVRPFILKSKEETYSCDACIIATGASAKRL
EIFCACNDEFWQKGVTACAVCDGASPIFKNKDLYVIFSGDSALEEALYLTRYGSHVYYVH
RRDKLRAIKAMEARAQNNEKITFLWNSEIVKISGDSIVRSVDIKNVQTOEITTREAAGVF
FAISHLFNTDFLJXQLTLDESGYIVTEKGTSKTSVFSVFAAGDVQDKYYROAVTSAGSGC
IAALDAFRFLG
```

CPn_0315   356977   358716
rpl31 Ribosomal Protein
```
MIKQAFYTWXXKKILDN[ECLTEDVAEFKDLLYTAHP[TSJEEEIDNEIQFCA[LKUTVV
DINKDFVVVIAVGLKGHIVIFMGEFIDSSEILVLLAEVEVYLDQAKDEEAIKVVLSREKATR
QRGWEYILAIKHEDSIVKGIQITRKVKQSLIVDIGMEAFLPCGQIDNKKIKNLLDYVGKVC
RRKILKINVERRNIVVIRRELLEAFRISKKAELIEQISIGEYRKAVVKNITDFGVFLDLD
GIDGLLJIITIMTWKRIHUPSFMVEINQELEVIILLSVIKEKGRVALAILKQKFHNFWEDIEK
```

CPn_0316   358784   360121
nusA-N Utilization Protein A
```
KYPFGKRVLGKIVKLLPYG,     IEEGIEGLIHIGEMSWVKNIVDFGEVVNKGDEVEAIV
LSIQKDEGKISLGLKQTERNPWGNIEEKYPIGLHVNAEIKNLTNYGAFVELEPGIEGLIH
ISDMSWIKKVSHRSELFKKGNSVEAVILGVDKESKKLTLCVKQLGSNPWNEIEAWRAGT
VISGVVTKITAFGGAFVELQNGIEGGIHVSELSDKPFAKIEDIISICENVSAKWIKLDPDH
KKVSLSVKEVLADNAYDQDSRTELDFKDSQGPKERKKKGK
```

CPn_0317   360045   362750
infB-Initiation Factor-2
```
SLLIRSLSKSANMEVKVLTKNLKLKIKNAQLTKAAGLDKLKQKLAQAGSSEAKSSSEKPS
AKEKSVKVALAATSTPTASAEQASPESTSRRIRAKNRSSFSSSEEESSAHIPVDTSEPAP
VSIADPEPELEVVDEVCDESPEVHPVAEVLPEQPVLPETPPQEKELEPKPVKPAEPKSVV
MIKSKFGPTGKHINMLLAKTFKAPAKEEKVVAGSKSTKPVASDKTGKPGTSEGGEQNNRE
KQFNPANRSPASGPKRDAGKKNLTDFRDRSKKSDESLKAFTGRDRYGLNEGGEEDRWRKK
RVYKPKKHYDEASIQRPTHIKISLPITVKDLAAEMKLKASEVIQKLFIHGHTYVVNDILD
SETAVQFIGLEFGCTIDIDYSEQDKLCLSNDTVRDEIQSTDPSKLVIRSPIVAFMGHVDH
GKTTLIDSLRKSNVAATEAGAITQHMGAFCCSTPVGDITILDTPGHEAFSAMRARGAEVC
DIVVLVVAGDEGIKEQTLEAIEHAKAADIAIVVAINKCDKPNFNSETIYRQLSEINLLPE
AWQGSTVTVNTSAKTGEGLSELLEMLALQAEVLELKADPSARARGLVIESELHKGLGPVA
TVLIQNGSLKLGEALVFNDCYGKVKTMHNEHNELMKEAGPSIPVLITGLSDIPKAGDPFF
VVKNEKTARDIIEARSAGQQRFALQQKKRPNFDSMLQNKKTLKLMIKADVQGSIEAVVSS
ISKIKSEKVDVEILTNSVGEISESDIRLAAASKAVLIGFHTGIESHAEPLIKSLGVRVEL
FTVIYHAIDAIKEIMTSLLDPIAEEKDEGSAEIKEIFRSSQVGSIYGCIVTEGIMTRNHK
VRVLRNKEILWKGTLSSLKRVKEDVKEVRKGLECGILLEGYQQAQIGDVLQCYEVIYHPQ
KL
```

CPn_0318   362704   363126
rbfA-Ribosome Binding Factor A
```
VMSYNVMKLSIIHKNYNLKYCMTENRRIKRVNALLQEAIAKVILKDVKHPKISNLWITVT
RVSLSKDLHSARVYVSVMPHENTKEEALEALKVSAGFIAHRASKNVVLKYFPELHFYLDD
IFSPQDYIENLLWQIQEKEKS
```

CPn_0319   363133   363879
truB-tRNA Pseudouridine Synthase
```
TIFFGNLNTIKDMTMDLAVELKEGILLVDKPQGRTSFSLIRALTKLIGVKKIGHAGTLDP
FATGVMVMLIGRKFTRLSDILLFEDKEYEAIAHLGTTTDSYDCDGVVGRSKKIPSLEEV
LSAAEYFQGEIQQLPPMFSAKKVQGKKLYEYARKGLSIERHHSTVQVHLQITKYEYPLLH
FVVSCSKGTYIRSIAHELGTMLGCGAYLEQLRRLRSGRFSIDECIDGNLLDHPDFDISPY
LRDAHGNSL
```

CPn_0320   363824   364783
ribF-FAD Synthase
```
TTPISIFLPTYEMPHEIAYSLTSSFSVDSVTVGFFDGCHLGHSNLLSILTSYSGSSGVTT
FDSHPQTVLSLNHTKLINTKEERLQLLQTFFPIDWLGVLTFDLNFANQSAEEFLTLLRNL
KCKRLILGYDSCIGKEQQSNTEALDTIGKGIEVIKIPPYRMDNIVVSSKAIRQFLSAG
NLECAHRFLGHPYAISGKITEGSGIGGSLGFATINLPREESLIPLGVYACEIRYDSTTCQ
GVMNLGTAPTFGRESLYAEAHIFSFAENLYGKEVSIIPRKFLREEKKFQSKETLIRAIEK
DILDAQGWFAKGSFNYEGTA
```

CPn_0321   365900   364767
ychF-GTP Binding Protein
```
YSKKHVIIFIFRCLMSHTECGIVGLPNVGKSGLFNALTGAQVASCNYPFCTIDPNVGIVP
VIDERLEALAKISNSQKIIYADMKFVDIAGLVKGASDGAGLGNRFLSHIRETHAIAHVVR
CFDDPDVTHVSGKVNPVEDIEVINLELIFSDFSSAKNIHSKLEKLAKGKREVGALLPLFD
TIIAHLEXGLPLRTLELTPEDIVALKPYPFLTMKPMFYIANVDESSLPDMDNDYVAAVRE
VAAKENSKVVPICVRIEEEIVSLPIEERLEFLMSLGLEKSGLHRLVRAAYDTLGLISYFT
TGPQESRAWTVVRGSSAWEAAGEIHTDIQKGFIRAEVITFEDMIECQGRAAARELGKLHI
EGRDYIVQDGDTMLFLHN
```

CPn_0322   366231   367328
yscU-YopS Translocation Protein U
```
SNLGNSMGEKTEKATPKRLRDARKKGOVAKSQDFPSAVTFIVSMFTAFSLSTFFFKHLGG
FLVSMLSQAPTRHDPVITLFYLKNCLMLILTASLPLLGAVAVVGVIVGFLIVGPTFSTEV
FKPDIKKFNPIENIKQKFKIKTLIELIKSILKIFGAALILYITLKSKVSLIIETAGVSPI
ITAQIFKEIFYKAVTSIGIFFLIVAILDLVYQRHNFAKELKMEKFEVKQEFKDTEGNPEI
KGRRRQIAQEIAYEDSSSQVKHASTVVSNPKDIAVAIGYMPEKYKAPWIIAMGINLRAKR
ILDEAEKYGIPIMRNVPLAHQLLDEGKELKFIPESTYEAIGEILLYITSLNAQNPNNKNT
NQPDHL
```

CPn_0323   367322   369460
lcrD- Low Calcium Response D
```
·SFIMNKLLNFVSRTLGGDTALMINKSSDLILALWMMGVVLMIIIPLPPPIVDLMITINL
SISVFLLMVALYIPSALOLSVFPSLLLITTMFRLGINISSSROILLKAYAGHVIQAFGDF
VVGGNYVVGFIIFLIITIIQFIVVTKGCAERVAEVAARFRLDAMPGKQHAIDADLRAGHID
ATQARDKRAQIQKESELYGAMDGAMKFIKGDVIAGIVISLINIVGGLTIGVAMHGMDLAQ
AAHVYTLLSIGDGLVSQIPSLLIALTAGIVTTRVSSDKNTNLGKEISTQLVKEPRALLLA
GAATLGVGFFKGFPLWSFSILALIFVALGILLLTKKSAAGKKGGGSGASTTVCAAGDGAA
TVGDNPDDYSLTLPVILELCKDLSKLIQHKTKSCQSFVDDMIPKMRQALYQDICIRYPGI
HVRTDSPSLEGYDYMILLNEVPYVRGKIPPHHVLTNEVEDNLSRYNLPFITYKNAAGLPS
AWVGEDAKAILEKAAIKYWTPLEVIILHLSYFFIIKSSQEFLGIQEVRSMIEFMERSFPDL
VKEVTRLIFLQKLTEIFKRLVQEDISIKDLRTILESLCEWAQTEKDTVLLTEYVRSSLKL
YIGFKFSQQQCAISVYLLDPEIEEMIRGAIKGTSNISYLALDPGSVNLILKSMRNTITPT
FACYQPPVLLTAIDVRRYVRKLIETEFPDIAVIGYQEILPEIRIQPLCRIQIF
```

CPn_0324   369468   370688
CT324 hypothetical protein
```
VVVANRRHHAAGCLTGGLGLCTGYNLAAVFAAAAKADAAEVVAGOEFHEMNMIQQSQDLT
NFAAATRTKKKKEEKFQTLESRKPGENIKAKFFIESTEEKFGTDIADKYAICNGEISCQEL
HALPLAIGDDAGPEDILALVQEFIKDIALGCTTAIJYLVUTFPPGXXKLKEAILQARNTHT
FOPYRTAIGAKNILFASQEYADGVKISCSILPGSIVIEVTFFDTHTCDQLLSMLQDDRYTYQD
HAIVSSFLMKGMATELKRQSFCFEGAQILVLISTFPHIJAVLGTHYDYFESIRVPILLDGLK
```

AEGIQTPEDLNFVKVAESYHKSHDKFPTASKV.   ANLIGDDVDSVTTSVLNLFFSALR
QTSSRLFGCAIDKRQQLGAMIANALDAVNTNNEDYPKASDFPKPYPWS

CPn_0325   370696   371148
CT325 hypothetical protein
KRIAMQNQYECLLESLAPLLNTTLAPDKNNSCLIRFSDTHVPVQIEEDGNSGDLAVSTLL
GTLPENVFRERIFKAALSVNGGFQSSIKGILGYGEVTQQLYLSDILSMNYLNGEKLFEYL
KLFSLHAKIWMESLRTTNLPDLHVLGIYYVA

CPn_0326   371118   ....
malQ-Glucanotransferase
PSCFGNLLRRVNVLKYTKHSPSAHAWKLIGTSPKHGIYLPLFSIHTKNSCGIGEFLDLIP
LISWCQKQGFSVIQLLPLNDTGEDTSPYNSISSVALNPLFLSLSSLPNIDTIPEVAKKLQ
DMHELCSTPSVSYTQVKERKWAFLREYYOKCCKSSLEGNSNFSEFLESERYWLYPYGTFR
AIKHHMHGEPINNWPKSLTDQENFPDLTKKFHDEVLFFSYLQFLCYQQLCEVKAYADQHH
VLLKGDLPILISKDSCDVWFRDYFSSSRSVGAPPDLYNSEGNMHLPIYNFSQLAKDDY
IWWKERLRYAQNFYSVYRLDHIIGFFRLWIWDSSGRGRFIPDNPKDYIKQGTEILSTMLG
ASSMLPIGEDLGIIPQDVKTTLTHLGICGTRIPRWERNWESDSAFIPLKDYNPLSVTTLS
THDSDTFAQWWLNSPKEAKQFAKFLHLPFQKTLTTTETQIDILKLSHESASIFHINLFNDY
LALCPDLVSKNLQRERINTPGTISKKNWSYRVRPSLEELAIHKKFNGYIEKILTGL

CPn_0327   372927   373211
r128-L28 Ribosomal Protein
RIHRKNMSRKCPLTGKRPRRGYSYTLRGIAKKKKGIGLKVTGKTKRRFFPNMLTKRLWST
EENRFLKLKISASALRHIDKLGLEKVLERAKSKNF

CPn_0328   373220   374992
CT085 hypothetical protein
LKYREIFHSFLRRHISLFRSQKQLIDVFAPVSPNLELAEIHRRVIEDQGPALLFHNVIGS
SFPVLTNLFGTKHRVDQLFSQAPDNLIARVAHLISSTPKLSSLWKSRDLLKRISSLGLKK
ARFRRFPFVSMSSVNLDHLPLLTSWPEDGGAFLTLPLVYTESPTLTTPNLGMYRVQRFNQ
NTMGLHFQIQKGGGMHLYEAEQKKQNLPVSVFLSGNPFLTLSAIAPLPENVSELLFATFL
QGAKLLYKKTNDHPHPLLYDAEFILVGESPAGKRRPEGPFGDHFGYYSLQHDFPEFHCHK
IYHRKDAYTPATVVGKPYQEDFYIGNKLQEYLSPLFPLVMPGVRRLKSYGESGFHALTAA
VVKERYWRESLTTALRILGEGQLSLTKFLMVTDQEVPLDRFSVVLETILERLQPDRDLII
FSETANDTLDYTGPSLNKGSKGIFMGIGKAIRDLPHGYQGGKIHGVQDIAPFCRGCLVLE
TSLEDRCIKSLLHHPDLKSWPLIILADNLRETIQSEKDFLWRTFTRCAPANDLHALHSHF
ATHRPNYNFPFVIDALMKPSYPKEVEVDPSTKQKVSERWHAYFPNKETFYI

CPn_0329   375085   376146
Phopholipase D Superfamily (leader (33) peptide)
KMNKRQKDKLKICVIISTLILVGIFARAPRGDTFKTFLKSEEAIIYSNQCNEDMRKILCD
AIEHADEEIFLRIYNLSEPKIQQSLTRQAQAKNKVTIYYQKFKIPQILKQASNVTLVEQP
PAGRKLMHQKALSIDKKDAWLGSANYTNLSLRLDNNLILGMHSSELCDLIITNTSGDFSI
KDQTGKYFVLPQDRKIAIQAVLEKIQTAQKTIQVAMFALTHSEIIQALHQAKQRGIHVDI
IIDRSHSKLTFKQLRQLNINKDFVSINTAPCTLHHKFAVIDNKTLLAGSINWSKGRFSLN
DESLIIILENLTKQQNQKLRMIWKDLAKHSEHPTVDDEEKEIIEKSLPVEEQEAA

CPn_0330   376930   376202
CT083 hypothetical protein
FISIEMLLLSRQLFSVLPSRFQDLHVYRFKESLKLLQFMTMVGGEIVVVLAEIKEEDLRA
RKLPVRKRREKNYLRIFRVLSRFIRVLIRFDPYGALSAQSIAKDSRQNSPLVEKISEEI
ATNEAIRLALLAIGDREQEEKKQRHRYKLLGQKQAKVLLSQLRHVHLDFKKLYCDSKKKE
DQEKDEKNKQKRSIKVTKKKKGISLGAAASQAIAAAAEAWVIARNKGVLETASTLFYQKD
EEA

CPn_0331   378452   376701
CT082 hypothetical protein
IQRIIMAVSGGGGVQPSSDPGKWNPALQGEQAEGPSPLKESIFSETKQASSAAKQESLVR
SGSTGMYATESQINKAKYRKAQDRSSTSPKSKLKGTFSKMRASVQGFMSGFGSARSRVSA
KRASDSGEGTSLLPTEMDVALKKGNRISPEMQGFFLDASGMGGSSSSDISQLSLEALKSSA
FSGARSLSLSSSESSSVASFGSFQKAIEPMSEEKVNAWTVARLGGEMVSSLLDPNVETSS
LVRRAMATGNEGMIDLSDLGQEEVSTAMTSPRAVEGKVKVSSSDSPEANPTGIPNSNTLE
PAEKEAEKQESREQLSEDQMMLARAMAGLLTGAAPQEVLSNSVWSGPSTVFPPPPKFSGTL
PTQRSGDKSKHKSPGIEKSTNHTNFSPLREGTVKSAEVKSLPHPESMYRFPKDSIVSREE
PEAVVKESTAFKNPENSSQNFLPIAVESVFPKESGTGGALGSDAVSSSYHFLAQRGVSLL
APLPRATDDYKEKLEAHKGPGGPPDPLIYQYRNVAVEPPIVLRSPQPFSGSSRLSVQGKP
EAASVHDDGGGGNSGGFSGDQRRGSSGQKASRQEKKGKKLSTDI

CPn_0332   378676   379536
CHLTR T2 Protein
YLDSRIRVIPLARQRCTLLHLLAVLCPPISFFTQGVSPCVFFCFLDF

CPn_0333   379117   378800
lcuB
VDFFVFVFFMGKPKKSRTDRALAQEIQKKSTEVLKKPARIKAKNRRKFLIAKEQKTLKHR
AQEYDQLVRSLLDSQKKDTDKVLIFNYENGFVFTDKDHFSKYSIRL

CPn_0334   379308   379823
CT079 similarity
TMSVHITPRKCFILCILSMFTLPTLFPKAHLILFSPYIVLCFYCFSKDKGLVLALGCGVL
CDLALGSRGVFLLLYPLTALITHKAHLIFSKESKAALVIVNMIFYGVFLLLTIPHCALFG
HEVRWCIDVLMIPLKCSFLDNLIFTSVIYILPCAINSGIHKMISFFRRLVCY

CPn_0335   379808   ....
folD-Methylene Tetrahydrofolate Dehydrogenase
EIGMLLPGIPAAEKILQRLKEEISQSPTSPGLAVVLIGNDPASEVYVGMKVKKATEIGII
GKAHKLPCDSTLSCVLKLIERLNQDPSIHGILVQLPLPKHLDSEVILQAISPDKDVQLH
PVNMGKLLLGNFDGLLFCTPAGIIELLNYYEIPLRGPHAAIVGRSNIVGKPLAALMMQKH
IVTNCTVTVLLIQSENLPEILKTADIIIAALGAPLFIKETMVAPHAVIVDVGTTRVPADN
AKGVTLLVDVDFNNVVTKCAAITPVPGGVGPMTVAMLMSNTWRCYQNFS

CPn_0336   380569   381591
yuiL
PCDKMPCHHESSWIRWSHHCRYAHEGYHAMLPKFFLVLLCLGIAECCQKTTTIECEQMFI
FYICIVIVTCILSAKEKASLESQQIDRCFHKIDSIYHMHNPYSELCSINRAPADVPITLCVEL
CKFFLVSVIVTLYKLCHICRFDIVGPLKTLWLLHILKCCQTLPPKDVWEQHYKDMVWQHLEFQS
ITTKTLIFYKNHIVQIDLACVVKPSYAVDCLNEICNTPFCPNNYVWKXIEIKTSCHIIPSGRPWR
IPCKAVSFILDIIAMAIATPCSNIIQKKWVPFIKIYTHIILDTRTYKILLELSSSYPIQSVSVVH
ICCAYALDAIATVLMTFDHCKLFAAKQWAEEHIILTYIHGGAGS

1n

CPn_0337   381575
smpB- Small Protein B
IEEIFPGNQGKRILIIVLRRKNCFLLYWFLSPIMGEDLMAQKEIVSNRKALRNYEVIETL
EAGIVLTGTEIKSTRDHGGRLGDAYVIVSRCEGWIENASIAPYREDKIIVHNECRIKRKLL
LHRYELRKLEGKIAQKGMTLIPLGMFLSRGYVKVRLCCCRGKKAYDKRRTIIEREKEREV
AAAMKRRHH

CPn_0338   382272   383375
....
FNMKFLTTRNEIIIIGIENARTPIITINLDLEIETTVTGLVSTATDLTGISTFTVTK
AKVYEKGAISIPGKRFFCLVKELTEANLEISSSAGEMAQITSGSSCFRLLSMEKEDFFHL
PDIQNALRFSLPAEQLKTMLCRTSFAVSREESRYVLTGVLLAIANGVATIVGTDGKRLAK
IDAEVTLDKSFSGEYIIPIKAVEEIIKMCSDEGEAAIFLDQDKIAVECDNTLLITKLLSG
EFPDFSPVISTESNVKLDLHREELITTLLKQVALFTNESSHSVKFSFLPGELTLTANCTKV
GEGKVSMAVNYSGELLEIAFNPFFFLDILKHSKDELVSLGISDSYNPGIITDSASGLFVI
MPMRLHDD

CPn_0339   383405   384034
CT339 hypothetical protein
VTTLPMFMKICSLKLKNFRNHSDLEISLAPKLNYAQGKTNLLEALYVLSLGRSFRTQHLT
DTITTFGSSHFFLETQFEKDHLPQALSIYTDKQGKKICYNQLPIKTLSQLIGKVPIVLFSS
KDRLLISGAPADRRLFLNLLLSQCDNHYTLCLSYYHRALQQRNALLKSKQTSTVASGMNS
WSNTAPTYPSNGFSVVVRNFQIYPKNFGLTT

CPn_0340   383842   384156
(frame-shift with 0339)
PLYPLLIVLSSRSSAEKCSLKKQANLNRGLWDEQLVKHGTYLSIQRFLCSQKLSDLSKEL
WSNNLKEQLALKFKSSLIKNSDISETAVAEEFHKQLSISLPRDLE

CPn_0341   384160   384495
(frame-shift with 0340)
GSTSVGPHREDFLLTMNQMPVSQFSSEGQKHSLLAILRLAECLYLKQSHHVSPLVCLDDI
HAGLLDNERVGQLLDPAPTLGQTLITSTHMHGELPKTSLVLSIENAQVSEQII

CPn_0342   384619   385062
predicted OMP (leader (19) peptide)
HMKKFLLTILFLAVGNPLFSETSVIQTLPSGIGGLKETSKQKESVVCVHAFLRSYTSLKP
IARVLEKEHYDVFIWNYETRKFTLEKHAEHLNRLLKKIAELKPGVPINFVTHSIGGVIVR
VALAHPDCPEEARKEKLFSWLLRTQGLH

CPn_0343   384999   385595
(frame-shift with 0342?)
LPRRSQKRKAILMAPPNAGSTLARRYRCVKFVQFVFGGKLGRQLLTYCPTKMLNVGKLPS
SLDVLILSGNRHSKFLPFRLPYENDGKVCTIETKLDTPHKAYVIHTSHTYIITNRKSLYL
MKEFLKEGNTTPIIEHVPEAALEQTVMEDKQKNSRLKPYPNQDIYVIHCFGSRPYNLYGF
PKKWSLNQKNEINPEKLEK

CPn_0344   387432   385558
yaeL-Metalloprotease
SSRYMTIIYFILAALALGILVLIHELGHLVVAKAVGMAVESFSIGFGPALFKKRIGGIEY
RIGCIPFGGYVRIRGMERTKEXGEKGKIDSVYDIPQGFFSKSPWKRILVLVAGPLANILL
AVLAFSILVMNGGRSKNYSDCSKVVGWVHPVLQAEGLLPGDEILTCNGKPYVGDKDMLT
SLLEGHLNLEIKRPGYLTVPSKEFAIDVEFDPTKFGVPCSGASYLLYSNQVPLTKNSPME
NSELRPNDRFVWMDGTLLFSMAQISQILNESYAFVKVARNDKIFFSRQPRVLASVLHYTP
YLRNELIDTQYEAGLKGKWSSLYTLPYVINSYGYIEGELTAIDPESPLPQPQERLQLGDR
ILAIDGTPVSGSVDILRLVQNHRVSIIVQQMSPQELEEVNSRDADKRFIASYHSEDLLQI
LNHLGESHPVAVGPYRLLDPVQPRPWIDVYSSESLDKQLEVAKKIKNKDKQRYYLERLD
AEKQKPSLGISLKDLKVRYNPSPVVMLSNITKESLITLKALVTGHLSPQWLSGPVGIVQV
LHTGWSVGFSEVLFWIGLISMNLAVLNLLPIPVLDGGYILLCLWEIVKRRRLNMKIVERI
LVPFTFLLIIFFIFLTFQDLFRFFG

CPn_0345   388587   387436
CT345 hypothetical protein
LKVACLKHLAVLGSTGSIGRQTLEIVRRYPSEFKIISMASYGNNLRLFFQQLEEFAPLAA
AVYNEEVYNEACQRFPHMQFFLGQEGLTQLCIMDTVTTVVAASSGIEALPAILESHXXGK
ALALANKEILVCAGELVSKTAKENGIKVLPIDSEHNALYQCLEGRTIEGIKKLILTASGG
PLLNKSLEELSCVTKQDVLNHPIWNMGSKVTVDSSTLVNKGLEIIEAYWLFGLENVEILA
VIHPQSLIHGMVEFLDGSVISIMNPPDMLFPIQYALTAPERFASPRDGMDFSKKQTLEFF
PVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRRFLCEEISWCDILRKLTTLMECHK
VYACHSLEDILEVDGEARALAQEI

CPn_0346   389690   388704
070-troD/ytgD-Integral Membrane Protein
KKGSLMALGPSPYYGVSFFQFFSVVFFSRLFSGSLFTGSLYIDDIQIIVFLAISCSGAFAG
TFLVLRKMAMYANAVSHTVLFGLVCVCLFTHQLTTLSLGTLTLAAMATAMLTGFLIYFIR
NTFKVSEESSTALVFSLLFSLSLVLLVFMTKNAHIGTELVLGNADSLTKEDIFPVTIVIL
ANAVITIFAFRSLVCSSFDSVFASSLGIPIRLVDYLIIFQLSACLVGAFKAVGVLMALAF
LIIPSLIAKVIAKSIRSLMAWSLVFSIGTAFLAPASSRAILSAYDLGLSTSGISVVFLTM
MYIVVKFISYFRGYFSKNFEKISEKSSQY

CPn_0347   391078   389678
069-troC/ytgC-Integral Membrane Protein
TFGTNPEALSRKTIWIVLIHLSCVFSDTIFLSSFLAVTLICMTTALWGTILLISKQPLLS
ESLSHASVPGLLVGALMACVVFSLQASIFWIVLFGCAASVFGYGIIVFLGKVCKLHKDSA
LCFVLVVFFAIGVILASYVKESSPTLYNRINAYLYGQAATLGFLEATLAAIVFCASLFAL
WWVYRQIVVTTFDKDFAVTCGLKTVLYEALSLIFISLVIVSGVRSVGIVLISAMFVAPSL
GARQLSDRLSTILILSAFFGGISGALGGYISVAFTCRAIIGGQAVPVTLPTGPLVVICAG
LLAGLCLLFSPKSGWVIRFVRRKHFSFSKDQEHLLKVFWHISHNRLENISVRDFVCSYKY
QEYFGPKPFPRWRVQILEWRGYVKKEQDYRLTKKCRSEALRLVRAHRLWESYLVNSLDF
SKESVHELAEEIEHVLTEELDIITLTEILNDPCYDPHPQIIPNKKKEV

CPn_0348   391815   391027
068-troB/ytgB-ABC transporter ATPase
FTWLLNVYDETFWSVHNLCMVEHAAVLYIILEFGLGKGSLTAIIGPNGAGKNTLLKASLG
LIFPSSGTVFFNQKFKKVRQPLAYMPQRACVIANDFPHTVLDLALMXVSYKGMMCRISS
DDPREAFHILERVGLVDCVADRQIVQLVYTQLQGPAFLAHALMQKADLYLMDELFIAIDMAS
FKTSVCVLQELRDGQKTIVVVHHDLSHVRQLFDHVVLLNKRLGCCPTDECLAGDTIFQT
YYXEIELLEQTLKLSRGKWFCC

CPn_0349   392747   391790
067-troA/ytgA-Solute Protein Binding Family

WILKHA::REMDAKMGYIFKVMRWIPCFVACGITI   .JSGFQNANSRPCILSMNRMIHDC
VERVVGNRLATAVLIKGSLDPHAYEMVKGDKDKIAGSAVIFCNGLGLEHTLSLRKHLENN
PNSVKLCERLIARGAFVPLEEDGICDPHIWMDLSIWKEAVIEITEVLIEKFPEWSAEFKA
NSEELVCEMSILDGWAKQCLSTIPENLRYLVGGHNAFSYFTRRYLATPEEVASGAWRSRC
ISPEGLSPEAQIGVRDIMAVVDYINEHDVSVVFPEDTLNQDALKKIVSSLKKSHLVRLAQ
KPLYSDNVDDNYFGTFKHNVCLITEELCGVALECQR

CPn_0350   393169   391684
....
EGLLKMLKTFILESETPRTINPKPRAPRCGSKKRRDFINFTKTDIERVLELARQVGDKDLL
ARFSPKKPLTSLKRELIRSIRNGIVSVELWNAYVEAVKAVSSPNLEVTSPFV

CPn_0351   393861   395432
adt-ADP/ATP Translocase
KIKVFQRVNMTKTEEKPFGKLRSFLWPIHTHELKKVLPMFLMFFCITFNYTVLRDTKDTL
IVGAPGSGAEAIPFIKFWLVVPCAIIFMLIYAKLSNILSKQALFYAVGTPFLIFFALFPT
VIYPLRDVLHPTEFADRLQAILPGLLGLVAILRNWTFAAFYVLAELMGSVMLSLMFWGF
ANEITKIHEAKRFYALFGIGANISLLASGRAIVWASKLRASVSEGVDPWGISLRLLMAMT
IVSGLVLMASYWWINKNVLTDPRFYNPEEMQKGKKGAKPKMNMKDSFLYLARSPYILLLA
LLVIAYGICINLIEVTWKSQLKLQYPNMNDYSEFMGNFSFWTGVVSVLIMLFVGGNVIRK
FGWLTGALVTPVMVLLTGIVFFALVIFRNQASGLVAMFGTTPLMLAVVVGAIQNILSKST
KYALFDSTKEMAYIPLDQEQKVKGKAAIDVVAARFGKSGGALIQQGLLVICGSIGAMTPY
LAVILLFIIAIWLVSATKLNKLFLAQSALKEQEVAQEDSAPASS

CPn_0352   395478   396830
No robust homolog present in Genebank/EMBL as of 11/7/98
WVGIFFINSHFTNSYAFFNQKVIITVRHSGCTMKCSPLTLVPHIFLKNDCECHRSCSLKI
RTIARLIGLVLALVSALSFVFLAAPISVAGLAAAIVILIITLVVALLAKSKVLPI
PNELQKIIYNRYPKEVFYFVKTHSLTVNELKIFINCWKSGTDLPPNLHKKAEAFGIDILK
SIDLTLFPEFEEILLQNCPLYWLSHFIDKTESVAGEIGLNKTQKHVYGLLGPLAFHKGYTT
IFHSYTRPLLTLISESQYKFLYSKASKNQWDSPSVKKTCEEIFKELPHNMIFRKDVQGIS
QFLFLFFSHGITWEQAQMIQLINPDNWKMLCQFDKAGGHCSMATFGGFLNTETNMFDPVS
SNYEPTVNFMTWKELKVLLEKVKESPMHPASALVQKICVNTTHHQNLLKRWQFVRNTSSQ
WTSSLPQYAFHAQTYKLEKKIESSLPIRSSL

CPn_0353   396893   397135
No robust homolog present in Genebank/EMBL as of 11/7/98
LRFRNIKKSLIFIKRIRYSQSGKEQKGARPFFKKSITSSLVILLLEAIFNENFSSIIQNN
FNKNFKNKNISINRIFVKFTI

CPn_0354   397062   398507
No robust homolog present in Genebank/EMBL as of 11/7/98
YKTISIKILKIKTFLLIGFLLNLRYNTQIDEPRKCMSNITSPVIQNNRSCNYYFELKNST
TIHIVISAILLCGALIAFLCVAAPVSYILSGALLGLGLLIALIGVILGIKKITPMISSKE
QVFPQELVNRIRAHYPKFVSDFVSEAKPNLKDLISFIDLLNQLHSEVGSSTNYNVSEELQ
QKIDTFEGIARLKNEVRTASLKRLESAASSRPLFPSLPKILQKVFPFHVLGEFISAGSKV
VELHRVKIGGSLEEDLSDYIKPEMLPTYWLIPLDFRPTNSSILNLHTLVLARVLTRDVF
QHLKYAALNGEWNLNHSDLNTMKQQLFAKYHAAYQSYKILSQPSLQEDEFYNLLLCIFKH
RYSWKQMSLIKTVPADLWENLCCLTLDHTGRPQDMEFASLIGTLYTQGLIHKESEAFLSS
LTLLSLDQFKTIRRQSTNIAMFLENLATHNSTFRSLPPITVHPLKRSVFSQPEEDESSLL
IG

CPn_0355   399955   398591
No robust homolog present in Genebank/EMBL as of 11/7/98
IRDFYLHIIYTAFNRSISKELAMSMTIVPHALFKNHCECHSTFPLSSRTIVRIAIASLFC
IGALAALGCLAPPVSYIVGSVLAFIAFVILSLVILALIFGEKKLPPTPRIIPDRFTHVID
EAYGLSISAFVREQQVTLAEFRQFSTALLCNISPEEKIKQLPSELRSKVESFGISRLAGD
LEKNNWPIFEDLLSQTCPLYWLQKFISAGDPQVCRDLGVPRECYGYYWLGPLGYSTAKAT
IFCKETHHILQQLTKEDVLLLKNKALQEKWDTDEVKAIVERIYTTYTARGTLKTEAGGLT
KETISKELLLLSLHGYSFDQLQLITQLPRDAWDWLCFVDNSTAYNLQLCALVGALSSQNL
LDESSIDFDVNLGLYVIQDLKEAVQAFSASDEPKKELGKFLLRHLSSVSKRLESVLRQGL
HRIALEHGNARARVYDVNFVTGARIHRKTSIFFKD

CPn_0356   400465   400109
No robust homolog present in Genebank/EMBL as of 11/7/98
KQVQLFQYMNESGWDWLCDFDSQGEGFOLSRLVGLLHSSWALYEAKEQFYLPEVSLLTWE
ELIEMQLLSKPTKHGVAKDLCNVFEKHFQRFRQYLGSLDLNQRFENTFLNYPKYHLDRE

CPn_0357   401341   400469
No robust homolog present in Genebank/EMBL as of 11/7/98
YSSHNGASMVNIQPVYRNTQVNYSQATQFSVCQPALSLIIVSVVAAVLAIVLVCSQSLL
SIELGTALVLVSLILFASAMFMIYKMRQEPKELLIPKKIMELIOEHYPSIVVDFIRDQEV
SIYEIHHLISILNKTNVFDKAPVYLQEKLLQFGIEKFKDVHPSKLPNFEEILLQHCPLHW
LGRLVYPMVSDVTPGTYGYWCGPLGLYENAPSLFERRSLLLLKKISFGEFALLEDGLKK
NTWSSSELVQIRQNLFTRYYADKEEVDEAELNADYEQFDSLLHLIFSHKLS

CPn_0358   401757   401578
No robust homolog present in Genebank/EMBL as of 11/7/98
EEVLSVSMKLIPTQDSIERETDSKRDKKIFTIYICSSKVLAGHFFSHLDKHNKIHESIGV

CPn_0359   401994   403817
lepA-GTPase
ITLQYILKEYKIENIRNFSIIAHIDHGKSTIADRLLESTSTVEEREMREQLLDSMDLERE
RGITIKAHPVTMTYLYEGEVYQLNLIDTPGHVDFSYEVSRSLSACEGALLIVDAAQGVQA
QSLANVYLALERDLEIIPVLNKIDLPAADPVRIAQQIEDYIGLDTTNIIACSAKTGQGIP
AILKAIIDLVPPPKAPAETELKALVTDSHYDPYVGIMVYVRIISGELKKGDRITFMAKG
SGFEVLGIGAFLPKATFIEGSLRFCQVGFFIANLKKVKDVKIGDTVTKTKHPAKTPLEGF
KEINPVVFAGIYPIDSSDFDTLKDALGRLQLNDSALTIEQESSHSLGFGFRCGFLGLLHL
KIIFERIIREFDLDIIATAPCVIYKVVLKNGKVLDIDNPSGYPDPAIIEHVEEMPVHVNI
ITIQEYLCNIMNLCLDKRCICVKTEMLDQHRLVLAYELPLNEIVSDFNDKLKSVTKGYCS
FDYRLGDYPKGSIIKLEVLINEEPIDAFSCLVHRDKAESRGRSICEKLVDVIPQQLFKIP
IOAAIHFKVIARETIRALSKNVTAKCYGGDITRKRKLWEKQKKGKKRMKEFGKVSIPNTA
FIEVLKLD

CPn_0360   405164   404922
CT160 hypothetical protein
VALQTHTGLLGLAVMCIKNLVLNMIDHGFSVLVVVNRTPEKTRDFLKEYPNIIRELVGFESLE
DFVRELERPHKIMLMLGWKKFVDQIDHALLPFLEIGDVIICCVNSYFKDSERPCKELQEK
GLLFLFFVILXXERIJARIRCSIMNYGNPEAWPLVAPIFQSIAAKVQRPCCSWVGTGXAC
ILVYKAVHHFIFYGPIQLICEAVGILRDFLKLSATAVATILKEWNTLELESYLIRIASEVL

ALKDPEGIPVIDTILGVVQ   JKWTAIDALNSIVPLILIDALLARFLISWKEIRECA
ARNYPGTPLIFEMPHDPSVFIQDVFHALYAGKIIGYAQGFMLLGEASKETAWGLDLGEIA
LMWRGGCIIQSAFLGVIHKGFAANRENTSLIFQEYFRGALRHAEMCMRRTAYTAIGAGLP
IPCLAAAITFYDGYRTASSSMSLAQGLRDYFGAHTVERMDRPRGEFSMTDMWKIKTTERV
K

CPn_0361   406650   405382
tyrS-tyrosyl tRNA Synthetase
....
.. ..
TLVNNADWLQEIILILFLDDIGKHFRDQMLVKETIIKGRVHJDEIIGYTEFGTYLILQSYD
FYHLFKNYGTILGGCSGSDGWGNITSGIDFIRRKGLQQAYGLTYPLLTNAQGKKIGKTESG
TVWLDSDLTSPFELYQYLLRLPDDTIPKIARTLTLLSNEEIQDIDRRVQTDPVAVKEFVA
QDILSAIHGDLGLEEALSVTRSMHPGNLSSLSEKDFHELFAGGMGASLDKSEVLGKRWLD
LFLVLGLCKSKGEIRRLIEQKGVYINNVPIANEHSVCEEQDICYGHYVLLAQGKKRKLVL
YLN

CPn_0362   407843   407055
fliA/rpsD-Sigma-28/WhiG Family
LDKKKFVKTQQTQNIIEVWNFYWETQEIEYRDSLIEFYLPLVKSVVHRLISGMPSHVKTE
DLYASGVEGLVRAVERYNPERSRRFEGYAVFLIKAAIIDDLRKQDWVPRSVHQKANKLSG
AMDSLRQSLGKEPTDLELCEYLNISQQELSGWFVSARPALIVSLNEEWPSQSDEGAGMAL
EERIPDERAETGYDVVRDKQEFSLCLANAIQOELEEKERKVMALYYYEELVLKEIGKVLGVS
ESRVSQIHSKALLKLRAALSAFR

CPn_0363   409700   407943
flhA-Flagellar Secretion Protein
EAVFVSGKKDGVRGHIFVPLSILVLIFLPLPQILLDFGLCISFALSLLTVCWVFTLNSSN
SAKLFPPFFLYLCLLRLGLNLASTRWIVSSGTASSLIVSLGSFFSLGSLWAATFACLLLF
FVNFLMVSKGSERIAEVRSRFFLEALPAKQMALDSDLVSGRASYKAVKKQKNALIEECDF
FSAMEGVFRFVKGDAIISCILLVNVVSVTCLYYTSGYALEQMMFTVLGDALVSQVPALL
TSCAAATLISKIDKEESLLNYLFEYYKQLRQHFRVVSLLIFSLCCIPSSPKFPIVLLASL
LWLAYRKEEPASEDSCIERAFSYVEGACPKEQESQFYQVYRAASEEVFEDLGRLVFPVLTS
LRIEERPWLRVFGQNVYLDEMTPEAVLPFLRNIAHEALNAEVVQKYLEESERVFGIAVED
IVPKKISLSSSLVVLSRLLVRERVSLKLFPKILEAVAVYQNSGDSLEIIAEKVRKSLGYWI
GRSLWDQKQTLEVITIDFHVEELINSSYSKSNPVMQENVIRRVDSLLERSVFKDFRAIVT
SCETRFEMKKMLDPHFPDLLVLSHDELPKEIPISFLGIVSDEVLVP

CPn_0364   409954   410238
fer4-Ferredoxin IV
KENSMAKLVITSDDEQQEFELEDNSEIAEPCESMGIPFACTEGVCGTCVIEVLEGRENLS
EFTEPEYDFLGEPEDSNERLACQCRIKGGCVKVTF

CPn_0365   410498   411544
No robust homolog present in Genebank/EMBL as of 11/7/98
FKGTQVNSLIHATISPISLTVDHPLVDTKKKSCSNFDKIQSRILLITAIFAVLVTIGTLL
IGLLLNIPVTYFLTGISFIAVVLSNPILYKRATTLLKPRACGKHKEIKPKRVSTNLQYSS
ISIAINRSKENMEHQPKDLQNLPAPSALLTDNPYEIWKAKHSLFSLVSLLPGGNPEHLLI
SASENLGKTLIEETSQNAPISSYVDTTPSPKSLLNEAIQETRVEINTELPAGDSGERLY
WQPDFRGRVFLPQIPTTPEAIYQYYYALYVTYIQTAINTNTQIIQIPLYSLREHLYSREL
PPQSRMQQSLAMITAVKYMAELHPEYPLTIACVERSLAQLPQESIEDLS

CPn_0366   411976   412440
No robust homolog present in Genebank/EMBL as of 11/7/98
MGYLPVSATDVLFESPAAPLINSANTQNQKLIELKGKQQAESSPRTITSVILEVLLVIGC
CLIVLSLLAIRPALQFTLETGHPAAIAVLAVSGTILLVAVIILFCFLAAVPFAAKKTYKY
VKTVDDYASWHSHQQTPTLGTIFSGIVYAESQAQL

CPn_0367   413078   413836
No robust homolog present in Genebank/EMBL as of 11/7/98
SFPLNRYFMTKTTSIPDVHENQSHLSVDERLISESPVLTKKEVIAKIIKLTALILALAIA
VGTAVVAGVLGMPLMAIATGAALLAAVVLSCLLLRRREPSKPTEELLGPGKNKYDIAAQ
VQPSVPLDYQKLLRNEWTLVNTLSEINISWTLQDFPNQRYYVWEHQGAPITLVATTGDIAK
PRLKTSGRVMIVNAANSNMQSGGAGTNAALSAATHPTCWNNTRTSGGKINTGKGLSVGEC
RSAPWINRDWTNK

CPn_0368   413766   414107
No robust homolog present in Genebank/EMBL as of 11/7/98
TLAKDYLWVNAAOHPGSIETGRINDTNPGEAHFLAQLLGPKYEGELKAHPEKLSNVIKKA
YLNCFDEALNNQATVVQOVPLISSSIYSPGGKLELEPVNQTKPNSSAYKLYHIRT

CPn_0369   414345   415562
CT058 hypothetical protein_2
NIMTDSNPLPSYTDASLYRTPAKHSYPIRLPLNRTDRIEKILKIVTLTLALACALGFSIA
AGILAMPIFSAVVVITLAIAAVSLYSLLKKPKLYEILPQIEPESEQSSLSPSPOPPEQOD
LPLQIDPLPDPESLFEVSLADLTTPPPEELTAITVTPGYEALLEQNWDLLPSLAAVDPSPT
TETPQQPCFIWKLKDSKLIFISTSGDIAVPRIKTQGRVMIVNAANENISREGGGTNKALS
LATSLQCWNASRLFRAHSRSCSQLQPGECRSAKWENSDHTSNDHVPGKAHFLAQLLGPEA
AKCNNDPKQAFEVSKKAFHNLFOEAEIIGVDVIQLPLIGCNLFAPSRLLNLGKTRAEWIE
AIKLALITSLQDFGWEQDNWEEQKIIILTDKDQPPIIPPRFDLTTP

CPn_0370   415755   416912
CT058 hypothetical protein_3
KRIFFKLFVFYLKSFMSTTEPNLTNVNLTMLISSESMPTQLASHKLKGLDLVAFILIIGI
AVSSGTAAIILGIFLLFILTALAVLAFSILLYFLLREPKSPISVTHQPTPIIKDTDLPPV
PPLALTPVPTEAVLEEPPLFSPRTHQTLLOENWDRIPDLQANTDMPFIAADNQTGYAWHL
KNSNLTLISTLGFIEKPRYKTQGIVMIVNAATPNMANNVKGTSLALAKATSVRCWENSKK
SPDPLRSKQPLQLGELRSAKWENLNGTTNAGKAGLPOFLGOLLGPKASDYNYNPNDAFTF
CRQAYLNCLNEAKRRKTTVLQLPLLGGHFPGGPKDEETTSLRLQWIDGVKLALIDALQTF
GSEAENQNQPWVILTTLARHPLITP

CPn_0371   417141   417750
No robust homolog present in Genebank/EMBL as of 11/7/98
KTMPVSSAPLPTSHRPSIGNLGLMEPHCKALYAPHQDYTFKTIKLLVKILVAILVIEVLG
IIAAFFIDGTPPICLIIGALILLTTIIVILLVIKLALVHKTHITPARXQIKRKLSGKSI
G

CPn_0372   417651   418061
No robust homolog present in Genebank/EMBL as of 11/7/98
NYRACHPNIGNHSSPVVTTCCACPVHGJVFIIVIEFLERLGCGIRCIKIAFAAITALLLLN
TFVGGIVAIAHIFVATSWIAYFTVIGPLFLCILILLAIMLIIMYKITHPGQNTPFSN

CPn_0373   418156   420218
ucpE
NSEIFEIFMTLITPAINSSPRKTHTVRIGNLYIGSDHSIKTQSMTTTLTTDIDSTVEQIY
ALAEHNCDIVRVTVQGIKEAQACEKIKERLIALGLNIPLVADIHFFPQAAMLVADFADKV
RINPCNYIDKRNMFKGTKIYTEASYAQSLLRLEEKFAPLVEKCKRLGKAMRIGVNHGSLS
ERIMQKYGDTIEGMVASAIEYIAVCEKLNYRDVVFSMKSSNPKIMVTAYROLAKDLDARG
WLYPLHLGVTEAGMGVDGIIKSAVGIGTLLAEGLGDTIRCSLTCGCPTTEIPVCDSLLRHT
....
/HGAPFVHFHASDPFIHTSRDFFEKQGHQCKPTKLVFSRDFDNKEEAAIIIATEFGALLL
DGLGEAVVLCLPNLPLQDVLKIAFGTLQNAGVRLVKTEYISCPMCGRTLFDLEEVTTRIR
KRTQHLPGLKIAIHGCIVNGPGEMADADFGFVGSKTGMIDLYVKHTCVKAHIPMEDAEEE
LIRLLQEHGVWKDPEETKLTV

CPn_0374   420209   420961
CT056 hypothetical protein
VDSMTLSFHTHPLNYWTFEEFDGLPIRHGVFSKQKDAEGTVFAAKNPEIASALQSPKYCD
LHQRHGTSVRCVTPTSPTYQPADGLCTQSPLLSLHIRHSDCQAAIFYDREHHAIANVHSG
WRGLLGNIYAVTVGTMKKLFHTKPQDLFVAIGPSIGPDYAIYPDYATLFPRSFLPFMNPK
NHFDLRAIARKQLTNLGISKDRIFISDLCTYTEHDAFFSSRYLAHHPDPNLTGQHSKNRN
NVTAVLLLPRD

CPn_0375   421112   421615
No robust homolog present in Genebank/EMBL as of 11/7/98
RLSMKLGASTNHKVHEPVKPKKAQLAEIEANKTQATEGTLRSKSLALQIARAVLYILFAA
LHLAAGITFVTFLALGFPLIOAYSIAGIITLVGLAIGLVLLILSLLPKEDEEADALSRNA
LLPLTIIVIEQQPITPKPEIPYSYLTKLALLTSLFLTLRRSSSQRKTH

CPn_0376   421680   422294
No robust homolog present in Genebank/EMBL as of 11/7/98
FKVVTAKAPNLTEIRDHGARVPSLFLLSPETSHWKGDKEVSAPLKQLQDLLGEEQWEAMK
TKMNSRKKAGQWAIFNSPTPGVSSTLVLAWTPWGYYDKDVQDILERKDPMSSSLSEKDSK
EFLKNLFVDLLENGFTSVHIHAEEAFTPLDHTGKPHFKRDNVYLPGKLLGALNEAAVQAN
VSADTQFTLFLTQDECNPFHDKKRG

CPn_0377   423441   422347
sucB-Dihydrolipoamide Succinyltransferase
IMTTEVRIPNIAESISEVTVASLLVTEGALIQENQGLLEIESDKVNQLIYAPVSGRIFWE
VSEGDVVPVGGVVGKIEPAGEGEELGDSQSKETIEAEIICFPQSGVRQSPPENKTFIPLR
DQMDQGSQGLSAGDRGETRERMTSIRKTISRRLLSALHESAMLTTFNEVYMTPLFHLRKE
KQEEFLSRYGVKLGFMSFFVKAVLEALKAYPRVNAYIDGEEIVYRHYYDISIAVGIDRGL
VVPVIRDCDKLSNGEIEQKLADLALRAREGLLAIAELEGGGFTITNGGVYGSLLSTPIIN
PPQVGILGMHKIEKRPVVLDNEIVIADMMYVALSYDHRLIDGKEAVGFLVKVKEGLENPA
SLLDL

CPn_0378   426195   423445
sucA-Oxoglutarate Dehydrogenase
IVFIEFNYFMDSEFVGQVYSSDMDWIESMYQRFMNHETLDPSWKYFFEGYOLGQAASPSE
ASTKISGNETIAMLQEQKSQFLCTIYRYYGYLQSQISTLAPTTDSRFIQEKIAKIDLDEQ
VPSAGLLPKAQVSVRELIEALKKCYCGSLTLETLTCTPELQEFVWNLMEKRQVERFAEQL
LRSYKDLCKATFFEEFLQIKFTGQKRFSLEGGETLVPMLEHLVHYGSALGISNYVLGMAH
RGRLNVLTNVLGKPYRYVFMEFEDDPAARGLESVGDVKYHKGYVLKSHQKDRETTFVMLP
NASHLESVDPIVEGVVAALQHQGHAGKEQSSLAILVHGDAAFSGQGVVYETLQLSRVPGY
STEGTLHIVVANYIGFTAVPRESRSTPYCTDIAKMLGIPVFRVNSEDVVACIEAIEYALQ
VRERFSCDVIIDLCCYRKYGHNESDDPSVTAPLLYDQIKRKKSIRELFRQYLLEGQFADI
SEETLASIEKEIQESLNREFQVLKGTDPEPFPKKECHHCDRLNNGELILHDCVVSLDRET
LFHMSSRLCGFPDNFHPHPKIKTLLEKRMKMAEGGVGYDWAMAEELAFASLLIEGYNLRL
SGQDSIRGTFSQRHLVWSDTVTGDTYSPLYHLSAEQGSVEMYNSPLSEYAILGFEYGYAQ
QALKTLVLWEAQFGDFANGAQIIFDQYISSGIQKWDLHSDIVLLLPHGYEGQGPEHSSSR
IERYLQLAAWNFQVVLPSTPVQYFRILREHAKRDLSLPLVIFTPKLLLRYPQCVSSIEE
FTEPCGFRAILEDADPNYDASILVLCSGKIYYDYAEMLPQDRRKDFSCLRIESLYPLALE
DLVSLICKYSHLKHFVWLQEESKNMGAYDYMFMALQDILPEKLLYIGRPRSSSTASGSAK
LSRQELVTCMETLFSLR

CPn_0379   426268   426765
CT053 hypothetical protein
KNKKMLCTCSRIODGNPWMKSERLKKLESELHDLTQWMQLGLVPKKEISRHQEEIRILEH
KIYEEKERLQLLKENGEIEEYVTPRRSPAKTVYPDGPSMSDIEFVEPTETEIDIDPGETV
ELELTDEGREDGAVEVDYSHEDDEDPFSDRNRWRRGGIIDPDANEW

CPn_0380   426671   427876
hemN-Coproporphyrinogen III Oxidase
KSTIPTKTMKTLSAIAIAGDAVVSLIPMLMNGKAPLALYIHIPFCTKKCRYCSFYTIPYK
SESVSLYCNAVIQEGLRKLAPIQETHFIETVFFGGGTPSLVSPLDLKRILKELAPHAREI
TLEANPENLTVSYLRQLQETPINRISVGVQTFDDSILQLLGRTHSSSAAITALQECQNHG
FSNLSIDLIYGLPTQSLEIFLSDLHQALTLPITHISLYNLTIDPHTSFYKHKILVPTIA
QEEILAEMSLLAENLLLSQGFQRYELASYAKPDYPAKHNLYYWTDRPFLGLGVSASQYLH
GERSKNYSHISHYLRAVRKNLPTQETSEILPKKERIKEALALRLRLLEGADLAEFPSTLI
CMLTQDVKLQNLFSVHGQCLALNRQGRLFHDTIAEEIMGYSF

CPn_0381   429836   428037
CT326 similarity
SLPNKFRALMTAPTESRSSPPTLLEETEPLSPNPIPADIQIPRITISPPSLDVSTVASSA
EDISVFIAGGPRSSSSASVASDVYELVCLCGGDEDPEPPDSEVRTLYVNGSWQTHQEAVQ
ELLYISEVRGEAVRLLYNDGSGMSPWPISPCRTLPTLDHPLCQALLTVWEQFFSAPENQN
REFLVIFYGDACPYIQQALTOSRHSPRIVVQISPTVFIQGDFRVHNYRVSGDFFSSLDC
PGTPAENTTILPYSSGLEGVFLPSIRCPSFTWAVRFGEQCLVANRGEDVEDRGGLSQDAE
PSGLPHGERDLAVVIDSTDPSSMSRLVEWLNQGSPSSDMEINPYPQRLPDVALSALYAIS
PVYKILAQEWILAGVHEGLDLDICYSLILMHTTFAVRYFFLLFTNYPQSRERFRTARIVAQ
XLTLPSIIVLVFIDCGNVLRKLWMPOEILRAIFISAJTISGSIVFVECTRWMGRGLRHRVQ
VFVKQRVIGGGLPVGTVRASYRDRACFIIGFLQTVHQGLYLPVGIMVLNQIAIQVPRILV
PHHRITAVPDLHNKSAEENWSSGDVLAVGQTLNFILCAFVLFVNLWFFVKSVLRHSRRRRR

CPn_0382   430752   410036
ydiB/yraL-SAM-Dependent Methyltransferase
IVTLYLLFHTIZTRAVETLEIVICELVIIRLDGILIVESDRGGRAFLSLWKIPEVIIKFPLAI
IGKHAPLIPKAWDFYLEPIVKHGENWGLICDALGLPCIADPGAGLVRRARALGIPVQAFSGP
CPITLALMLGGLPNQPFFFLYIYLPQGPKERVKSIKKAATGKEVIITSVVIETGYRNVVTFSPE
GLLLTLPGYAEDAVAGDLRGPSELVLTROVQSWRTTEDLGGVKQSITKVPTIFLPHIPN

CPn_0383   430741
CT047 hypothetical protein
VQDTTFLTLPMQKGLTGFDDFSQAYAEKVPAIALIGIALEDDKDALIELINGESFKELCG
QGLMPATLMGWTETFALFQEHETLGLIHAEKFPLATKEFLGRYKENKOPREITLIEITKQ
ECFRELSKALPSALGLSLFGEWPADROKRIIRLLLOAERVGISCSCGLAGLFLRALAST
SLPDILSEFDKLLCSVGKKTSLDHSDIKELVVKKEKASLWKFRDSLLKRDPVEGHQQLHF
LLEDGEDPLGIITFLRTQCLYGLRSIEEGSKENKHPMFVLYGKERLHCALNGLFYAETLI
KNNVQDPIVAVETLVIRMVNL

nCCB-Histone-like Protein I
VITCLIRGIKMIGAQKKGSCKKTASRAVRKPAKKVAAKRTVKKATVRKTAVKKPAVRKTA
AKKTVAKKTTAKRTVRKTVAKKPAVKKVAAKRVVKKTVAKKTTAKRAVRKTVAKKPVARK
TTVAKGSPKKAAACALACHKNHKHTSSCKRVCSSTATRKHGSKSRVRTAHGWRHQLIKMM
SR

CPn_0385   434042   432522
pepA-Leucyl Aminopeptidase A
FLVIKGEFVVLFHAQASGRNRVKADAIVLPFWHFKDAKNAASFEAEFEPSYLPALENFQG
KTGEIELLYSSPKAKEKRIVLLGLGKNEELTSDVVFQTYATLTRVLRKAKCSTVNIILPT
ISELRLSAEEFLVGLSSGILSLNYDYPRYNKVDRNLETPLSKVTVIGIVPKMADAIFRKE
AAIFEGVYLTRDLVNRNNADEITPKKLAEVALNLGKEFPSIDTKVLGKDAIAKEKMGLLLA
VSKGSCVDPHFIVVRYQGRPKSKDHTVLIGKGVTFDSGGLDLKPGKSMLTMKEDMAGGAT
VLGILSALAVLELPINVTGIIPATENAIDGASYKMGDVVVGMSGLSVEICSTDAEGRLIL
ADAITYALKYCKPTRIIDFATLTGAMVVSLGEEVAGFFSNNDVLAEDLLEASAETSEPLW
RLPLVKKYDKTLHSDIADMKNLGSNRAGAITAALFLQRFLEESSVAWAHLDIAGTAYHEK
EEDRYPKYASGFGVRSILYYLENSLSK

CPn_0386   434543   434046
ssb-SS DNA Binding Protein
KSKGYLMMFGKFAGYLGADPEERMTSKGKRVITLRLGVKTRVGMKDETVWCKCNIWHNRY
DKMLPYLKKGSGGVIVAGDISVESYMSKDGSPQSSLVISVDSLKFSPFGRNEGSRSPSLED
NHQQVGYESVSVGFEGEALDAEAIKDKDMYAGYGQEQQYVCEDVPF

CPn_0387   435229   434699
CT043 hypothetical protein
NNNNLLQGDSLMSRQNAEENLKNFAKELKLPDVAFDQNNTCILFVDCGEFSLHLTYEEHSD
RLYVYAPLLDGLPDNTQRKLALYEKLLEGSHLGGOMAGGGVGVATKEQLILMHCVLDMKY
AETNLLKAFAQLFIETVVKWRTVCADICAGREPSVDTMPQMPQGGGGMQPPPTGIRA

CPn_0388   435323   437320
glgX-Glycogen Hydrolase (debranching)
STMEKVSSYPSVPLPLGASKISPNRYRFALYASQATEVILALTDENSEVIEVPLYPDTHR
TGAIWHIEIEGISDQSSYAFRVHGPKKHGMQYSFKEYLADPYAKNIHSPQSFGSRKKQGD
YAFCYLKEEPFPWDGDQPLHLPKEEMIIYEMHVRSFTQSSSSRVHAPGTFLGIIEKIDHL
HKLGINAVELLPIFEFDETAHPFRNSKFPYLCNYWGYAPLNFFSPCRRYAYASDPCAPSR
EFRTLVKTLHQEGIEVILDVVFNHTGLQGTTCSLPWIDTPSYYILDAQGHFTNYSGCGNT
LNTNRAPTTQWILDILRYWVEEMHVDGFRFDLASVFSRGPSGSPLQFAPVLEAISFDPLL
ASTKIIAEPWDAGGLYQVGYFPTLSPRWSEWNGPYRDNVKAFLNGDQNLIGTFASRISGS
QDIYPHGSPTNSINYVSCHDGFTLCDTVTYNHKHNEANGEDNRDGTDANYSYNFGTEGKT
EDPGILEVREROLRNFFLTLMVSOGIPHIQSGDEYAHTAEGNNNRWALDSNANYFLNDQL
TAKPTLMHFLCDLIAFRKKYKTLFNRGFLSNKEISWVDAMGNPMTWRPGNFLAFKIKSPK
AHVYVAFHVGAQDQLATLPKASSNFLPYQIVAESQQGFVPQNVATPTVSLQPHTTLIAIS
HAKEVT

CPn_0389   438254   437319
CT041 hypothetical protein
TVFNFKRFYQKDSQRQNGNTTCLRPFKKTCKELIEFRRRTVKLLKNVLLGLFFSMSISGF
SEVKVSDTFVKQDTVVEPKIRVLLSNESTTALIEAKGPYRIYGDNVLLDTAIQGQRCVVH
ALYEGIRWGEFYPGLQCLKIEPVDDTASLFFNGIQYQGSLVHRKDNHCIMVSNEVTIED
YLKSVLSIKYLEELDKEALSACIILERTALYEKLLARNPQNFWHVKAEEEGYAGFGVTKQ
FYGVEEAIDWTARLVVDSPQGLIIDAQGLLQSNVDRLAIEGFNARQILEKFYKDVDFVVI
ESWNEELDGEIR

CPn_0390   439171   438134
ruvB-Holliday Junction Helicase
RKSDREGSYMTHQVAVLHQDKKFDVSLRPKGLEEFYGQHHLKERLDLFLCAALQRGEVPG
HCLFFGPPGLGKTSLAHIVAYTVGKGLVLASGPQLIKPSDLLGLLTSLQEGDVFFIDEIH
RMGKVAEEYLYSAMEDFKVDITIDSGPGARSVRVDLAPFTLVGATTRSGMLSEPLRARFA
FSARLSYYSDQDLKEILVRSSHLLGIEADSSALLEIAKRSRGTPRLANHLLRWVRDFAQI
REGNCINGDVAEKALAMLLIDDWGLNEIDIKLLTTIIDYYQGGPVGIKTLSVAVGEDIKT
LEDVYEPFLILKGFIKKTPRGRMVTQLAYDHLKRHAKNLLSLGEQQ

CPn_0391   439701   439510
No robust homolog present in Genebank/EMBL as of 11/7/98
KDQLYKQEKPIPKATILSRNLEVMLDNPKGKRQTLFLGRTSGRSALYSYSRRILVLLNAF
MRGP

CPn_0392   439814   440383
dcd-dCTP Deaminase
MSIKEDKWIREMALNADMIHPFVNGQVNVNEETGEKLISYGLSSYGYDLRLSREFKVFTN
VYNSVVDPKCFTEDIFISITDDVCIVFPNSFALARSVEYFRIPRNVLTMCIGKSTYARCG
IIVNVTPFEPWEGHVTIEISNTTPLPAKIYANEGIAQVLFFESSTTCEVSYADRKGKYQ
KQQGITVPCV

CPn_0393   440229   440723
CT038 hypothetical protein
KFLTLRHCORKFTLMKGLPRSYGLSLVRPARFLMQTEKESIKSNKASPYLVSKVSVRKKN
WGFRLLEEVMIKSWWVIFSILICGFVTDRAIQELRTEELRLQSKVSSLCQDILSAQEKQR
OLQLHLQHWNDSAAIEAALIQRLGLIPYGYKKLCVSPKQQSENKD

CPn_0394   440727   441048
tlyC-CBS Domain protein (Hemolysin Homolog)
KETHIPTMLMFFIICFTLGGGFIGLGGIALFGLFTGLLGHYKRGKGKKQQRVATLLLHPH
HLLITLIFCDIGLNIAIQNCFAILFGLAAGWWFFASLFLAITLIIAEILFKAVALPFNTQ
IAGGVAPLIGLGVTKIFKPLLHWGIVGLIGVVVGWILGKGGIDIIQIQELKEVLGVGKDFGV
VNQEESRLLLYGVLSLSDCSVKERMQFFQDIIFYDIQYTIFENLYLLFGKOIRGRVPICNDN
LQNLIGICTADCLLLIDKPLQGGDGLLIHLLYFIYYMFGTIIAKMALLCUMAAEDETIIMIII
DRYILIIEGLITQEDLFEIVAGEIVDGFIJIKIITFTGGADVFIAGTLELREFGEIFDINL
PTNNHIATIGKWLIFQIGTIPTTMKLGWHHLLPGVIJMAAIHICIRRVYIRKLYD

CPn_0395   441955   441175
CT257 hypothetical protein
GNCMTNSALFWIGVNIICIVLQGFYSMMEHACVSFNRVRLQYYLTKDHKKARYINFLIRR
PYRLFCTVMLGVNIALQVCGESSRNCYRALGITPDYAPFTQIFIVVIFAELLPLTISRKI
PEKLALWCAPILYYSHYIFYPLIQLIGSLTEGLYYLLNIRKEKLNSTLSRDEFQKALETH
HEEQDFNTIATNIFSLSATCADQVCQPLEQVTMLPSSANVKDFCRTIKNTDINFIPVYHK
ARKNVIGIAHPKDFVNKALDEPLINNLHSPWFITAKSKLIRILKEFRDNRSSVAVVLNAS
GEPIGILSLNAIFKILFNTTNIAHLKPKTISVIERTFPGNSRIKDLQKELDIQFPQYPVE

CPn_0396   444359   443241
yhfO-NifS-related protein
YSMIYLDWNAMTPPERGLLEFLQKTFLIEGTYANPSSVHQLGKKSRQLVLEASHWMQKVL
SFQGRVLYTSGATESLNLAIASLPKDSHVITSGSEHPAILEPLKHSSLSVSYLNPEEGRC
VLTIEQIERAVTPKTSAIILGVVNSETGAKADIAAIAHFAQERQLQFIVDATANVGKERI
VLPSGVTMAAFSGHKFHALSGIGALLVSPGVKLHPQLWGGGQQGGLRAGTENLWGIASLL
YIFKYLDLHQERISQEILTHRNGFEKAIKARIPDVHIHCADQPRANNVSAIAFPPLEGEV
LQIALDIEGVACGYGSACSSGATAPFKSLVSMGVDEELTLATLRFSFSHLLLQEDVERAV
GIIEKVVERLKNS

CPn_0397   445124   444381
PP2C phosphatase family
EHFVDFDYFGLSDIGRVRARNEDFWQVNLMSQVVAIADGVGGRLGGDIASQEAVTSLMEL
IDEQQSKLMGYGDDOYKETLKKILLEVNGVVYEHGGMEEHLQGMGTTLSFIQFRKDRAWL
FHVGDSRIYRIREGELRRLTEDHSLENQLKNRYGLPKQSDKVYSYRHILTNVLGSRPYVH
PDIRNLPCEKEDLYCLCSDGLTNMVPDIDIRDILNQPATLEERGNALISLANTRGGDDNA
TVVLVRIQ

CPn_0398   445518   445700
No robust homolog present in Genebank/EMBL as of 11/7/98
IEELPMQIENSSILFAEVVMKWFIFSVISAPVVFLPGCTLIPKEKVTKVPSQLWSESLSQ
P

CPn_0399   445759   446523
CT253 hypothetical protein
YKLMRVLNGKSLNCESIDLKSKNFPRARIFCKISNLRTVTMRKMLVLLASLGLLSPTLSS
CTHLGSSGSYHPKLYTSGSKTKGVIAMLPVFHRPGKSLEPLPWNLQGEFTEEISKRFYAS
EKVFLIKHNASPQTVSQFYAPIANRLPETIIEQFLPAEFIVATELLEQKTGKEAGVDSVT
ASVRVRVFDIRHHKIALIYQEIIECSQPLTTLVNDYHRYGWNSKHFDSTPMGLMHSRLFR
EVVARVEGYVCANYS

CPn_0400   446527   447306
CT254 hypothetical protein
SKEMSKFILLLSLGVAALASKNFFIWPAPSGKTPLKLRQVLFGGALLVFSSLVALSVSSQ
TAELLSTMTGISLAFAFLFYLLFLPKDITRAILFSGERPVKTSWRALGSAIRMWIIIIPV
TQLIGIMMSKFLTLVLPTQEIHTQEVTQEVQNSLPITGHYISMILNLGVLTPFGEEVFFR
GILQTFLKNKMTRIAAVLCSSIIFSFIHIEHSLGSWVFVPVLFVFSLSAGFLYEKDRHIL
SPIALHGLFNLTSLLFLGIK

CPn_0401   447884   447495
CT255 hypothetical protein
MRDHAFSKLIGTVRAMVVEGRCPWSLQQSLVSMVEHILGECQEFHEAVLQGKTVQEVGSE
AGDVLTLVLILCFLLEREGVLASEDVANEAMEKLRRRAPYIFAEDYKPVSIEEADRLWEL
AKHREKNEST

CPn_0402   449012   447888
mutY-Adenine Glycosylase
NFKRFCMTKIAFSEKAKNFPVEALKKWFEKNKRSLPWRDNPTPYSVWVSEVMLQQTRAEV
VIDYFNQWMERFPTIESLAAAKEEDVIKLWEGLGYYSRARHLLEGARMVMEEFHGKIPDD
AISLAQIRGVGPYTVHAILAFAFKRRAAAVDGNVLRVLSRIFLIETSIDLESTRTWVSRI
AQALLPHKSPEVIAEALIELGACICKKVPQCHRCFVRQACGAWRENKQFVLPVRHARKKV
IFLHRLVAIVLYDGSLVVEKRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTTKKMELSLES
PLEFLGNLKEQRHAFTNHKVHLCPIIFKATSLPQFGELHLLSDIDHLAFSSGHKKIKDAL
LIYLGDVRSRESIGV

CPn_0403   449009   449710
ycec-predicted pseudouridine synthetase family
NFMQLSNDKRAALQYFMENFSWLATQVSRLSSFLRSQLPNHSKQEILASIRQHRCRVNGF
IERFESYKVQPGDRVSLSLIPSTKQQPSILWEDDYSIIYKPPHLTTEQMAHMTRFFTVH
RLDKGTSGCLLMGKSKQAATELMKLFKQRKIHKQYIAFVFGHPKKKFGTVKSYTAPVYRR
CGAVIFGAAGPSQGEPIKSAYKWDCWVILLSEMSTTDLKNSLPRSSALSSMLTP

CPn_0404   450962   449871
No robust homolog present in Genebank/EMBL as of 11/7/98
ELEALEQKYGKAVLLIALSELGIDTMSLLSGHRLEGFPPIAEVMAACDRCSMDFCEILKS
QSMDLWADAASCVDGLLQDDPFWSTAIASGIAKSSLQETEFECESKVNVLSSWGEQGAQVC
SPFNLERICMSFPSLKVFSLKKNGCENMGIOLSASCMNLLMSIFFVATNGGSTPIWITKE
NLMALVALVLSHYQCYFVPATGDPORGNILGNPEVNAILARGMGMRVDLERKRQGESSSS
RYLELAARCFENSLTKTSLLSDANNVQERDKCLLQMSTSLMHTAGLNLQRPPVVPTPSGVT
AHPOPOPDPVVTSQPSLLGARERSPVSSRGRFPVVLPLSVISPRSHPGRVERRDLEDEEE
EVMF

CPn_0405   451814   450966
CT105 hypothetical protein
NIQTSHSRVLLKKFSKEFTIRTYRSLGFTDYLGGCLTNPLGKFPSPQNPQVVTIAPSSTT
PQAVSSAVQFLQTGGAASSTATTTTASGASALGLSPDQVQALLTNLLNVGQPSVGQPST
SAGTSGAGSSSASMQQOLLQLILDKTTGSGGSSVSSEQLOQLLSLVSQMTTSQGGSGQTQ
AGQAASVLLNLLSATGSAAANPLGTAASLAQIIYAAVTSPGAKKTSEFCYNYCGETCQGN
CGCPTCGCPDGQCCCGGFGRFFCGVWKNCCGIGECSQEPAIPL

CPn_0406   451960   452865
fabI-Enoyl-Acyl-Carrier Protein Reductase
CKIFMLKIDLTVKVAFVVAIIGDDQGYGWIIAKLLAEAGATIIVGTWVPIYKIFSQSWELCK
FNEJRKLINGTLEIAKIYFMDACFDIPFDVPEDIAEHKRYKGITGFTLGEVAEQVKKDF
HIIDILVHGLANSPEGKILLETSRKGYLAALSAMYCFVSLLLHESMIHGKGSTIGLT
YLAIMRAVGIVGGMOAKAALESDTKTLAWEACKPWGIRVNTIIALPLASRAGKAIGFI
ERMVDYYQFWAPIPEAMNAEQVGAVAAFLAGPLACAITGETLYVDHGANVMKGIGPEMFPK
L

CPn_0407   451757   452858
HAD superfamily hydrolase/phosphatase

NYGDAMEKLLVTDIDVTVT   HLDKKVYERLYALHQAVWKLFFLTIRYVKYAAPLFSD
FOAPYLLCCQNCASVWNVTSUNLLYSKSLFDDLVIILCQCMEGATALFSVESCAPYGDHY
YRFSPTPIAQDLHEYVDFRVFFPNAKERETLFETRGLKDDYAEFGFAAAKVRGLADEMIRI
QKELERQEALTSVATMTLMRWBFDFRVKILFLTDKGVSKGKALDGVURILDGKKFENMA
SGDDANDLDLIERGDFKIVMGSSAPEEMHVHADFLAPPADKNGILGAWEAGVRYYDDLMSL

CPn_0408   454090   454591
CT102 hypothetical protein
LPVLHMPETTHTT   TF AHLANTIDKGTTMGWRNEMWKLMEFEWRMIZISFTFT
FSVWARFTTTPTTHTSLLFFPTTSPTTPRTVLFFTHTVPSMAWTPF
EFPPDTUINHLLUJEMIKUSSSSATJCPLSPAILRILKKUVIRVL

CPn_0409   454645   455127
CT260 hypothetical protein
MTTWTLNQNNLTKFLKSSDEEPFLERESGLTYINIQANGNELPLFFVIRSEGEILQLICY
LPYQLHESHKASTARLLHLLNRDIDIPGFGMDEECGLIFYRLVLPCLNGEIHDTLLRIYI
DTIKLVCDSFSHAIGLISSGMNLDELRRQALQEQQEKRNE

CPn_0410   455087   455833
dnaQ-DNA Pol III Epsilon Chain
DVRLFKSNKKNVMSSQTMDVLIFYDTETTGTQIERDRIIEIAAYNSVTDESFLTYVNPEI
PIPDEASKIHGITTDAVLSAPKFPEAYEGFRKFCCGEDSILVAHNNDGFDFPLLGKECRRH
SLEPLTNRTIDSLKWAQKYRPDLPKHNLQYLRQVYGFAENQAHRALDDVVILHKVFTSLI
GDLPPQQVLDLLQQSYHPKVFKMPFGKYKCQPLVDIPKSYFEWLENQGALDKPENKDIKA
AIALLHQPT

CPn_0411   455794   456609
CT262 hypothetical protein
RHQSRYSSITSTDMILTAAFSPCPNDIFLFRSFLKDPQFRPLLNQVTIADIETLNTLALQ
RRLSLMXMSAALFPVLVSDYYNLMDVGNTLGYNSGPIVLSLDPECSLDTLATPGMTTAHA
LCKLYYPKAKLIPMPYDKILSAILQGKVDGGALIHEERFSYDLQLTLRADFGELWRRKTI
FPLPLGCLAIAKYVPMATVDALTAALRKSLICSLKDPITAGAKAVEYSKNKNVTVIHRFI
GTYINKETFQLSKTGKKALHMLWKANECCQYT

CPn_0412   456515   457246
CT263 hypothetical protein
EPISTKKPFNYLKLGKKLYICSGRPMNAVNTPKKILCIVADYREISPLIEQLDFTQINEH
LYSYRCTDYHLDLYIVHVWGSTAVLNALQSYCQAYTDYDLWINPGFVGACSPEIPLGQCY
TIEKIANLTTDTPPVLSEDPPYIFDALPDSLPKSSLVTSPVLYHYGFHKTFKLLDMEGYA
IASQAAEHHIPCSFLKITSDYTVPGDCPFSRLEEVSQKLTQTLVELLPELMERAIPPKLL
LPCP

CPn_0413   459209   457227
msbA-Transport ATP Binding Protein
VFMKLLLKAVLRHKNHLVILGCSLLAILGLTFSSQMEIFSLGHIAKTGPDAFLLFGRKES
GKLVKVSELSQKDILENWQAISKDSETLTVSDATTYIAEHGKSTASLTSKLSKFVRNYID
VSRFRGLAIFLICVAIFKAVTLFFQRFLGQVVAIRVSRDLRQDYFKALQQLPMTFFHDHD
IGNLSNRVMTDSASIALAVNSLMINYIQAPITFILTLGVCLSIWKFSILICVAFPIFIL
PIVVIARKIKNLAKRIQKSQDSFSSVLYDFLAGVMTVKVFRTEKFAFTKYCEHNNRISAL
EEKSAAYGLLPRPLLHTIASLFFAFVVVIGIYKFAIPPEELIVFCGLLYLIYDPIKKFGD
ENTSIMRGCAAAERFYEVLNHPDLHSQKEREIEFLGLSNTITFENVSFGYQEDKHILKNL
SFTLHKGEALGIVGPTGSGKTTLVKLLPRLYEVSQGKILIDSLPITEYNKGSLRNHIACV
LQNPFLFYDTVWNNLTCGKDMEEEAVLEALKRAYADEFILKLPKGVHSVLEESGKNLSGG
QQQRLAIARALLKNASILILDEATSALDAISENYIKNIIGELKGQCTQIIIAHKLTTLEH
VDRVLYIENGQKIAEGTKEELLQTCPEFLKMWELSGTKEYNRVFVPDHKLVANPTDMAIT
T

CPn_0414   460203   459172
accA-AcCoA Carboxylase/Transferase Alpha
LCLRIVCIKMILFIRGEHILMELLPHEKQVVEYEKAIAEFKEKNKKNSLLSSSEIQKLEK
RLDKLKEKIYSDLTPWERVQICRHPSRPRTVNYIEGMCEEFVELCGDRTFRDDPAVVGGF
VKIQGQRFVLIGQQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLAEKFGLPVVFLVDTPG
AYPGLTAEERGQGWAIAKNLFELSRLATPVIIVVIGEGCSGGALGMAVGDSVAMLEHSYY
SVISPEGCASILWKDPKKNSEAASMLKMHGENLKQFGIIDTVIKEPIGGAHHDPALVYSN
VREFIIQEWLRLKDLAIEELLEKRYEKFRSIGLYETTSESGPEA

CPn_0415   461522   460221
CT266 hypothetical protein
SQTGFLPGLTLIFVIIIVWCNAFLIKLCVIMGLQSRLQHCIEVSQNSNFDSQVKQFIYAC
QDKTLRQSVLKIFRYHPLLKIHDIARAVYLLMALEEGEDLGLSFLNVQQYPSGAVELFSC
GGFPWKGLPYPAEHAEFGLLLLQIAEFYEESQAYVSKMSHFQQALFDHOGSVFPSLWSQE
NSRLLKEKTTLSQSFLFOLGMOIHPEYSLEDPALGFWMQRTRSSSAFVAASGCQSSLGAY
SSGDVGVIAYGPCSGDISDCYYFGCCGIAKEFVCQKSHQTTEISFLTSTGKPHPRNTGFS
YLRDSYVHLPIRCKITISDKQYRVHAALAEATSAMTFSIFCKGKNCQVVDGPRLRSCSLD
SYKGPGNDIMILGENDAINIVSASPYMEIFALQGKEKFWHADFLINIPYKEEGVMLIFEK
KVTSEKGRFFTKMN

CPn_0416   461871   461557
himD/ihfA-Integration Host Factor Alpha
EALSNMATMTKKKLISTISQDHKIHPIHVRTVIQNFLDKMTDALVKGDRLEFRDFGVLQV
VERKPKVGRNPKNAAVPIHIPARRAVKFTPGKRMKRLIETPNKHS

CPn_0417   463047   462244
amiA-N-Acetylmuramoyl Alanine Amidase
REKGMKLTKYLNTKQLRSMISRLFVRYSLFMSKQLSFFALCVLGSHPIFAQTPNPPQRVR
RGEVIFIDFGHGGKDQGTASKELHYEEKSLTLSLALTVGGYLKRMGYKPQLTRSSDVYVD
LGKRVALSNRQQCDVFISIHCNHSSNAAAFGTEVYFYNGKVGSPTRNRMSEVLGKNILAA
MEKNGILKSRGLKTANFVVIRDTSMPAVLVETGFLSNSPERAALQDARYRMHVAKGIAEG
VHNFLGGPSFQKPKQNIAKIRKPQIQAN

CPn_0418   464401   462953
murE-D-Acetylmuramyl alanyl glutamyl DAP Ligase
MDLKELLLRVQAKIYGKVRPLEVRNLTRDSRCVSVGDIFIAIKCQPYLKNDFAVDALANG
AIAIAGGGLYNPFIGVVQIITPNLEELEAELSAKYYEYPCEKLHTIGYDSTNGFTVTCLI
KALLLSVGKIEGILSFIIEHLLGKIVIVPGGFTTTPTPALLGYYLATMVIQNRDAVMEVGSI
GLAGKVAVTHFVPAVLPNLTLDHLDFGCTFETYVAAKAPLFSLVIRGGMVVIFTDSPYA
GQFIELAKAIVITVGLLFAALVPATDIGLSSSSTKYTLVIGDLKLVCGDDKIIFMGYNL
LAAIGTVFIILRIGTKIGKLEKLCHLGKPHPIRLDPVLNGPCFVVIDYAIFFDALLNVLTGL
HELLPFZIRLLVVFASSGRERKRYLMAQVVERYGFAVVTHDNIASPFPELLVNEIGG
FYIKNYFIELIKKQAIYYAIGIIAIBADIVLLAGKGHEAYGIFKIIGFIAFDQFVTAVEVLA
TVV

CPn_0419   466897   464876
pbpJ- transglycosilase/transpeptidase
QLFPNTNIWNIPOKKVSVFYPMSYRKRSTLIVLGVFALYALLVLRYYKIQICEGDHWAAE
ALGGHEFCVRDPFRRCTFFANTTVRKCDKDLQOPFAVDITKFHLCADPLAIPECHRDEII
CGILQFIEGCTYCDLSLKLDKKSRYCKLYPLLDVSVHDRLSLWWKGYATKHRLPTNALFF
ITDYQRSYPFGKLLCQVLJITLREIKDEKTGKAFPTGGMEAYFNHILEGDVGERKLLRSPL
NRLDTNRVIKLPKDTSDIYLTINPVIQTIAEEELERGVLEAKAQGGRLILMNSCTGEILA
LAL.VFPDF.PTWTCTTT.FTTV.VDTITTTTTTTTTVVZZTTTT.MFF.VTVZTTTTTT.LTTT.T
FTITTFEED.D.TTTTTTT.TTTTT.VTTTV.DT.V.VDTDT.VT.V.TTTTVTAGLAOR.T.TTTT
VAWYQQKLLALGFGRKTGIELPSEASGLVPSPHRFHINCSLEWSLSTPYSLAMGYNILAT
GIQMVQAYAILANGGYAVRPTLVKKIVSASGEEYHLPTKEKTRLFSEEITREVVRAMRFT
TLPGGSGFRASPKHHSSAGKTGTTEKMIHGKYDKRRHIASFIGFTPVESSEGNFPPLVHL
VSIDDPEYGLRADCTKNYHGGRCAAPIFSRVADRTLLYLGILPDKKLRNCDEEAAALKRL
YEEWNRSPKQGGTR

CPn_0420   467120   466824
CT271 hypothetical protein
KSFFPMNKSRFLRLCCCLCFCGSLFYFYINKQNSLTKLRLEIPCLSVRLRQLEQONISLRF
LIDKIERPDHLMEIAALPEYQYLEYPSEESISLLSYELP

CPn_0421   468007   467108
yabC-PBP2B Family methyltransferase
EILMSERAHIPVLVEECLALFAQRPPQTFRDVTLGAGGHAYAFLEAYPSLTCYDGSDRDL
QALAIAEKRLETFODRVSFSHASFEDLANQPTPRLYDGVLADLGVSSMQLDTLSRGFSFQ
GEKEELDMRMDQTQELSASDVLNSLKEEELGRIFREYGEEPQWKSAAKAVVHFRRHKKIL
SIQDVKEALLGVFPHYRFHRKIHPLTLIFQALRVYVNGEDRQLKSLLTSAISWLAPOGRL
VIISFCSSEDRPVKWFFKEAEASGLGKVITKKVIQPTYOEVRRNPRSRSAKLRCFEKASQ

CPn_0422   468323   468784
CT273 hypothetical protein
GLAMVEIFNYSTSIYEQHASNNRIVSDFRKEIQHEGISIRDVAKHAQILDMNPKPSALTS
LLQTNQKSHWACFSPPNNFYKQRFSTPYLAPSLGSPDQQDEDIEKISSFLKVLTRGKFSY
RSQITPFLSYKDKEEEEDEDPEEDDDDPRVQQGKVLLKALDLGVKSTNVMIDYVISRIFQ
FVQG

CPn_0423   468788   469216
CT274 hypothetical protein
CMLDNEWKAILGWGDDELEELRISGYSFLRQGHYSKAILFFEALVILDPLSIYDHQTLGG
LYLQIGENSQALAVLDQALRMOGDHLPTLLNKTKALFCLGRIEEATAIATYLSSCPIPAI
ANDAEALLMSYSKATKKNAALVR

CPn_0424   469528   470961
dnaA-Replication Initiation Factor
SRCNEIFSPSLMGWVDCIWESFINKESGMLTCNECTTWEQFLNYVKTRCSKTAFENWISP
IQVLEETQEKIRLEVPNIFVQNYLLDNYKRDLCSFVPLDVHGEPALEFVVAEHKKPSAPV
ASQKESNEGISEVFEETKDFELKLNLSYRFDNFIEGPSNQFVKSAAVGIAGKPGRSYNPL
FIHGGVGLGKTHLLHAVGHYVREHHKQNLRIHCITTEAFINDLVYHLKSKSVDKMKNFYRS
LDLLLVDDIQFLQNRQNFEEEFCNTFETLINLSKQIVITSDKPPSQLKLSERIIARMEWG
LVAHVGIPDLETRVAILQHKAEQKGLLIPNEHAFYIADHIYGNVRQLEGAINKLTAYCRL
FGKSLTETTVRETLKELFRSPTKOKISVETILKSVATVFQVKLNDLKGNSRSKDLVLARQ
IAMYLAKTLITDSLVAIGAAFGKTHSTVLYACKTIEHKLQNDETLKRQVNLCKNHIVG

CPn_0425   470965   471564
CT276 hypothetical proteins
FRGCPMFRRTGKGPFEDVQTLYEEETSSPSSYSPSYSRSERPETPPSLFDNPKASEARPLN
HNLTEESSLPQWSSTPRTESLLPLEEPETTLGEGVTFKGELAFERLLRIDGTFEGILVSK
GKIIIGPKGVVKADIQLQEAIIEGVVEGNITVSGKVELRGGAIIKGDIQANTLCVDEGVR
ILGYLAIAGITDHSERERDL

CPn_0426   472111   471536
CT277 similarity
MVLFSLLFPKLCYGCOAPGAYFCSNCLEKLLVEDREGRCLHCFRYLGSSETRLCSQCSPS
SQLQAFSLYLPSQTALSVYARACEGKRPALQFFSKSIAFELASLDETPSCIAYITSTISR
KIVVEVAKLEKLLRIPLWPWLPKKRQIEKLPKGEGICFLSAYPLSQKWMQTIVGGSASPL
VSISLFLSQNDQ

CPn_0427   472153   473715
nqr2-NADH (Ubiquinone) Dehydrogenase
AVCYVFERVEASTFLSITHLKKFINSLWKLCQQDKYQRFTPIVDAIDTFCYEPIETPSKP
PFIRDSVDVKRWMMLVVIALFPATFVAIWNSGLQSIVYSSGNPVLMEQFLHISGFGSYLS
FVYKEIHIVPILWEGLKIFIPLLTISYVVGGTCVLFAVVRGHKIAEGLLVTGILYPLTL
PPTIPYWMAALGIAFGIVVSKELFGGTGMNILNPALSGRAFLFFTFPAKMSGDVWVGSNP
GVIKDSLMKHNSTGKVLIDGFSQSTCLQTLNSTPPSVKRLHVDAIAANMLHIPHPTQD
VIHSQFSLWTETHPGWVLDNLTLTQLQTFVTAPVAEGGLGLLPTQFDSAYAITDVIYGIG
KFSAGNLFWGNIIGSLGETSTFACLLGAIFLIVTGIASWRTMAAFGIGAFLTGWLFKFIS
VLIVGQNGAWAPARFFIPAYRQLFLCGLAFGLVFMATDPVSSPTMKLGKWIYGFFIGFMT
IVIRLINPAYPEGVMLAILLGNVFAPLIDYFAVRKYRKRGV

CPn_0428   473719   474681
nqr3-NADH (Ubiquinone) Oxidoreductase. Gamma
NMSKGSSKHTVRINQTWYIVSFILGLSLFAGVLLSTIYYVLSPIQEQAATFDRNKQMLLA
AHILDFKGRFQIOEKKEWVPATFDKKTQLLEVATKKVSEVSYPELELYAERFVRPLLTDA
QGKVFSFEEKNLNPIEFFEKYQESPPCCQSPLPFYVILENTSRTENMSGADVAKDLSTVQ
ALIFPISGFGLWGPIHGYLGVKNDGDTVLGTAWYCQGETPGLCANITNPEWQEQFYCKKI
FLQDSSGTTNFATTDLGLEVVKGSVRTTLGDSPKALSAIDGISGATLTCNGVTEAYVQSL
ACYROLLINFCNLTHEKKTCE

CPn_0429   474666   475319
nqr4-NADH (Ubiquinone) Reductase 4
EENPPMTCKKCVKGYFFDPLWGNNQILIAILGICCALAVTTTVQTAITMGIAVGIVTGCS
SFFVCLLRKFTPDSVRMITQLIIISLFVIVIDQFLKAFFFDICKTLCVFVGLIITNCIVM
GRGELCLARIIVTPIFAFLDCFASGLYGWVLLVIGVIRELFGFGTLMGFRIIPOFVYAGET
HPCFVCHLCNMVLADPGAFFLLCIHIWLCNIRDCKYFFR

CPn_0430   475323   476094
nqr5-NADH (Ubiquinone) Reductase 5
FMWIZIAYIWLNVFILLLQQAAFICNILLANFLCHACYILACCTRVCTANCILCHCVALVLTVT
CSIIMFVIIAFITIPKALCIWICPGLACVNLGFLELCIFIVVIAAFIQILELLLEKVCRNLY
ICICIIFLPLCIAVNCAILZCVLFCCITRCYPFIPMMIFICCIACCZWWIAIVCLATIKEKLAY
IDIIFYRIIIACIHCICFITPCILCAMAFMCLTCCIDICKICACIQHAFLETEVVFNTTNPLKECC

CPn_0431   476489   476151
No robust homolog present in Genebank/EMBL as of 11/7/98
KIHTTLFKYVPRSRQNPDTLTFLKRYSSVLLHSENSLSYRIFAKVLAILLTSLAVAFAVT
LFSCEGSQLRLCALYIGIALAICVLLTIVVYCIASKIATACKKPPSISRIEIV

CPn_0432   476817   476514
CLFLTGSAPLCJLSIWIAASCITTLSMLVCACWAYKLCNALEKFRVAHES

CPn_0433   477327   476929
gcsH-Glycine Cleavage System H Protein
RTFRILYGTLYRTGSRKVMWYSDYKVVILPVHERVVRLCLTEKMQKNLGAILHVDLPSVG
SLCKEGEVLVILESSKSAIEVLSPVSGEVIDINLDLVDNPQKINEAPEGEGWLAVVRLDQ
DWDPSNLSLMDEE

CPn_0434   479471   477276
CT283 hypothetical protein
RPWVRIYQODLFCRLCRDPAWFFSLLSFTLRFYCLGRGWTLLSFFYKHQKKFIGIVIAVV
CVSGIGVGWGRFSRKGSAESTSRRTVFTTASGKRYVEKDFMAMKKFFAHEAYPFTGNPRA
WNFINEGLLTDYFLTTRVGEKLFLKVYHPGEKIFSKEKAYOPYRRFDAPFISSEEVWKSS
APQLLEILKVFQOIENPISKEGFLARAKLFLEERRFPHYVLRQMLEYRRQMFALPPDEAL
SRGKDLRLFGYQTIODWFGDAYLSAAVELLIRFIDEOKKVLPRPSKQEARDDFYDKAKHA
YTKISKNKEFSLGFEEFVNSYFQFLEISESEFFNMYRDILLCKRALLLLQGGVSFDFQPL
TTFFVQGKDSIQVEFFRLPKEYSFKTKQELKAFEVYLKLVSLPKSDSLDVPNEILPIATI
KAKEPRLVGRRFSIDYKRVALQDLAATVPMVEVLHWQONSEHFOEILQQFPDVETCQSYK
DFQHLKPALRDKISLFTRKEILRARPERILQSLQOVPKQSOEVLLSAGKNSALPGISDGQ
QLAKVLLENEVLDLYSQDAETYYTIIVNSSFEKEEVLPYREVLKRDLASQLLTSHGHLVD
MERLESALRTRYPGEEGASLWQRRLWKVVENHRLGRHLEGSFSWSLDRSLKTFSRGDKEL
PQEFDRIFSMKVGDYSSVFMSPNEGPCYYQCLSHLLYDRPASVDKLFLAKSQLDEELLGS
YMERFIEQGVVR

CPn_0435   480908   479475
Phospholipase D superfamily (uncleavable leader peptide)
GVMMSRLRFRLAALGIFFILLVPNSVSAKTIVASDKEKVGVLVYDNSVEAFQQILDCIDH
ANFYVELCPCMTGGRTLKEMVDHLEARMDLVPELCSYIIIOPTFTDAEDOKLLKALKERH
PNRFFYVFTGCPPSTSILAPNVIEMHIKLSIIDGKYCILGGTNFEEFMCTPGDEVPEKVD
NPRLFVSGVRRPLAFRDQDIMLRSTAFGLQLREEYHKQFAMWDYYAHHMWFIDNPEQFAG
ACPPLTLEQAESTVFPGFDKHEDLVLVDSSKIRIVLGGPHDKOPNPVTQEYLKLIQGARS
SVKLAHMYFIPKDELLNALVDVSHNHGVHLSLITNGCHELSPAITGPYAMGNRINYFALL
YGKRYPLWKKWFCEKLKPYERVSIYEFAIWETQLHKKCMIIDDEIFVIGSYNFGKKSDAF
DYESIVVIESPEVAAKANKVFNKDIGLSIFVSHGDIFSWYFHSVHHTLGHLQLTYMPA

CPn_0436   481633   480902
lplA-Lipoate Protein Ligase-Like Protein
FYVCYMKVRIVDSGKSSAASHMAKDRDLLESLQDGELILHLYEWENPCSLTYGHFMRPEK
FLLSNYADLGLDAAVRPTGGGFVFHKGDYAFSVLMSATHPSYSSSVLENYHTVNSFVAKV
LEKVFRIQGHLAPEDENSSSRDSGNFCMAKTSKYDVLFGDKKIGGAAQRKVQQGFLHGGS
LFLSGSSSEFYQRFLXPEVLEEIIEQIQIHAFFPLGLEAADEVLQEARQOVKEAPIKLFC
GEGL

CPn_0437   481810   484350
clpC-ClpC Protease
VFMFEKFTNRAKQVIKLAKKEAQRLNHNYLGTEHILLGLLKLGQGVAVNVLRNLGIDFDT
ARQEVERLIGYGPEIQVYGDPALTGRVKKSFESANEEASLLEHNYVGTEHLLLGILHQSD
SVALQVLENLHIDDPREVRKEILRELETFNLQLPPSSSSSSSSSRSNPSSSKSPLGHSLGS
DKNEKLSALKAYGYDLTEMVRESKLDPVIGRSSEVERLILILCRRRKNNPVLIGEAGVGK
TAIVEGLAQKIILNEVPDALRKKRLITLDLALMIAGTKYRGOFEERIKAVMDEVRKHGNI
LLFIDELHTIVGAGAAEGAIDASNILKPALARGEIQCIGATTIDEYRKHIEKDAALERRF
QKIVVHPPSVDETIEILRGLKKKYEEHHNVFITEEALKAAATLSDQYVHGRFLPDKAIDL
LDEAGARVRVNTMGQPTDLMKLEAEIENTKLAKEQAIGTQEYEKAAGLRDEEKKLRERLQ
SMKQEWENHKEEHQVPVDEEAVAQVVSLQTGIPSARLTEAESEKLLKLEDTLRRKVIGQN
DAVTSICRAIRRSRTGIKDPNRPTGSFLFLGPTGVGKSLLAQOIAIEMFGGEDALIQVDM
SEYMEKFAATKMMGSPPGYVGHEEGGHLTEQVRRRPYCVVLFDEIEKAHPDIMDLMLQIL
EQGRLTDSFGRKVDFRHAIIIMTSNLGADLIRKSGEIGFGLKSHMDYKVIQEKIEHAMKK
HLKPEFINRLDESVIFRPLEKESLSEIIHLEINKLDSRLKNYQMALNIPDSVISFLVTRG
HSPEMGARPLRRVIEQYLEDPLAELLLKESCRQEARKLRATLVENRVAFEREEEEDEAAL
PSPHLES

CPn_0438   485455   484334
ycbF-PP-loop superfamily ATPase
NLTLPMPPQVREIMQQTVIVAMSGGVDSSVVAYLFKKFTNYKVIGLFMKNWEEDSEGGLC
SSTKDYEDVERVCLQLDIPYYTVSFAKEYRERVFARFLKEYSLGYTPNPDILCNREIKFD
LLQKKVCELGGDYLATGHYCRLHTELQETQLLRGCDPQKDQSYFLSGTPKSALHNVLFPL
GEMNKTE/RAIAAQAALPTAEKKDSTGICFIGKRPFKEFLEKFLPNKTGNVIDWDTKEIV
GQHQGAHYTIGQRRGLDLGGSEKPCYVVGKNIEENSIYIVRGEDHPOLYLRELTARELN
WFTPPKSGCHCSAKVRYRSPDEACTIDYSSGDEVKVRFSQPVKAVTPGQTIAFYQGDTCL
GGGVIDVFMIPSEG

CPn_0439   485523   486077
No robust homolog present in Genebank/EMBL as of 11/7/98
IISSNIPVLFVSSTLNGVFPSSLPEESADLFITNKEIVALGEKGNVFLTHSIPMHIAAIT
ILVIVALAGIAIICLGCYSCOSILLIAVGIVLTILTLLCLQALVGFIKFIRQLPQQLHTTV
QFIREKIRPESSLQLVTNAQRKTTQDTLKLYEELCDLSQKEFKLQSTLYOKRFELSHKNE
KTNQN

CPn_0440   486081   486740
No robust homolog present in Genebank/EMBL as of 11/7/98
LATIPGRSMATCVAPSFVPECCPLCHATEVLHLPHAYITOPHPIPAAFWETFRSKLSTKH
TLCFALCLLLTUICTIACIVACVTCYNMCIOICICLCIIVLTLILALLLAIPLKNKQTTTKL
IDRICCLCICSICCCFVQRYCLMFCTICCVHLICELTTCNQEKTPILNEIEAKKECIQNLEL
YITRCCCVLACKQPKRKCCOKCFMPCIKILCCKNPVILFDC

CPn_0441   486876   487818
CT007 hypothetical protein
MWHILCSMFKLLFIIAAFACHVLCTFCIFIVQCAVCCICEEENCKHPPPRDFCIACVVYLKVND
AKFKKLCHPJTICYRUYDCTFLCTLPICTTGISCRLLFSTYCYICADIQWKCCLFCLFTOPNGLG
HATFQLTCCFYNVVLLCICCIAYTLCCLKMMCWCIITLCCLLVDIKIICFMCYGLYQCVLICKYOAT
EKICAIFCVINETILIIQFKAWILCICVCCYKATIACLTLICICYPCMIFCICDYRCTCVCNLCCLAY

RLTRFRRKLHKHHLICOPGIFEC/CRKELEANVK.   DLSFIKGF/CWSIGNDISIADDH
NNNKTSHTFKTSAFFGCCAVMQIF

CPn_0442   487992   489528
CT006 hypothetical protein
NILFQTDMGFKNIICKGCGGLYLMGIFPERIILARKLKNCAKSYPRTALTIEVLVSSVLGAL
KVILIFCASTYAALTLPLRALFHAIKTKGCQHLASYAMAWLCHILTIAVIIGLVFSLVFI
PPPVVFISLCLLMEVTTVTVTLFCVHKNLFPPYEPPPSRPHTPPPFADEYVPLISESYFD

_443
CT005 hypothetical protein
VDSMSQPPINPLCQPQVPAAASPSCQPSVVKRLKTSSTGLFKRFITIPDKYPKMRYVYDT
GIIALAAIAILSILLTASGNSLMLYALAPALALGALGVTLLISDILDSPKAKKIGEAITA
IVVPIIVLAIAAGLIAGAFVASSGTMLVFANPMFVMGLITVGLYFMSLNKLTLDYFRREH
LLRMEKKTQETAEPILVTPSADDAKKIAVEKKKDLSASARMEEHEASORQDARHRRIGRE
AQGSFFYSSRNPEHRRSFGSLSRFKTKPSDAASTRPASISPPFKDDFQPYHFKDLRSSSF
GSGASSAFTPIMPASSRSPNFSTGTVLHPEPVYPKGGKEPSIPRVSSSSRRSPRDRQDKQ
QQQQNQDEEQKQQSKKKSGKSNQSLKTPPPDGKSTANLSPSNPFSDGYDEREKRKHRKNK

CPn_0444   490266   494507
pmp_6-Polymorphic Outer Membrane Protein
KAFPQRHMKYSLPWLLTSSALVFSLHPLMAANTDLSSSDNYENGSSGSAAFTAKETSDAS
GTTYTLTSDVSITNVSAITPADKSCFTNTGGALSFVGADHSLVLQTIALTHDGAAINNTN
TALSFSGFSSLLIDSAPATGTSGGKGAICVTNTEGGTATFTDNASVTLQKNTSEKDGAAV
SAYSIDLAKTTTAALLDQNTSTKIGGALCSTANTTVQGNSGTVTFSSNTATDKGGGIYSK
EKDSTLDANTGVVTFKSNTAKTGGAWSSDDNLALTGNTQVLFQENKTTGSAAQANNPEGC
GGAICCYLATATDKTGLAISQNQEMSFTSNTTTANGGAIYATKCTLDGNTTLTFDQNTAT
AGCGGAIYTETEDFSLKGSTGTVTFSTNTAKTGGALYSKGNSSLTGNTNLLFSGNKATGP
SNSSANQEGCGGAILAFIDSGSVSDKTGLSIANNQEVSLTSNAATVSGGAIYATKCTLTG
NGSLTFDGNTAGTSGGAIYTETEDFTLTGSTGTVTFSTNTAKTGGALYSKGNNSLSGNTN
LLFSGNKATGPSNSSANQEGCGGAILSFLESASVSTKKGLWIEDNENVSLSGNTATVSGG
AIYATKCALHGNTTLTFDGNTAETAGGAIYTETEDFTLTGSTGTVTFSTNTAKTAGALHT
KGNTSFTNKALVFSGNSATATATTTTDQEGCGGAILCNISESDIATKSLTLTENESLSF
INNTAKRSGGGIYAPKCVISGSESINFDGNTAETSGGAIYSKNLSITANGPVSFTNNSGG
KGGAIYIADSGELSLEAIDGDITFSGNRATEGTSTPNSIHLCAGAKITKLAAAPGHTIYF
YDPITMEAPASGGTIEELVINPVVKAIVPPPQPKNGPIASVPVVPVAPANPNTGTIVFSS
GKLPSQDASIPANTTTILNQKINLAGGNVVLKEGATLQVYSFTQQPDSTVFMDAGTTLET
TTTNNTDGSIDLKNLSVNLDALDGKRMITIAVNSTSGGLKISGDLKFHNNEGSFYIDNPGL
KANLNLPFLDLSSTSGTVNLDDFNPIPSSMAAPDYGYQGSWTLVPKVGAGGKVTLVAEHQ
ALGYTPKPELRATLVPNSLWNAYVNIHSIQQEIATAMSDAPSHPGIWIGGIGNAFHQDKQ
KENAGFRLISRGYIVGGSMTTPQEYTFAVAFSQLFGKSKDYVVSDIKSQVYAGSLCAQSS
YVIPLHSSLRRHVLSKVLPELPGETPLVLHGQVSYGRNHHNMTTKLANNTQGKSDWDSHS
FAVEVGGSLPVDLNYRYLTSYSPYVKLQVVSVNQKGFQEVAADPRIFDASHLVNVSIPMG
LTFKHESAKPPSALLLTLGYAVDAYRDHPHCLTSLTNGTSWSTFATNLSRQAFFAEASGH
LKLLHGLDCFASGSCELRSSSRSYNANCGTRYSF

CPn_0445   494739   497579
pmp_7-Polymorphic Outer Membrane Protein
FNFLVSKKCLQMKSSVSWLFFSSIPLFSSLSIVAAEVTLDSSNNSYDGSNGTTFTVFSTT
DAAAGTTYSLLSDVSFQNAGALGIPLASGCFLEAGGDLTFGGNQHALKFAFINAGSSAGT
VASTSAADKNLLFNDFSRLSIISCPSLLLSPTGQCALKSVNSLLTGNSQIIFTQNFSSD
NGGVINTKNFLLSGTSQFASFSRNQAFTGKQGGVVYATGTITIENSPGIVSFSQNLAKGS
GGALYSTDNCSITDNFQVIFDGNSAWEAAQAQGGAICCTTTDKTVTLTGNKNLSFTNNTA
LTYGGAISGLKVSISAGGPTLFQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNN
NQVTNGSTSTRNAINIIDTAKVTSIRAATGGSIYFYDPITNPGTAASTDTLNLNLADANS
EIEYGGAIVTFSGEKLSPTEKAIAANVTSTIRQPAVLARGOLVLRDGVTVTFKDLTQSPGS
RILMDGGTTLSAKEANLSLNGLAVNLSSLDGTNKAALKTEAADKNISLSGTIALIDTEGS
FYENHNLKSASTYPLLELTTAGANGTIITLGALSTLTLQEPETHYGYQGNWQLSWANATSS
KIGSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGEPFERELWLSGIA
NFFYRDSMPTRHGFRHISGGYALGITATTPAEDQLTFAFCOLFARDRNHITGKNHGDTYG
ASLYFHHTEGLFDIANFLWGKATRAPWVLSEISQIIPLSFDAKFSYLHTDNHMKTYYTDN
SIIKGSWRNDAFCADLGASLPFVISVPYLLKEVEPFVKVQYIYAHQQDFYERHAEGRAFN
KSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMAYGTN
LARQGFSVRAANHFQVNPHMEIFGQFAFEVRSSSRNYNTNLGSKFCF

CPn_0446   497602   500415
pmp_8-Polymorphic Outer Membrane Protein
LIEPKHLSMKIPLHKLLISSTLVTPILLSIATYGADASLSPTDSFDGAGGSTFTPKSTAD
ANGTNYVLSGNVYINDAGKGTALTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAAS
TTADKALTFTGFSNLSFIAAPGTTVASGKSTLSSAGALNLTDNGTILFSQNVSNEANNNG
GAITTKTLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQLVFMNNKGETGGGAL
GFEASSSITQNSSLFFSGNTATDAAGKGGAIYCEKTGEPTPTLTISGNKSLTFAENSSVTQ
GGAICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIAIADSGSLSLSANQGDITFLGNTLT
STSAPTSTRNAIYLGSSAKITNLRAAQGGSIYFYDPIASNTTGASDVLTINQPDSNSPLD
YSGTIVFSGEKLSADEAKAADNFTSILKQPLALASGTLALKGNVELDVGHPFTQTEGSTLL
MQPGTKLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLTSPLVFQDSSGNFYE
SHTINQAFTQPLVVFTAATAASDIYIDALLTSPVQTPEPHYGYQGHWEATWATSTAKSG
THTWVTTGYNPNPEPRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFF
HKDKSGTNQAFRHKSYGYIVGGSAEDFSENIFSVAFCOLFGKDKDLFIVENTSHNYLASL
YLQHRAFLVGGLPHPSFGSITDMLKDIPLILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNN
SGALELGCGGLALYLPKEAPFFQVYFPFLKFQAVYSRQQNFKESGAEARAFDDGDLVNCSI
PVGIRLEKISEDEKNNFEISLAYICDVYRKNPRSRTSLMVSGASWTSLCKNLARQAFLAS
AGGSHLTLSPHVELSGEAAYELRGSAHIYNVDCGLRYSF

CPn_0447   500541   503351
pmp_9-Polymorphic Outer Membrane Protein
FVKPPIALYMKSSLHWFLICSSLALPLSLNFSAFAAVVEIHLGFTNSFSGPGTYTPPAQT
THAGTIYNLTGDVSITNAISPTALTASCFKETTCNLCFQGHGYQFLLQNIDAGANCTFT
... (illegible) ...NPNLTFAKNKATQKGQALYGTYQGIITHHTLNGAGFSENTAANHGGAIYTEAS
... (illegible) ...FICQIFAIIEFINNEVTATVATAIACYCGSTGAPKFVLTLCCNIELNFIGHTAITSGGAI
... (illegible) ...VTTGNLVIISSIPTLFKNNSAIDTAAPVZGAIAIADCGSLSLSALVIDITFEGNTVVKCAS
... (illegible) ...CGVITTHGIINDENTNAKIVQLRAGQNTIYFYDFIFTGSTAALSDAINLVGPDLAGNPA
... (illegible) ...VVTTVFIGEKLSEAEAAFADNLKFTIQQPLTIAVZQLSLKGVVTLVAKSFSQHPGSTLL
... (illegible) ...MUVTFTIFLFTANTTINNLVINVDELKETKKATIKATVQASQFFTLANLSLVDPSGNVYED
... (illegible) ...VDWNHLVFESCLTLTAHDHANIHITDLAADPLFKNHIHWVZVINWALSWQEDTATKSKAA
... (illegible) ...TLTWTFEYNPNIEPRGTLVANTLWNIVRQPIOQLVATYHIRQVQETRGIWCEFISNFF
... (illegible) ...HKIZTKIHKSFHIIGHYVVATTTLAGDNLLTTAAFCOLFCKDRGHIFINKNRAGAYAASL
... (illegible) ...HLQHLATICNIILLKYLASIFEQPVLFDAQIEYFCKHTMKTYYTQAPKGEISWYNDKIC
... (illegible) ...ALRLACLIHTTALCIGSILFHAYFCFIKVFEACYIGLZFKKEPHTTLVRSFDCGDLINVSVP
... (illegible) ...ICITTFFFPFCSRNFACYEATVIYVADVYRKNIIXTTTALLIIIIFSWKTFDSTNLGRQACIGRA

GIFYAFSPNLEVTRCLSME   SRGYNAGLCSKFQF

CPn_0448   504876   503698
*yxjG_Bs_2   Hypothetical protein
FIQPSRREIHEWKCILLGSSLRMEMHSPFCQPEQCHFDVVGSFLRPESLTRARSDFEEGR
IVYEQMRVVEDAAIPNLIKKQTEAGLIFFTDGEFRRYSWDFDFMWCFHGVDRRRDSNDPE
ICVYLKDKISVSKHPFIEHFEFVKTFEKGNAKAKQTISPSPSQFFHEMIFAPNLKNTRKFY
PTNQELIDDIVFYYPQVICQLYAAGCRNLQLDDCAWCRLLDIRAPSWYTVDSHDRLQEIL
... (illegible) ...
CGFASCEGDHRMTEEEGWKKIAFVKEIAKEIWG

CPn_0449   507231   505330
pmp-10-PMP_10 (Frame-shift with 0451)
EAYTGFRGGGGISFSNNIVQGTTAGNGGAISILAAGECSLSAEAGDITFNGNAIVATTPQ
TTKRNSIDIGSTAKITNLRAISGHSIFFYDPITANTAADSTDTLNLNKADAGNSTDYSGS
IVFSGEKLSEDEAKYADNLTSTLKOPVTLTAGNLVLKRGVTLDTKGFTGTAGSSVIMDAG
TTLKASTEEVTLTGLSIPVDSLGEGKKVVIAASAASKNVALSGPILLLDNQGNAYENHDL
GKTQDFSFVQLSALGTATTTDVPAVPTVATPTHYGYQGTWGMTWVDDTASTPKTKTATLA
WTNTGYLPNPERQGPLVPNSLWGSFSDIQAIQGVIERSALTLCSDRGFWAAGVANFLDKD
KKGEKRKYRHKSGGYAIGGAAQTCSENLISFAFCOLFGSDKDFLVAKNHTDTYAGAFYIQ
HITECSGFIGCLLCKLPGSWSHKPLVLEGQLAYSHVSNDLKTKYTAYPEVKGSWGNNAFN
MMLGASSHSYPEYLHCFDTYAPYIKLNLTYIRCDSFSEKGTEGRSFDDSNLFNLSLPIGV
KFEKFSDCNDFSYDLTLSYVPDLIRNDPKCTTALVISGASWETYANNLARQALQVRAGSH
YAFSPMFEVLGQFVFEVRGSSRIYNVDLGGKFQF

CPn_0450   508121   507180
pmp_10-Polymorphic Outer Membrane Protein
SGFMKSQFSWLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTYTPKNTTTGIDY
TLTGDITLQNLGDSAALTKGCFSDTTESLSFAGKGYSLSFLNLKSSAEGAALSVTTDKNL
SLTGFSSLTFLAAPSSVITTPSGKGAVKCCGDLTFDNNGTILFKQDYCEENGGAISTKNL
SLKNSTGSISFEGNKSSATGKKGGAICATGTVDITNNTAPTLFSNNIAEAAGGAINSTGN
CTITGNTSLVFSENSVTATAGNGGALSGDADVTISGNQSVTFSGNQAVANGGAIYAKKLT
LASGGGGVSPFLTI

CPn_0451   508158   511058
pmp_10-PMP_10 (Frame-shift with 0451)
KTQRVKIKILDSCFVIFNLIYLFCFYIDANSSLKNKSITHKTSIPWVLVSSVLAFSCHLQ
SLANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVFFYEPGKGTPLSDSCFKQTTDN
LTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGGGTLSS
AGGVNLENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGA
RIANNTGYVRFLSNIASTSGGAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNTKASGSP
ELIISNNKTLIFASNVAETSGGAIHAKKLALSSGGFTEFLRNNVSSATPKGGAISIDASG
ELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGKFTELRAAKNHTIFFYDPITSE
GTSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTOPVSLSGGKLLLQ
KGVTLESTSFSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASN
KVIVSGKLNLIDIEGNIYESHMFSHDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSE
YGFQGQWNVNAFTEGKETYEGTISFSGLCLDDHEVCAENLTSTILQDVTLAGGTLSLSD
GVTLQLHSFKQEASSTLTMSPGTTLLCSGDARVQNLHILIEDTDNFVPVRIRAEDKDALV
SLEKLKVAFEAYWSVYDFPQPKEAFTIPLLELLGPSFDSLLLGETTLERTQVTTENDAVR
GFWSLSWEEYPPSLDKDRRITPTKKTVFLTWNPEITSTP

CPn_0452   511304   512860
pmp_12-Polymorphic Outer Membrane Protein (truncated)
FNEETMTILRNFLTCSALFLALPAAAQVVYLHESDGYNGAINNKSLEPKITCYPEGTSYI
FLDDVRISNVKHDQEDAGVFINRSGNLFFMGNRCNFTPHNLMTEGFGAAISNRVGDTTLT
LSNFSYLAFTSAPLLPQGQGAIYSLGSVHIENSEEVTFCGNYSSWSGAAIYTPYLLGSKA
SRPSVNLSGNRYLVTFRDNVSQGYGGAISTHNLTLTTRGPSCFENNHAYHDVNSNGGAIAI
APGGSISIVKSGDLIFKGNTASQDGNTIHNSIHLQSGAQFKNLRAVSESGVYFYDPISH
SESHKITDLVINAFSGKETYEGTISFSGLCLDDHEVCAENLTSTILQDVTLAGGTLSLSD
GVTLQLHSFKQEASSTLTMSPGTTLLCSGDARVQNLHILIEDTDNFVPVRIRAEDKDALV
SLEKLKVAFEAYWSVYDFPQPKEAFTIPLLELLGPSFDSLLLGETTLERTQVTTENDAVR
GFWSLSWEEYPPSLDKDRRITPTKKTVFLTWNPEITSTP

CPn_0453   513156   516152
pmp_13-Polymorphic Outer Membrane Protein
NCVLLYLFFYSLSLICRIIWFHLYVQMKTSIRKFLISTTLAPCFASTAFTVEVIMPSENF
DGSSGKIFPYTTLSDPRGTLCIFSGDLYIANLDNAISRTSSSCFSNRAGALQILGKGGVF
SFLNIRSSADGAAISSVITQNPELCPLSFSGFSQMIFDNCESLTSDTSASNVIPHASAIY
ATTPMLFTNNDSILFQYNRSAGFGAAIRGTSITIENTKKSLLFNGNGSISNGGALTGSAA
INLINNSAPVIFSTNATGIYGGAIYLTGGSMLTSGNLSGVLFVNNSSRSGGAIYANGNVT
FSNNSDLTFQNNTASPQNSLPAPTPPPTPPAVTPLLGYGGAIFCTPPATPPPTGVSLTIS
GENSVTFLENIASEEQGALYGKKISIDSNKSTIFLGNTAGKGGAIAIPESGELSLANGGQ
DILFNKNLSITSGTTFTRNSIHFGKDAKFATLGATOGYTLYFYDPITSDDLSAASAAATVV
VNPKASADGAYSGTTVFSGETLTATEAATPAHATSTLNQKLELEGGTLALRNGATLNVHN
FTQDEKSVVINDAJTTLATTNGANNTDGAITLNKVINLDSLDGTKAAVVNVSTDKSALT
ISGTLGLVKNSQOCIDNHGMFNKDLQQVPILELKATSNTVTTTDFSLGTNGYQQSPYGYQ
GTWEFTIDTTTHTVTGNWKKTGYLPHPERLAPLIPNSLWANVIDLRAVSQASAADGDVP
GKQLSITGITNFFFAANHTGDARSYRHMGGGYLINTYTRITPDAALSLGFGOLFTKSKDYL
VGHGHSNVYFATVYSNITKSLFGSSRFFSGGTSRVTYSRSNEKVKTSYTKLPKGRCSWSN
NCWLGELEGNLPITLSSRILNLKQIIPFVKAEVAYATHGGIQENTPEGRIFGHGHLLNVA
VPVGVFGKNSHNRSDFYTIIVAYAPDVYRHNPDCOTTLPINGATWTSICNNLTRSTLLV
QASSHTSVNDVLEIFGHCCGCDIRRTSRQYTLDIGSKLRF

CPn_0454   516179   519115
pmp_14-Polymorphic Outer Membrane Protein
GHFLSFKICCCFCLLALLCSASCAFAETRLGGNF/PPITHQGEEILLTSDFVCINFLGASF
... (illegible) ...GCSFINSSGHLSLLSSILSLTFTSCQAPTNGHFALLSAAETLTFKNFSSINFTGNQSTGL
... (illegible) ...QGLIFYCKDIVFQSIKDLIFFTNRVAYSPASVTTGATPAITTVTTDAASALNITQSLTVEHI
... (illegible) ...QQLIFTANGKVHFSKGVTFSSGTYALCGGAICIPTGTFELKNNQGKCTFGYNITPNDAG
... (illegible) ...AIYAETVNIVFJKVALLLDSNTAAPNCIAICAFVLNICGRGPIEFSRNRAEKIIALFIGP
... (illegible) ...SVGFPAKQTLTLTILAIFGDIAFCYNMLNTYFGIRNAITVEAGGEIVSLSAQIISHLVFY
... (illegible) ...DFITHGLPTTGSKSDITINANIAISSVVFTCYILSSTELLLPANTTTLLUTVKIAGGE
... (illegible) ...LKITLIAVVFFIAFADYISILTIISSIFILSLATPTGAPAAVDFTICKLAFDPFSFLYRD
... (illegible) ...FVSAGYNAIFFHTICTGALVLDEHIAFHLTLIZGLQSIVAIPIAVFKSATVFDNSHFLGE
... (illegible) ...IATPCIVGVGYGKWSNTWCRFLLLFADYFIFVYISPSGANTLYAVWNSTLVRITYILLPE
... (illegible) ...HYGEIFCNSLHIFPLSGAFSDITLDQVILIIDIILGLSITAKALGAYVFHTFPRCFSIRGFFSR

YG:VQAAL:MI:'TDH:''UGL:F'QOLYCKTNAHF   .:3EOHYLLSFFGOFPIVTQKSEA
LI.WKAAYG:':KNHLNTT'/LRPDKAPKGQCQWHNNSYYVLISAEHPFLNMCLLTRPLAQA
WDL:GFISAEFLCGWQSKFTET'TDLQRSFSRGKGYNVSLPIGCSSQWFTPFKKAPSTLTI
KLAYKPDIYRVNPHN(/TVVSNQESTSISGANLRRHGLFVQIHDVVDLTEDTQAFLNYTF
GGKNGFTNHRV:T'GLKGTF

CPn_0455   520363   519458
No robust homolog present in Genebank/EMBL as of 11/7/98
.: ::::: ::::::: :: ::::::::::::::::::: ::::::::::::: :::::::::::::::::
.: :::: :::::::::::::::::::: :::::: ::::::::FGLHPPIRNL:.A:FP::'?PEKEAADAY
ASGCKVVAFDDEHLPWVGSHIAYAEEIREKQEQTMQGSLTEEQLIGALLLNTVSTEKNLAF
ALDAVIKQSVWRFRNPDLFAYEREALEASVTDALVSVSNLDMIPYTSSQGIVIEDSSIV
RTSQEHTLIVNCAAFDKLASQIEFLCPSDVLPISGKDPLISDDEDEELNPKVSSAADSKD
KT

CPn_0456   521568   520327
No robust homolog present in Genebank/EMBL as of 11/7/98
IPCTFESKRKFLMTHCLHGWFSVVRHHFVQAFNFSRPLYSRITHFALGVIKAIPIVGHLV
MGVDWLISHCFERGVSHPGFPSDIAPILKVEKIAGRDHISRIENOLKSLRKTIEVEDLDK
VHGQYQENPYADMASSEVLKLDKGVHVSELGKAFSRVRNRITRSYSYAPTPOLDSIAIVG
ICLVSPEEQENLVRLANEVIQLYPKSKTTLYLLIDFNKEWVGDISSDKEKQLRSLGLHSE
VCCLSVLEEDGSEGEDTKHFDLMVGCYGKDSYLREGKILQQALGTSLGTVPWVNVHHTLP
SRYRSRLSLPINTEKDKTELYKEISRTHHQLHTLGMGLGAQDSGLLLDRQRLHAPLSOGS
HCHSYLADLTHEELKILLFSAFVDAKNISKKELREVSLNFANDTSVECGCAFYF

CPn_0457   523886   522120
No robust homolog present in Genebank/EMBL as of 11/7/98
VFLPSRVMASCLSAWFSIVREHFYRAFDFSLPFCARITEFVLGVIKGIPVVGHIIVGIEW
LVSRYLESFVTKPTFVSDVVSLLKTEKVAGRDHIARVVETLKRQRVAVAPEDEDKVHGKI
PVHPFGGIQPVEVLTLYPEVQDATLGLAFSKIRNRVRQAYLQAPRPKLQKYIIIGNDMNP
FEVDDFLHLARLCNETQRLYPDATISLYLTASGGRNAMDKKNRKLLSDCELNPKIACLDF
NQGDVVKQATCDCWMVYHGENDQGTLNQIQEELEKSGEETPWIHVGQKPLSQSLWDFSPF
SSLEMKGDKEKALEYSELEKEQLYSRLVYVGERSSVLSLGFGDSRSGILMDPKRVHAPLS
SGHYCHSYLADLENPGLQKTILAAFLNPKELSSTILQPISLNLILNSKTYLRQHFGFFER
MSRSDRNVVVVVCDVTDWKEEPSFQHFIMELECRGYSHFNIFAFRSNSMCVEERRIL
NESSQEKAFTMIFCEDSVSQGDIRCLHLASEGMLCGKECYAVDVYTSGCANFMMEEVLTL
ERESNLWNRKHGLWKREVRKQKQEAALDQDESEIYVCNQLTAQQNFACS

CPn_0458   526344   524236
No robust homolog present in Genebank/EMBL as of 11/7/98
YFLCCYLKLFVSNFIFFVVMPIPYISSWISTVRQHFVKAFDFSRPFCSRVTNFALGVIKA
IPIVGHIVMGHEWLVSSCVAGIITRSSFTSDVVQIVKTEKALGRDHISRVAEILQRERGT
:TPENQDKVGFKFPVCPFGRLKSEETLKLKPGEREGTLDTVFSPIRTRVTRAYLQAPRPE
IRTISIVGSKLKTPQDFSQFVSLANETQRLHPEALVCLYLTGLNRESQMCDTTTAEKKQY
LHNSGLDSRIQCKDSKEDDAGSPENFYWIGYYSREQOHNIDGOYIQQCLGKSADPIPWI
HVTEDTKDFYYPPNFTSYSHTRQSTDPTSPPRLPESEGDKDSLYGQLSRSYHHEYMLGLG
LKPEDAGLLMDPDRIYAPLSQGHYCHSYLADIENEDLRTLVLSPFLDPGNLSSEDLRPVA
FNIARLPLELDSLFFRLVAGQQEGRNIVTLAHGTPRPEDLDPDSMNILTRRLQMSGYSYL
NIFSYKSRKMIVKEROFFGDRSEGKSFTLILFEDPISAADFRCLQLAAEGMVAKDLPSVA
DICASGCSCIQFSEMOSPQAIEYRQWEARVEDEAGEEAREPVTYSQODLSSMLTTQQNFV
FSLDAVVKQAIWRFRSKGLLTHERKALGEEFLTAIFSYLGSQERNENMGKRTTEEHEVVI
SFEELDRMVQVLPAEVPADSGNDPTRPVPNPDSNPDSSQNEGS

CPn_0459   527062   526619
No robust homolog present in Genebank/EMBL as of 11/7/98
STKIQMHPGLRNWRTSTNKLREEGSVSFREYFRAYMCDKIVAQKNFLFTLDAVIKQAGWR
SQEKLNLFYVESOALGREIKVSLEEYIQSMVGILGSQRTKKSFKFSVDFTPLEQALQERC
SSDDDEDATATSTATGATASPTDMHEDE

CPn_0460   527840   526992
No robust homolog present in Genebank/EMBL as of 11/7/98
VIQHLLNFALEETPSISVQYQEQEKLSPCDHSPEIGKKKRWNKLESFSTYCSLFMSVKDH
YKLNLGIQNSLGWLLDPYRVCAPLSSPYSCPSYLLDLQNKELRRSLLSTFLDPKNLTSE
TFRSVSINFGNSSFGQRWSEFLSRVLHDEKEKHVAVVCNDAKLLEEGLSPEALSLLEEDL
RESGYSYLNILSVSPEGVSKVQERQILRRDLQGRSFTVMITDLPLGSEDIRSLQLASDRI
LVSSSLDAADACASGCKVLVYENPNASWAQELENFYKQVERRR

CPn_0461   528647   527844
No robust homolog present in Genebank/EMBL as of 11/7/98
ISIVACPSISSWFTVVRQHFVNAFDFTHPVCSRITNFALGIIKAIPVLGHIVMGIEWLIS
WIPRHVRHGMFTSDVSSAIKVEQTRGHNCLAPLEAYLSSLRVPISQEDLKYHGRTPED
PFVDITPTEIVQLLPDEELSTVDEALQGVRSRLTYAYRSVEKPMIQDLALVGFGLRDSAD
LINFVRLANGVQNHYPHTKVKLYLAKNLADVWDCEISEEEKGQLRALGLDPKIESISLTS
AGLPSVPEVATVDFMITCYGKDQEVQDP

CPn_0462   531124   529037
No robust homolog present in Genebank/EMBL as of 11/7/98
LIFYLFLNLYIACVRFHFQCWFDPMACYISIWISTVKQHFIRAFDFTRPLGSRITNFALG
VIKAIPILGCVVIGVSWLVSTCSARRFGKPAFTSDVASIVKIEKTRGYNPLAWVEQYLRQ
LRVRLPEGDLCKIHGKVSRDYVCDRTPQENLNMVPHQYLGELGRAFYGIRNRVTKAYORV
TPLEVPCLTLVGFDILDPEDQVNFVRLANGIQTQYPQTQIKLYLISIQKIWNQCDGTISQ
EKEQQLRSLGLDAKIKCVSAPALLLQKYLQSENLPSCDLLINYYGKQQSVRDVDSIKSLL
NLGSEHIPAISVTYRPDDPFYSYYFFPGSQGGTAPDQRIPWSEQEHLQTYTTLSNPRCDR
YAVHLGMEDFASGVFLDPLRVSAPLSGEYSCPSYLLDLKSEELRCFLSAFIDPNNSGQG
NPRPMSINFGNSPLGQRWSEFLSRVLHDETEKHVAVVCNNPOLIKKSFPSHSLSLLENEL
EEGGYSYLNIVSVSQERTCVKERRILSSDPSGRSFTVILTDLPEGSSDIRNLQLASDRIL
VGSALDAADACASECKILEYEDPEQEWAQQYASFYPNIDRAGDLQROGIPGEPLGVSAST
RVVLEKDIVFNLNAVIOQAMWKFKKRDLFAVESOALGDDMRRALEGYIGSSLLVEGTIQP
QVAVMVNVGFATLDEAVCAACDSAQDAPSEENNTDD

CPn_0463   532480   531191
No robust homolog present in Genebank/EMBL as of 11/7/98
L:::PYEKTEQLLGTPNCRTPRVNISTVGIPIDETSHAFVDGMMKQ:VCQDAKELYTFLSR
:HIRVQNG:LEELLFLFDEKMLCAPLSEDHY:GHGYLVDLVDQHLKDLILGMFLDPQ
HI:WIELLKV:IHVR:F:LQQKDFL:HVLRDET:KNVVVVFKGVSLLPATOVCKLVEE
HEGYDIIYE:C:H:GS:FQLLFRKELEGTSCGRYFTVICALYL:DTOMRSLQLASERIM
H:E:HEFLVDNYAAH:KILK:DHTNWRDCFTFGRHADFADAVDV:AGFNSREFKLITQANGG
ILFE:HEL:L:PK:KTFWR:FLAFCDRVTVTRHFIFMLDAAIKQAVWTHKHPSLIDKECEALD
LFTV:LG:IV:TYLEYVTN:HEKT:KGPF:QKEIIADCGFLKEALFFCSDEDVPGTGEDPS
II:4IF:CHLEU:

CPn_0464   5   :   :::::
No robust homolog present in Genebank EMBL :: :: :: :7'99
GLETRGRFTEICLGLLFFDPOGLKFLQLPGETTALNLFR:FAPERHB:::TSYSRARQPDL
HRIAIVYIGVLDSESSKILEPLISYMSC:YSEGOMYLRPFMGKMVNGAVLGRLMVENLH
IRCCGFFSEDAVPESEPFDLG:YVHTDRSCPLPTKKRS:GWELQTVELPESIYPQSEFLLM
RPRMLS

CPn_0465   533278   512971
:: ::::::::::: ::::::::: ::::::::::: ::::: ::::::: :::::::::::::::::::::
::::::::: ::::::::::::: :: :::: :::::::::::::::::::::::::::::::::NFALTT'
ALLIE:GLT'GLDWLLDGH:FPK:SFI:DVLQIS:KV::H:::GHOHKGRVEDILKRORLSLEF
RDEGKVHGDLPSAPFF

CPn_0466   533718   536537
pmp_15-Polymorphic Outer Membrane Protein
TSMRFFCFGMLLPFTFVLANEGLQLPLETYITLSPEYQAAPOVGFTHNQNQDLAIVGNHN
DFILDYKYYRSNGGALTCKNLLISENIGNVFFEKNVCPNSGGAIYAAQNCTISKNQNYAF
TTNLVSDNPTATAGSLLGGALFAINCSITNNLGQGTFVDNLALNKGGALYETNLSIKQN
KGPIIIKQNRALNSDSLGGGIYSGNSLNIEGNSGAIOITSNSSGSGGGIFSTQTLTISSN
KKLIEISENSAFANNYGSNFNPCGGGLTTTFCTILANNREGVLFNNNQSQSNGGAIHAKSI
IIKENGPVYFLNNTATRGGALLNLSAGSGNGSFILSADNGDIIFNNNTASKHALNPPYRN
AIHSTPNNNLQIGARPGYRVLTYVFYDPIEHELPSSFPILFNFETGHTGSVTLRSLHSQSL
DEMNFFSYLRNTSELRQGVLAVEDGAGLACYKFFQRGGTLLLGQGAVITTAGTIPTPSST
PTTVGSTITLNHIAIDLPSILSFQAQAPKIWIYPTKTGSTYTEDSNPTITISGTLTLRNS
NNEDPYDSLDLSHSLEKVPLLYIVDVAAQKINSSQLDLSTLNSGEHYGYGQIWSTYMVET
TTITNPTSLLGANTKHKLLYANWSPLGYRPHPERRGEFITNALWQSAYTALAGLHSLSSW
DEEKGHAASLOGIGLLVHQKDKNGFKGFRSHMTGYSATTEATSSQSPNFSLGFAQFFSKA
KEHESQNSTSSHHYFSGMCIENTLFKEWIRLSVSLAYMFTSEHTHTMYQGLLEGNSQGSF
HNHTLAGALSCVFLPQPHGESLQIYPFITALAIRGNLAAFOESGDHAREFSLHRPLTDVS
LPVGIRASWKNHHRVPLVWLTEISYRSTLYRQDPELHSKLLISQGTWTTQATPVTYNALG
IKVKNTMQVFPKVTLSLDYSADISSSTLSHYLNVASRMRF

CPn_0467   536528   539434
pmp_16-Polymorphic Outer Membrane Protein
NEILTISDQNRKIKEPLVSKTPPKFLFYLGNFTACMFGMTPAVYSLQTDSLEKFALERDE
EFRTSFPLLDSLSTLTGFSPITTFVGNRHNSSODIVLSNYKSIDNILLLWTSAGGAVSCN
NFLLSNVEDHAFFSKNLAIGTGGAIACQGACTITKNRGPLIFFSNRGLNNASTGGETRGG
AIACNGDFTISQNQGTFYFVNNSVNNWGGALSTNGHCRIQSNRAPLLFFNNTAPSGGGAL
RSENTTISDNTRPIYFKNNCGNNGGAIQTSVTVAIKNNSGSVIFNNNTALSGSINSGNGS
GGAIYTTNLSIDDNPGTILFNNNYCIRDGGAICTQFLTIKNSGHVYFTNNQGNMGGALHL
LQDSTCLLFAEQGNIAFQNNEVFLTTFGRYNAIHCTPNSNLQLGANKGYTTAFFDPIEKQ
HPTTNPLIFNPNANHQGTILFSSAYIPEASDYENNFISSSKNTSELRNGVLSIEDRAGWQ
FYKFTQKGGILKLGHAASIATTANSETPSTSVGSQVIINNLAINLPSILARGKAPTLWIR
PLQSSAPFTEDNNPTITLSGPLTLLNEENRDPYDSIDLSEPLQNIHLLSLSDVTARHINT
DNFHPESLNATEHYGYQGIWSPYWVETITTTNNASIETANTLYRALYANWTPLGYKVNPE
YQGDLATTPLWQSFHTMFSLLRSYNRTGDSDIERPFLEIQGIADGLFVHQNSIPGARGFR
IQSTGYSLQASSETSLHQKISLGFAQFFTRTKEIGSSNNVSAHNTVSSLYVELPWFQEAF
ATSTVLAYGYGDHIHSLHPSHQEQAEGTCYSHTLAAAIGCSFPWQQKSYLKFHVPTEWTLELSYQPVLYQ
QNPQIGVTLLASGGSWDILGHNYVRNALGYKVHNQTALFRSLDLFLDYQGSVSSSTSTHH
LQAGSTLKF

CPn_0468   539608   540432
pmp_17-Polymorphic Outer Membrane Protein
IYKLLDNKLMIFYDKLYFHIKVWMFMRPICLSILSTALCCSLSGNEVPNLASCOMSRKDI
SAFHTSPSFRLNVTPEPLVSSFRPSNLLNGFGHDITQDITITGNSINSVIDYNYHYEDGG
ILACKNLFISENKGNLSFERNSSHSSGGALYSVRECWISKNQNYSFISNAASLATTTTSG
FGGAIHALDSYITNNLGEGQFLDNVSKNRGGAIYVGVSLSITDNLGPIVIKKNQTLEDSS
FGGGIFCRAVNIERNYQNIQINDNASGQGVVYFLP

CPn_0469   540399   541460
pmp_17-Polymorphic Outer Membrane Protein (Frame-shift with
0469)
CFRTRGGIFSALGVIISSNKEIIEISNHSASSINTASGKLYPGGGGIMCTSLVIENNPKG
LIFNNKTAALSGGAIHTRSFIFQNNGPTAFINNSATSGGALINLSGIGSTPQNFFLSADY
GDILFNNNTITSSSPOPGYRNALYAAPGINLKLGARQGYKILFYDPIDHDQTTTDPIVFN
YEPHHLGTVLFSGCINVDSNATNPLNFLSKFSNSSRLERGVLAIEDRAAISCKTLSQTGGI
LRLGNAALIRTKGPGSSINFNAIAINLPSILQSEASAPKFWIYPTLTGSTYSEDTSSTIT
LSGPLTFLNDENENPYDSLDLSEPRKDIPPPLPPRCDCKKNRYFESHCRSHELR

CPn_0470   541357   542532
pmp_17-Polymorphic Outer Membrane Protein (Frame-shift with
0470)
ISLNLERISPLLYLLDVTAKKIDTSNLIVEAMNLDEHYGYQGIWSPYWMETTTTTSSTVP
EQTNTNHRQLYVDWTPVGYRPNPERHGEFIANTLWQSAYNALLGIRILPHQPQNLKEHDLEA
SLQGLGLLINQHNREGRKGFRNHTTGYAATTSAKTAARHSFSLGFAOMFSKTREROSPST
TSSHNYFAGLRFDSLLFRDFISTGLSLGYSYGDHHMLCHYTEILKGSSKAFFNNHTLVAS
LDCTFLPARITRTLELQPFISAIALRCSQASFQETGDHIRKFHPKHPLTDLSSPIGFRSE
WKTSHHIPHLWTTEISYVPTLYRKNPEMFTTLLISNGTWTTQATPVSYNSVAAKIKNTSQ
LFSRVTLSLDYSAQVSSSTVGQYLKAESHCTF

CPn_0471   542561   545401
pmp_18-Polymorphic Outer Membrane Protein
TVQNNRSLSKSSFFVGALILGKTTILLNATPLSDYFDNQANQLTTLFPLIDTLTNMTPYS
HRATLFGVRDDTNQDIVLDHQNSIESWFENFSQQGGALSCKSLAITNTKNQILFLNSFAI
KRAGAMYVNQNFDLSENHGSIIFSGNLSFPNASNFADTCTGGAVLCSKNVTISKNQGTAY
FINNKAKSSGGAIQAAIINIKDNTGPCLFFNNNAAGGTAGGALFANACRIENNSQPIYFLN
NQSGLGGAIRVHQEE:ILTKNTG:VIFNNNFAMEADISANHSSCGGAIYCISCSIKDNPGIA
AFDNNTAARDGGAICTOSLTIQDSGPVYFTNNQGTWGGAIMLRDDGACTLFADQGDIIFY
NNRHFKDTFSNHVSVNCTRNV:GLTVGAGQGHCATFYDPILQRYTIQNSIQKFNPNPEHLG
TILFSSTYIPDT:TSRDDFISHFRNHIGLYNGTLALEDRAEWKVYKFDUFQGTLRLGSRA
VFHTDEE:S:::V:SVININNLAINLFG:IU:NRVAPKLWIRPTGS:APYGEDNNPIINL
SGFL:H:DDENI:DGVDFADLA:F:IAEVPLLYLLDVTAKIIINTDNFYPDLNTTOIIYGYGQ
VWGHYW:ET:TT::ECDTNATHJIROLQ:HWTPTGYFVMPENKGDIALSOOFHNLF
ATLPYUTQ:QIAITA:G:EACDLF:HQHENNDAKGFHMEATGYSLATT:NTA:NH:FGVN
FCQLFNLYE:HE:PNSVA:HTTFFALI:IHHIIWLQERFITGASLAYGY:NHIHIKAT:Y:YK
IQTFDLKGY:TFL:AASLI:G:GLS::AWR:DFH:FDTTF:QAIAVRSNUTAFQEXGDFARKFGVH
KFL/NLTV:I::IG:AWE::KFKLFPFWHIELAYUFMYLYQUNPEINV:LC::T::WLJJ:TT
LAPNAIAFKGRO::IF:FPKI:VFLGYG:GVV::TTTHIYLHAGTFFKF

CPn_0472   5   4   5   5

No robust homolog present in Genet. /EMBL as of 11/7/98
EVFMAJG(?????GCGKIPPKDNGDRSR?PSPKGELGSHEISLPPOEHGEECASGSSHIHS
JSSFLPEDUE?OSSSSAASSPGFFSRVRSGVDPALKSFGNFFGAESTGQARETRQAFVRL
SKTITADERRDVDSSSAAATEARVAEDASVSGENPSOGVPETSSGEPQRLFSLPSVKKQ
SGLGRLVQT'VRDRIVLPSGCAPPTDSEPLSLYELNLRLSSLROELSDIOSNDOLTPEEKAE
ATVTIOQL:IQITEFOCGYMEATOSSVSLAEARFKGVETSDEINSLCSELTDPELQELMSD
RDSLONLLDETACDLEAALSHTRLSFSLDDNPTPIDNNPTLISQEEPIYEEIGGAADPQR
TRENWSTRLWNOIREALVSLLGMILSILGSILHRLRIARHAAAEAVGRCCTCRGEECTSS
[illegible line]
[illegible line]
FGDYEVPITJAEPSKDKNIYMTPRLATPAIYDLPSRPGSGGSSRSPSSDRVRSSSPNRRG
VPLPPVPSPAMSEEGSIYEDMSGASGAGESDYEDMSRSPSPRGDLDEPIYANTPEDNPFT
QRNIDRILQERSGGASASPVEPIYDEIPWIHGRPPATLPRPENTLTNVSLRVSPGFGPEV
RAALLSESVSAVMVEAESIVPPTEPGDGESEYLEPLGGLVATTKILLQKGWPRGESNA

CPn_0473   549602   548070
No robust homolog present in Genebank/EMBL as of 11/7/98
GSIMAVGGVGGSRSPSPIPPNRRNSEDGKVSPKDNLGEHTVSSSDSSLASOGPTIEERKA
QLGGTDKIPLPSVKEPGDSQTSGRSGVLQRIWKGVKGVFKKTPQARPEVSSPRLPSHVQH
GQRLPGLEGFRDRIOKRSENPEADLGDKMKRSYSDGDLDRVGHDSNEDSTEDSRSGGEPS
SKSSSFLSGVRGAVSKVHGALGDIKGKFQRSASEDDLTTQGEDSAGDTVKERRSEEAEAS
SKSSSFLSGVRGATSTVQGALGDAKEKVSAFGEQAAGAIRSAPGNIRTRFQRSSSEGDLS
NVNKAAKHLRKALENLEKVAPEQVSPEVASRVQSLLARMEQLTHQEPPTVEDLITFVESN
VGSDSVEYASIVPODGSQAPAETAEAPETGGVEGSAAQGAWKALRDFVVSIFQAVASFFR
AIASRLSSARRESAVDDLASESNTQWFVEQEGVSNPSAAPSLSFAEEIARRAAEMSNRNA
QSLEKLESGNVTDPVIQQGLGLARSFAPEGQ

CPn_0474   551600   549807
CT365 hypothetical protein
LKIIISISFMSTSPISNDPRYLSLSNATEKTSLLANSRSLSPVPNSLVPSNPEDTGLRKS
IFTHSVTLFAGLVVLLVAVSVVVVALTVLAPGVPQAILLGIAISGVGIGGFSIMKSLVYM
VRDYMSPRMQESSRIKSALAVGTGFTVMGLVMKVGANFVPGGYGGLVGSLGSSAYSRGSQ
TTLASFSHYIYTKFFRSEKVAKGEKLTEAEIIKEAKKLHYITLSIATIGVGLAVLGILLA
IAGTVLLGGAPATIAIILAPPLISIGLTTVLQTILHSSIGKWRAFLLTQEKKDLFVDTSL
KDIRLEKLPPSEVEESETSQSVIEVPDSEGIAETRISAEEIDTRLSLTTRQKVIFALATL
LLLASIAAFIVTGFOGGLTVMQVLLVASVGSAVASVTLPMVSSGFSYVAYQLKARLNISKL
RWKEAKNKKRVROFLIESGVIASDREFNQMWKTVYKKQIQKTDAAIREEVRNFEKGGEVN
SALVGGILLGVGTGIMLLALVPAFAPIVPGILALGGSTLGIAGSILMRKFVNWLYDELVK
LYERRRNRRELLYGPESKMRSIATDLVVEALAASHDHLFDLDGPVDFIDVDVDIDGAA

CPn_0475   553850   551685
glgB-Glucan Branching Enzyme
PSMVDKLIHPWDLDLLVSGROKDPHKLLGILASEDSSDHIVIFRPGAHTVAIELLGELHH
AVAYRSGLFFLSVPKGIGHGDYRVYHQNGLLAHDPYAFPPLWGEIDSFLFHRGTHYRIYE
RMGAIPMEVOGISGVLFVLWAPHAQRVSVVGDFNFWHGLVNPLRKISDOGIWELFVPGLG
EGIRYKWEIVTQSGNVIVKTDPYGKSFDPPPQGTARVADSESYSWSDHRWMERRSKQSEG
PVTIYEVHLGSWQWQEGRPLSYSEMAHRLASYCKEMHYTHVELLPITEHPLNESWGYOVT
GYYAPTSRYGTLQEFQYFVDYLHKENIGIILDMWPGHFPVDAFALASFDGEPLYEYTGHS
QALHPHWNTFTFDYSRHEVTNFLLGSALFWLDKMHIOGLRVDAVASMLYRDYGREDGEWT
PNIYGGKENLESIEFLKHLNSVIHKEFSGVLTFAEESTAFPGVTKDVDQQGLGFDYKWNL
GWMHDTFHYFHKDPMYRKYHQKDLTFSLWYAFQESFILPLSHDEVVHGKGSLVNKLPGDT
WTRFAQMRVLLSYQICLPGKKLLFHGGEFGQYGEWSPDRPLDWELLNHHYHKTLRNCVSA
LNALYIHQPYLWMQESSQECFHWVDFHDIENNVIAYYRFAGSNRSSALLCVHHFSASTFP
SYVLRCEGVKHCELLLNTDDESFGGSKGNRAPVVCQDQGVAWGLDIELPPLATVIYLVT
FF

CPn_0476   554877   553858
CT865 hypothetical protein
GRGRRADWGDCMIDIMQHFKPYTMVPGQKLPIPGSLLYAQVFPTLWRLFSSKHEILNEQT
LQVQGPLKRFAVFQDLHRGGLAVTSERYKYYLLPSGECTQSIKGKLPSAAQAGPLLSLGV
HKHADWQKVRCRRDLKEILPLWFRFAAMAPKGSYRDLETTAIGSLVKTAHQRVLHRETTE
IAPALLSIALAGFSECFLPRSYDEEFQGILPQDGDPEGGVPFELLSYSFGMIQDIFLRHQ
GQLVEILPALPPEFPCGRLIHVALPNLGTLSIVWTKKTIRQVELHAEYSGEVFLKFCSSL
CSARLREWSERRLSGSKRLSLGETLEIKAGTTYLWDCFHK

CPn_0477   556112   554844
*yqeV_Bs Hypothetical Protein
RYMTVAEVKGTFKLVCLGCRVNQYEVOAYRDQLTILGYQEVLDSEIPADLCIIINTCAVTA
SAESSGRHAVROLCRQNPTAHIVVTGCLGESDKEFFASLDRQCTLVSNKEKSRLIEKIFS
YDTTFPEFKIHSFEGKSRAFIKVQDGCNSFCSYCIIPYLRGRSVSRPAEKILAEIAGVVD
QGYREWVIAGINVGDYCDGERSLASLIEQVDRIPGIERIRISSIDPDDITEDLHRAITSS
RHTCPSSHLVLQSGSNSILKRMNRKYSRGDFLDCVKFRASDPRYAFTTDVIVGFPGESD
QDFEDTLRIIEDVGFIKVHSFPPFSARRRTKAYTFDNQIPNQVIYERKKYLAEVAKRVGQK
EMMKRLGETTEVLVEKVTGQVATGHSPYFEKVSFPVVGTVAINTLVSVRLDRVEEEGLIG
EIV

CPn_0478   557640   556210
hflX-GTP Binding Protein
WHCGPLDTIDTPGEOGSQSFGNSLGARFDLPRKEQDPSOALAVASYQNKTDSQVVEEHLD
ELISLADSCGISVLETRSWILKTPSASTYINVGKLEEIEEILKEFPSIGTLIIDEEITPS
QORNLERKLGLVVLDRTELILEIFSSRALTAEANIQVQLAQARYLLPRLKRLWGHLSRQK
SGGGSGGFVKGEGEKQIELDRRMVRERIHKLSAQLKAVIKQRAERRKVKSRRGIPTFALI
GYTNSGKSTLLNLLTAADTYVEDKLFATLDPKTRKCVLPGGRHVLLTDTVGFIRKLPHTL
VAAFKSTLEAAFHEDVLLHVVDASHPLALEHVQTTYDLFQELKIEKPRIITVLNKVDRLP
QOSIPMKLRLLSPLPVLISAKTGEGIQNLLSLMTEIIQEKSLHVTLNFPYTEYCGKFTELC
DABVVASSRYOEDFLVVEAYLPKELQKKFRPFISYVFPEDCGDDEGRGPVLESSFGD

CPn_0479   558434   557616
phnP-Metal Dependent Hydrolase
AIGMVRDIOSESIGKLVFLGTGNPEGIPVPFCSCRVVQNTGIHRLRSSVLIOYQNKTLVI
DACPDFRTQMLVAGVSELDVVFLTHPHYDHIGGIDDLRAWIVTQRSLPLVLGACTYRFL
NKAKEYLFATPNVESSLPAVLEFTILNEDCQQEFG/IPVTVVYYQKSCHVTGFRFGNL
AYLTDLCVYDAKIFYLDNVETLILSACFSETPIFFG/IHKGSHLTVREEAKAFANHAGIKN
LIITHGSHGLEAERDQHPEVTFAYDGMEVLWTL

CPn_0480   559375   558650
CT384 hypothetical protein
SDEHIGWIISRLCGEPVGKKEQDGMLGSLECYDGACHIIEEYKNRYFYCCLCAEVVGPYVV
IVIVVDVGGAPPTGILQVLRCKQHKFG/GLPVKGPITGLWALEPGVCKGAIGLECGAMYELCS
GVRNFDIGGIVGWVGIRCLGFAGLIVGVMVEAPLIVSGLSAWVINGGRXVVGAILCLFAIL
HAYLGGGPVREWLHGGGHEYITOGHGRQIQAIGGQNYGVITEYPAWVAIGGPITKLPNGSRR

CN

CPn_0481   [illegible]   559210
No robust homolog present in Genebank/EMBL [illegible]
SCLRIEGILMATSVPVTSSTSVGEANSSNERFTERTSRMYYAALVLGALSCLIFIAMIV:
FPQVGLWAVVLGFALGCLLLSLAIVFAVSGLVLGKTLEPSREATPPEIVAQKEWTTQCSV
LGNEYWRSELISLFLRGGLHESL:VGSKDRGLGIDGGLGNILKLEPLGTTLLLKKDCVH
INIILHLVROWNLLGVGLSPEVTAHAEELLLFLIEECYYSFDILKLIRYGDALQATSPLM
[illegible line]
[illegible line]
YESANGHLDNLFIAFGGGVFAMRKLFDKTLGVVRVGHRGVIREGILSNTEILENEGJFLLS
LYEYPLSYLICWAVLLDCVPGTEISLEDQADYTVTLOGLGDSMLSQFASRLQSGQKVLNPR
DVLSEQAAVMLVHGLAAQGVSFOGLKALMYLTAVPQRMWLGALPLFESFPVFNRMKEFLG
ESLGD

CPn_0482   561764   560961
artJ-Arginine Periplasmic Binding Protein
NLAYRAQTFMIKQIGRFFRAFIFIMPLSLTSCESKIDRNRIWIVGTNATYPPFEYVDAQG
EVVGFDIDLAKAISEKLGKQLEVREFAFDALILNLKKHRIDAILAGMSITPSRQKEIALL
PYYGDEVQELMVVSKRSLETPVLPLTQYSSVAVQTGTFQEHYLLSQPGICVRSFDSTLEV
IMEVRYGKSPVAVLEPSVGRVVLKDFPNLVATRLELPPECWVLGCGLGVAKDRPEEICTI
QQAITDLKSEGVIQSLTKKWQLSEVAYE

CPn_0483   561830   564964
No robust homolog present in Genebank/EMBL as of 11/7/98
IILIKKRAIFERMFPIPPPHCPPNNKNNFYHLTTDTKDPLLLRILRTIGYVLLHIITLGL
LLLLIHYYKHHRVVRKEGLPTPPTLPKGPEPKTIEIAKQPPKDGEDKKPDVPKPGTPPPED
TPPPPPKAPSPASPKVPKQPADKKPTPPPEAPPPPVRVATPMPLRPSSQGYWOCLNRVNN
MVLRRAPLPLPAMQVDPILGDFNPHFVASYPNRIDNEPMYFQIKQFKKIAQNPDLPQQHR
RLAQLSLEQALYLNDNYYLVNVPGDGNCFYRAYAVGWLSALYEESSRNDIVFEQEATRLL
DLPFASSSPANANLCAEMAELLQLCSTYCSFIDLYDGVILSQKHTATLIAFLRKLSAYAI
RQQIAASSNEETARALFISDMCDDLLPSVLEFLAANRPYSELFQNLIDHSALPYMQSRDK
LFLLLEHLPALFLTDAELQKMSPEDQQLRKQYEREIREAFAKLSRRIADSGWDTERFNAI
VKDHLPEAIRCQYSRFLATIENRRSGDLPWSPALSFFAFLCTCPSVRFHKLCATFYKSLE
DIIIASAPPQRSIQEILQISNASLSYLNEDLDSSWQREVISSNIMTILTTHESLTLESSM
PQLETLHKRIANLLKNVISTSFETPPLSNQPDLLSNLVNKLLVAIHSLKRSPAATLEEWLCAAE
ARSLRLTRDEGSGLSQEQDLLYTQAVQLLFFILQHPQVNNRPETKDAVKELKMLLLPFLQ
YAFKKVENEKKLQKLLRSILGSLVLKPPARYPSTPSNKDKETFCKFWSRHPEVMVLDPIL
EKNCMQFLRATFPNYQLETEAILLEKEIESTFRNGWNVFLTRLNLFGSKLGSPSSPTALS
DQFSKSFLIFCFLNNYPKLLQKKTPLAARLDAFQREASHRFTQVKDKLLLSLKYGFPLAT
ATINQYSRARDQLICNLLKNTVTASDGFCRSGFRQSLIGYLHSLSSNELGDILDDVKEQA
EANDVAAMTTVPLQPFAVCLIHSDRDTVSEENIENFVAMHGFLNTISPERDARIFLIRFP
NHYGCLLPRNPRTEDQNSKPDSSNP

CPn_0484   564931   565824
aroG-Deoxyheptonate Aldolase
RSELKTGQLKSLVLHEVLILTFTYPLPRTLKQHPDEVHTVPISPNLSFGEGSPILIAGPC
TLESYEHTVSSALTVKEAGAQVFRGSIRKPRTSPFSFOGWEKECVLWHKEAQSIHGLPTE
TEVLDVRDVEITAEHVDILRIGAKNMHNTPLLQEVSKSHRPIILKRSPAATLEEWLCAAE
YILASSPSCPGVILCERGIRTFEHSTRYTLDLNTVALLKEISSLPVIVDPSHAAGKRSLV
LPLASAGLSVGADGLHIEVHAHPEKALCDAKQQITPEELHLFAKKHFCPSESRAHAIS

CPn_0485   565993   566229
CT382.1 hypothetical protein
QPIGRTPTRVFLWRFHIKQACKFYLLQCLLCALYWLLKYCRKLLKGTLHHSEETLYQALL
SSLIDLLYQLKQLPAPTNE

CPn_0486   567799   566405
hypothetical proline permease
AQHRSLLKGNIFHLGCGVLYFMNFSLFLFFLIAIQGICLYVGRRGSKKVEDRESYFLAGR
SLKIFPLMMTFIATQIGGGVLLGAAEEAFCYGYGGILYPLGVALGLIFLGMGPGKRLAEG
SLTTVVSIFEVFYGSKKLRKIAFLLSAGSLFFILVAQVIALDRLFSSFPFGYVTVAFWI
VLASYTSTGGFRGVVRTDVIQAGFLLIAVLVCGVSVWLSVPKSLSVLDPFQSLPCAKLSN
WIFMPHLFMLVEQDMVQRCVAASSPKRLQWAAVGAGLVLLLFNFIPLFLGSLGAKAGLKA
GCPLIDTIAYFCNPSLAAVMAAAIGVAILSTADSLMNAVSQLIAEEYPTLKAPYYRYLVL
GLAVAAPLVAIGFTNIVDVLILSYSLSVCCLSVPVGFYLLAPKGRRVSGAAAWAGVLVGA
LGYGWVQIVSLGMFGELLAWVGSLVAFSFVGFIEITWKNKVKTQT

CPn_0487   569833   568112
CT384 hypothetical protein
RRTGGISLTYSSFRWASFRCYSLIFFCFCGSLFGSESLRYOLLIQDFAKVSEEGIGLLES
KEYSLLQAKLVLRALAQNSSFDDWFRSFKKCQISYPELAHDRDVLEEFGIQVLREGIENP
SVTVRAVSVLAIGLARDFRLVPLLLQSCNDDSAIVRSLALQVAVNYGSESLKKAIVELAR
NDDSIHVRITAYQVVALLQIEELLPFLRERAENKLVDSVERREAWKACLELSSQFLETGV
AKDDIDQALFTCEVLRNGMLPETTEIFTELLSVEHPEVQESLLSALAWSHQLQNHKEFL
SKVRHVMCTSPFAKVRFQAAALLHLHGDPLGRDSLVEGLRSPQPLVCEAASAALCSLGIH
GVPLAKEHLESLSSRKAAANLSILLLVSREDIERAGDVIARYLSQNPEMCWAIEYFLWDAQ
WNLRGDTFPLYSDMIKREIGRKLIRLLAVARYSQAKAVTATFLSGOQAQGSFFSGMFWE
EGDVKTSEDLVTDACFAAKLEGALASLCQKKDQGASLQRVSQLYNDSRWQDKLAILESVAF
SENLDAVPFLLDCCHHEAPSLRSAAAGALFSIFK

CPn_0488   570147   569767
hitA-HIT Family Hydrolase
RKLPTCFAVNVTRSRDHMTVFKQIIDGLIDCEKVFENENFIAIKDRFPQAPVHLLIIPKK
PIPRFQDIPGDEMILMAEAGKIVQELAAEFGIADGYRVVINNGAEGGQAVFHLHIHLLGG
RPLGAIA

CPn_0489   571037   570099
CT387 hypothetical protein
RIVFAIENYFCLVIHIELWLRRI/F24PJIFRSIVFIHDGSFHADEVTACALLIIFDLVDENKI
IRGRDPVVLGKLGFVVVDVGAXVGIENKRFDHIGVGYGGZGWGGANIMILIYLKERGYMDCEE
YHFIANITLVHGVDEGNWIRFFGGKEIFCGFGDIIKIYNPGREEFETNGDADPGGALIIFTIDF
LCRLPFFFOYDRVVIGGIVRFAMETEDMGGLYFDPILAWGENFFFLYGEKIPAAFVCFPGCD
QWILGGITPGNIDRRHIVPVFSFFIRWGGGLILKELGGKVGGIIFGAVFCHKGLFISVWINRGGCC
QRALRLTIGOHGGTI

CPn_0490   [illegible]   571155
CT497 hypothetical protein
IMYNLLHAHHDAALGFTGGPLASGLFYILGGFHITYEGGEVLIEHIFAYFFGFHLLGGGIQVNLKGI
SIWQWIVRAVLHHILELHFAKKEAGGLIFVLFGGGDDLFIATAMLELLLGPGFSGVGKLFAAHHRRI
VIGGHGGYHINRGGFHITFTDRGGHGGTLLPFGGCKMLEHFITLEIIHGRLVVFLLGGLLGGTIGGYEETETYG

FLPLMJKJHJTRPHLKIRKFLPLYGMVTDRPPVPE.   LLIKTEPLHIRTVFARVVQDLL
PQILRHTAADILEPTTQESGDIYEFYGTTSEPIERLPLEFFTLEPYKEHSFFFYRDMLQE
TLEGPQEVFRVFESIPEGEDQAAMFISKCGELLELSGQDSWIIKPRISPSDERHAREIOKH
IEDQPCFPFLKAMETDHITGQGVLFSRYFPSAGLKGMFLSNYSRYYLQHIYFQIPSPTSG
EFFSNRDRSFLLDLYFAGISVFWADLESKRLLOYIKRRNKDVGMFVPKHQAEQFAQSYFI
GIHGSCLIAGDYDEFLRELLTGMHTLSQQFTIPEFPPQTPLAILTGQGSGAMELANRVAT
ELGILSCGNLIILDTTNAYVEAKMSYAIPDLLERQADFHVDLAVFVIGGMGTDFELLLEL
IRLKTGKKALVFVFLIGPVDYWKSKITALYNSNHAVGTIRGSEWVHNCLFCLSSAKAGIA
     MIEPIIITIQLBEGAFAY

CPn_0491   574595   573336
CT389 hypothetical protein
ILSSLYTVFTMKTAFHSCYSWFCWLFSFLVLFVCGIAGGEPLCPDCKYETKSVLRSDOLP
DHLWNYENDCYLTGYVQSLLDMHFLDSRTQVVIEKNRAYLFSLPVDSSLSEAITNFVRDL
PFICAVEICERPYGECITRSSAERPLLPKEKTLGMPIFCGKEGVWLPQNTILFSPLIADP
RQVTNSAGIRFNEKVVGNRVGATIFGGDFILLRLFDVSRFHVDCDFGIQGGVFSVFDLDH
PESCHVNSDFFVAGLWSGAIDKWSFRFRLWHLSSHLGDEFILTHPNFPRFNLSDEGVDLF
ISFRYTPQIRLYGGCGYIVSRDLTFPERPFYCEWGAELRPFGLREGNLHAQPIFAMHFRC
WEEQKFGLDQSYILGMEWAKFQEIGRKIRAVLEYHQGFSKEGQFIREPCNYYGFRLTYGF

CPn_0492   574643   574804
No robust homolog present in Genebank/EMBL as of 11/7/98
LFSLIFPICEERNSQQTYKHLHVESACFLLESPLKIHWSSPYGFPPFYRRDLKL

CPn_0493   575142   574855
No robust homolog present in Genebank/EMBL as of 11/7/98
SKTEGSHSKTSKGFVGRFVQWIRTFTGRGSKKRSPSSFSPTHPYIRLRTYTRSPKQSGVE
RXQEDAETSFIETPKGILKKPGNKDPKGKHVHWKDS

CPn_0494   575370   575146
No robust homolog present in Genebank/EMBL as of 11/7/98
VIMIRVNPYGSYRGRNPSPEDGKKDVPLSGNSRLHRRGGIRRKHKSASVGVTSGSKTGKA
SLEKKVKGISEAHFK

CPn_0495   575507   576793
aspC-Aspartate Aminotransferase
RRLKKNQKMAIQKAGAFLRCLPSESRPYLEHAMRRNPHFSLLKPQYLFSEISKKLAQFRK
ENPEISVIDLSIGDTTQPLCRSITQAIKEFCVSQEKQETYRGYGPETGLEKLRTKIASEV
YENRISPEEIFISDGAKPDIFRLFSFFGSEXTLGLODPVYPAYRDIAHITGIRDIIPLAC
RKETGFIPELPNQOSLDILCLCYPNNPTGTVLTFQQLQALVNYANQHGTVLIFDAAYSAF
VSDPSLPKSIFEIPEAKYCAIEINSFSKSLGFTGMRLAWNVIPKELTYDNNEPMINDWKR
LFATTFNGASLLMQEAGYYGLDLFPTPPAISLYLTNAQKLKKSLETAGFSVHGGDHAPYL
WVELPEGISDEEAFDFFLHQYHIAVTPGHGFGSCGQGFVRFSALTQPQNIALACDRLCTA
SLKETMVLA

CPn_0496   576751   577812
CT391 hypothetical protein
PPLYRFTKRNDGSCMTILRKLSQYLFFFSLFCSFIYVATCGSQPDSVSSPKIAIFLSFPH
PLLEDCSKSCIETLKDFENLPEIVVLNAEDSIVKARKIARSLHTDKNVVAIVTLGTIATK
VMSHIETQKFVIYAAVPDRESLTLPKNTHNIYGVNDTLDINQYCFAIQAVATNAQSIVYL
KPSEPFPSDLQKEIVKKLHASGIEVIEISITSSTFKTRIRQAIDKRPSAIFIPLSPLSHK
EGTAFLQEILKEKIPIITDDTSLISEGACIACSVDYKKSGKQIAKIVHHLLYNNHDVDSL
RKIIAQRLSPTTTFNEDIIKYLGIKLHKTERNQFLSFKSKKLEKSEKGKNVAVS

CPn_0497   578107   577820
CT388 hypothetical protein
IFQRVVLDDSWILEVKVTPKAKENKIVGFDGQALKVRVTEPPEKGKANDAVISLLAKALS
LPKRDVTLIAGETSRKKKFLLPNRVQDIIFSLHIDV

CPn_0498   579062   578085
No robust homolog present in Genebank/EMBL as of 11/7/98
YCRLRRAPFMNRRKARWVVALFAMTALISVGCCPWSQAKSRCSIDKYIPVVNRLLEVCGL
PEAENVEDLIESSSAWVLTPEERFSGELVSICQVKDEHAFYNDLSLLHMTQAVPSYSATY
DCAVVFGGPLPALRORLDFLVREWQRGVRFKKIVFLCGERGRYQSIEEOEHFFDSRYNPF
PTEENWESGNRVTPSSEEEIAKFVMMQMLLPRAWRDSTSGVRVTFLLAKPEENRVVANRK
DTLLLLFRSYQEAFPGRVLFVSSQPFIGLDACRVGQFFKGESYDLAGPGFAQGVLKYHWAP
RICLHTLAEWLKETNCCLNISEGCFG

CPn_0499   580404   579205
No robust homolog present in Genebank/EMBL as of 11/7/98
LSVYLLIFYFCNCSTHSSVNQSSGTPNPEEVTSPESTEENKNVVSSDEAQATHAVALPIV
TOLSLPEGSVTSSEETASNPRVDEIVAEVSSSRAVADQISSLVERVGELLDDLKGAQSLF
TSFQSELKNCLPAWKSSTRRLETRGAGDNADIARLELFRSDYEAVLGHANQFHGKAHLIL
SKLTDVHHKLQGLSREDLSLAFDWNDRVLEHLGSLGLDVDAEGNWSLSCERGIPRLVLTA
DSMLVQIKKVNLPTVEELRTLQGTTESSSDPRVEESLSCCERLLNELRRLWANFVGFISS
CYDNIVFVLMWIVRRINLLPGLCCLPFHNPDASQEDQRSSSGERSTRRERLSRRSDLSEE
EMIVRAEGESIHPESPHCDGRNQPSRGDKQDSDSEEETEL

CPn_0500   580647   582362
proS-Prolyl tRNA Synthetase
QPHSMKTSQLFYKTSKNANKSAAVLSNELLEKAGYLFKVSKGVYTYTPLLWRVVSKMMNI
IREELNAICGQELLLPLLHNAELWQHTGRWEAFTSEGLLYTLKDREGKSHCLAPTHEEVI
CSFVAQWLSSKPQLPLHLYQIATKFRDEIRPRFGLIRSRELLMEDSYFTSDSPEQMNEQY
EKLRSAYSKIFDRLGLAYVIVTADGGKIGKCKSEEFQVLCSLGEDTICVSGSYGANIEAA
VSIPGHAYDREFLFVEEVATPGITTIEALANFFSIPLHKILKTLVVKLSYSNEEKFIAI
DMPGDRQVNLVKVASKLNADDIALASDEEIERVLGTEKGFIGPLNCPIDFFADETTSPMT
NFVCAGNAKDKHYVNVMWDRDLLPPQYGDFLLAEEGDTCPENPGHPYRIYOGIEVAHIFN
LHTPYTDHFEVHFQDEHCQTQCCWMGTYGIGVGRTLAACVEQLADDRGIVWPKALAPFSI
THAFHYFDTVSQELAETIYHELDHCQYEFLLDDRDERLGFKLKDCDLIGIPYKLILGKSY
QETHIFEIEHRCUEKYTVSPEAFPTWCQNILA

CPn_0501   582424   583650
hrcA-HTH Transcriptional Repressor
ILLTFKHPFPIMLRVTIVLVGLHMARHKVSKRDHKILDILFATTGLYLKTGQPVGSKTLK
ESPCDLEHTATIHNYFAELEALHFLKKNHTHGIRIFTDLALRHYVHNQDKPEAEISADI
KDKLCQLEGRNIIKDIUKATELLCEILDLPTFFCHPRFENDHVTNIQITGVDKQRAVT
ILCTEPFYJIFTDFLWLHEACDTLHIKRIEKFLQNYIPPLPTNEELHKKEEHLCMCLYNEV
VVKYLTRQVNFCMEEDLYQHMIKLLKYEAFKDPEVLAUGLSLFEHRRVMVELLHHGMIIKC
KATAFLGKELGILTCHHNQSVITIPYYMNRSPLGALGILLQRENLHYKFALPLLKLFAN
KIHFHMGHFYKFKIFPRPGHCNCKLGNEPILRTEYGGIKLLPGKETL

CPn_0502   586   584201
drpE-HSP-70 Cofactor
GDVMTDTPPENEEDHHLRNMQNFNEVEHLQQEIVTLKFGLKEKNDKVLMALAESENSRKRL
QKERQELMQYALSNTLLDFLNPIESHEKALCFATCNLDDVKNWALCHGHTLNQEKQLPEE
KGIIEYSSIGQKFNPFLHEAVQTESTSEVPEGTILEEFAKGYKIGERPIRVAKVKVAKAP
TPKENKE

CPn_0503   584225   586213
PTPE1A superfamily
PAKRQAVTNFEKTLSSTKRFIGRKYSEVAJEIGTVFITVTSGSKGDAVFEVDGKQYTPEE
IGAQILMKMKETAEAYLGETVTEAVITVPAYFNDSQRASTKDAGRIAGLDVKRIIPEPTA
AALAYGIDKVGDKKIAVFDLGGGTFDISILEIGDGVFEVLSTNGDTLLGGDDFDEVIIKW
HIEEFKKQEGIDLSKDNMALQRLKDAAEKAKIELSGVSSTEINQPFITMDAQGPKHLALT
LTRAQFEKLAASLIERTKSPCIKALSDAKLSAKDIDDVLLVGGMSRMPAVQETVKELFGK
EPNKGVNPDEVVAIGAAIQGGVLGGEVKDVLLLDVIPLSLGIETLGGVMTTLVERNTTIP
TQKKQIFSTAADNQPAVTIVVLQGERPMAKDNKEIGRFDLTDIPPAPRGHPQIEVSFDID
ANGIFHVSAKDVASGKEQKIRIEASSGLQEDEIQRMVRDAEINKEEDKKRREASDAKNEA
DSMIFRAEKAIKDYKEQIPETLVKEIEERIENVRNALKDDAPIEKIKEVTEDLSKHMQKI
GESMQSQSASAAASSAANAKGGPNINTEDLKKHSFSTKPPSNNGSSEDHIEEADVEIIDN
DDK

CPn_0504   586418   588514
vacB-ribonuclease family
ATQFTSETTGFLVQCPKLTGGAQLLKKPKRKPGRRTYGKSLKIFIPGTLFVHARKGFGFV
SPDNPEEYPFDIFVPARDLRGALDGDHVIVSVLPYPRDGQKLKGTISEVLARGKTTLVGT
ITSLVSPTSALAYTSHSGSQSLIPVELLPGRTYKIGDRILLSTPPWVDKPQEGASPALQM
LEFIGHITNAKADFQAIQAEYNLAEEFPPEVIEEASLFSQKHITQVLHSRKDLRDLLCFT
IDSSTARDFDDAISLTYDHNNNYILGVHIADVSHYVTPHSHLDKEAAKRCNSTYFPGKVI
PMLPSALSDNLCSLKPNVDRLAVSVFMTFTKSGHLSDYQIFRSVIRSKYRMTYDEVNII
EKRHSHPLSKILNEHATLSKKFSDIREERGCIRFVLPSVTMSLDNLQEPVALIENHQTFS
HKLIEEFMLKANEVVAYHISHQGVSLPFRSHEPPNDENLLAFQELAKNMGFDITFTPTQE
PDYQYLLQTTSAGHPLEQVLHSQFVRSMKTASYSTENKGHYGLKLDYYTHFTSPIRRYID
LIVHRLLFNPLSIDQTHLEIIVRACSTKERVSAKAENSFENLKKTRFINKFLQEQPRTTY
HAYIITANHEGLSFVVTEFCHEGFIAAAELPKEYSLKKNALPESIPDKMKPGASIKVTID
SVNLLTQKIVWSIATTTEDKPKKIKKTPSKKKGTKKRAS

CPn_0505   588471   589106
*3-methyladenine DNA glycosylase
RKRLLRKKERKKEPRNVLQEHFFLSEDVITLAQQLLGHKLITTHEGLITSGYIVETEAYR
GPDDKACHAYNYRKTQRNRAMYLKGGSAYLYRCYGMHHLLNVVTGPEDIPHAVLIRAILP
DQGKELMIQRRQWRDKPPHLLTNGPGKVCQALGISLENNRQRLNTPALYISKEKISGTLT
ATARIGIDYAQEYRDVPWRFLLSPEDSGKVLS

CPn_0506   589055   589840
CT421 hypothetical protein
CPMEISPIPRRFGKSFILNNLKLYSKETNAHFLISCRRIMKKYFITGLVILLPLAITIAI
VTMIMNFLTQPFVGLASEFFEKFSFYTKHRALLKFVLQIILLGFLKGLFFATVLLGFLTRIMI
FKSLLSIYDKILHRIPIIKTVYKAAQQVMTIFGSKSGSFKQVVMVPFPNANVQCIGLVA
GDAPTVCCTGEKEDDPLVTVFIPTTPNPTSGFLTLFRKSDIVFLDMKIEDAFKYIISCGV
LSTPMACPSSPLPDELHQDQGS

CPn_0507   589898   590122
CT421.1 hypothetical protein
STPYPQFPLSGEIKKFNIELFHTRMSKQARRRAKSPKKRKPKYAIVHPAPAPRIVYKLHT
NALSTSDSIFIPKIG

CPn_0508   590133   590300
CT421.2 hypothetical protein
SRIHSRHRSYGKSVKGVTKRNVLKRFERVEVLRKLGRWNDSTAKKVTGLPKTPILK

CPn_0509   590299   590808
(predicted Metalloenzyme)
NKFVFLYGNFIRVTQEKIKIHVSNEQTCIPIHLVSVEKLVLTLLEHLKVTTNEIFIYFLE
DKALAELHDKVFADPSLTDTITLPIDAPGDPAYPHVLGEAFISPQAALRFLENTSPNQED
IYEEISRYLVHSILHMLGYDDTSSEEKRKMRVKENQILCHLRKKHALLTA

CPn_0510   590804   591973
tlyC-CBS Domains (Hemolysin homolog)
QLNMLHILLAIFCILLFLAFGLTQPSCHGSSKFLKTLNQRFFKDKGREYPPFSAPTILA
TLLCILYGALGTKLYTLLPPKTAHKDLLFWPLYSLSALIAYGFLPWISTKVPKETTAHL
RFLASVFQLGLFPLOLLFYRRRPNQQVRSSTSFQSQLSEALSAFDNLIVREVMIPKVDIF
ALPEETTLQEALVLVSEEGYSRVPVYKKNLDNITGILLVKDLLLLYTSSHDLSQPISSVA
KPPFYAPEIKKASSLLQEFRQKHRHLAIIVNEYGFTEGIATMEDIIEEIIGEIADEHDVQ
ENTPYKKIGSSWIVDGRMNISDAEEYFHLKIDHENSYDTLGGHVFHKVGAVPQKGHRIHH
ENFDIEIITCTERNVGKLKITPRKRKFHIS

CPn_0511   592141   592488
rsbV-Sigma Regulatory Factor
MSDIQKEEHGSTTIFHLHGKLDGISSPEVQENISQSLAAGSKNIILDCAHLDYMSSAGIR
VLLQSYHQVGQHSGKIVLTTVPKTIEQTLYVTGFLSYFKIFNTVDEAIQTLNKDGD

CPn_0512   592538   594412
CT425 hypothetical protein
SLPLTMRRSVCYVNPSIARACQISTWKFLYSLATPLPAGTKCKFDLAGSGKPTDWEAPAT
DLSQTRHVIYAEMPEGEIIEATAIPVKDHIPVPQFEFTLPYELQVGETLTIVMGASPNHPQ
VDDACNGAQLFAQRRKPFVLYIDPTGEGNYDEPDVFSMDIPGNVLKKIEIFTPSVVVGNK
RFDITVRFEDEFCGNLTNFSFEETRIELGTEHLPEHLNWQLFIPETGFVILPNLYFNEPGI
YRIQLKNLSTQEIFISAPIKCFADSAFHLMWGLLHGESERVDSEENIETCHRYFRDDRAL
NFYACCGFENQENLGPDIWKLINQTVGDFNEEDPFITLSCFOYSGEPHLEGVRHILHTKE
TKSHEHKKEYKHIPLAKLYKHTVNIIDMEJIDGFTASKEHGFDFENFYPEFERVVEIYNAW
GSFTTAALHNPFFIGKKDGERHGTVIEGLKKHLRFGFVAGGLDDRGIYKDYFDSPQVQ
YSHGHTAIICHKYTRFHHAYEALFARHGYATTGPPIVLGFHITGSAPHGSELGTSGKPGLNV
NRHHHYHVAHTALLKTVEIIRHHEVLHTFFFFPDGHRILDYEYCDMVPLSGVTLKDPHGKAPF
VFYYIRVTGAIANAHAWRSHIWDGIN

CPn_0513   594515   594753
Ker-3 oxidoreductase
VPHHTAVHGCLKVKNGIAAKKPHVTKQGFVLQHLER IVHGCVHQHTTCLHQPPKTGPLYG
IFFKILAUGEFHGSEIAUHLLIJINKEIGAPTHWIFADQVPRGPVCGTVVYGGTLYLYPTNF
CDFGKFGGFYAKHGHGKMLYGHGDLLGIQIGHIHTPITEVHIVGGKCFPGGNLQYYGDLF

25

TKIKEYDIOIIIKALTAIEYAYLSDLDNLSIRD: LKDAGLDSIPCCGAEILVDKIRN
FLAPKRLSSSDFLNIHKMAIIGLGIHSNITHLCYHKEGPEDLVTHMVKVRDLQODETQGFKN
FILLKFAQENNVLCKRLRKSSCCHAIPLKSLMAVARIFLDNFSNMKALWNYLGIEAALDL
LSCCANDLSGTIIMCEKVFQMASSKEPIKMDAECMAALITQQGRTPCLTNSSHV

CPn_0514   595690   596520
CT437 hypothetical protein
GNCGPHHTTRENAMCIIGLOPCIGLCCVSTYINSFPLSLDLIKRNDIRCVLAPPADLLNLLI
....
....
ASGWYDLTKLPFVFALLLIISTSWKEHPLPNLAMEEALQQFESSPEEVLKEAHQHTGLPPS
LLQEYYALCQYRLGEEHYESFEKFREYYGTLYQQARL

CPn_0515   596450   597181
ubiE-Ubiquinone Methyltransferase
EKNTTKALKNSGNIMEPSTNKPDCKKIFDSIASKYDRTNTILSLGHHHFWNRSLIQILGS
GYSLLDLCAGTGKVAKRYIAAHPOASVTLVDFSSAMLDIAKOHLPQGSCSFIHSDINQLP
LENHSYPLAAMAYGLRNLSDPHKALQEISRVLMPSGKLGILELTPPKKTHPTYSAHKLYL
RAVVPWIGKSVSKDPDAYSYLSKSIQQLPKDHDLEDLFSKSGFYIAKKKKLFLGAATIWL
LEKQ

CPn_0516   598904   597255
No robust homolog present in Genebank/EMBL as of 11/7/98
RISISFRVSWFVKIILAVLGRAIAKAYYVCMVARGLCDFPTLVPNERLPIGPFFVPQHTS
GAKGKEFAKRNFSIISGLDDILKLCILQRRRPFALQWDNLSVKSDYEEAGPAIGIRSLEPQ
VSQISPAHGRLCSTLVQWAPILGSEEQLVWLEETHKRLKFPKSLGSKDAVIVDSEHVPVN
ANPTQEIPAASETVESSPVAPGNTTDTMPAASGTTDTTSGVSEAAAAEAAVDSTPGTEEE
PSFSLRYALVVQNVPYPEPPKEPEVMFTDEEKSLILEATRARRMELDLYNGYLADYELSK
DEIQKHVPDLPENWRTNWRWSERLYKFFFKTKKEGLEEIFLNKELGNMILARGLAATOSQ
ARIKVFNSLVAWLLQSFNVGRSCTAKPLPTSKLDLFKSEFESKPKNNILTEFLVASDEEI
LFKGLRVLEPGIEGWYDHPDQAGEIRSVLEGLVQAGRISGYWENQPFGRFVLRGVGERRT
ELVELLESLVASGEIMQFFESSDEEGAFIIDNEPSKTAMLKQRFKSCVRTKLVGSFADES
LPRGRFTILV

CPn_0517   599637   598795
No robust homolog present in Genebank/EMBL as of 11/7/98
FIMSSLLSCGRIEPTRVTCSLKTYLEDTSONQLSTRLVRASVIFLCALLIILVCVALSSL
IPSIMALATSFTVMGLILFVMSLLGDVAIISYLTYSTVTSYRQNKRAFEIHKPARSVYYE
GVRHWDLGRSSLGTGEIPIVRTLFSPFQNHGLNHALAAKIFLFMEHFSPEPPNEPLVDWA
CLIRDFRPHVSSLCFVIEKQGSSLRTKEGNTICEAFRSDYDAHFAMVDCYRLIHSKLIIE
KMGLKNIDIIPSVMVREDYPSRPGEGYREGLLRMYGGKGAL

CPn_0518   600806   599832
CT429 hypothetical protein
FMMTYPVPQNPLLLRILRLMDAFSKSDDERDFYLDRVEGFILYIDLDKDQEDLNKIYQEL
EENAERYCLIPKLTFYEVKKIMETFINEKIYDIDTKEKFLEILQSKNAREOFLEFIYDHE
AELEKWQQFYVERSRIRIIEWLRNNKFHFVFEEDLDFTKNVLEQLKIHLFDAKVGKEITQ
ARQLLSNKAKTYYSNEALNPRPKRGRPPKQSAKVETETTISSDIYTKVPOAARRFLFLPE
ITSPSSITFSEKFDTEEEFLANLRGSTRVEDQLNLTNLSERFASLKELSAKLGYDSLSTG
DFFGDDDEKVVTKTKGSKRGRKKSS

CPn_0519   601707   600904
dapF-Diaminopimelate Epimerase
QPTKLRILVYWMAFYSPSTISKYFIYSGAGNRFLLGETLPEVEDVRFLCQETRVDGFLYL
KPSSCADAQLIIFNSDGSRPTMCGNGLRCAIAHLASQKGKSDISVSTDSGLYSGYFYSWD
RVLVDMTLADWRASVHRLESRPDPLPKEVVCIHTGVPHAVVILPEISTLDLSILGPFLRY
HQTFSPDGVNVNFVQILGHCQLRVRTYERGVEGETAACGTGALASALVVSNSYGWKESIQ
IHTWGGELMTVSQNRGRVYLQGSVTRDL

CPn_0520   602233   601646
clpP-CLP Protease
ERHYFMADGEVHKLRDIIEKELLEARRVFFSEPVTEKSASDAIKKLWYLELKDPGKPIVF
VINSPGGSVDAGFAVWDQIKMLTSPVTTVVTGLAASMGSVLSLCAAPGRRFATPHSRIMI
HQPSIGGPITGQATDLDIHAREILKTKARIIDVYVEATNQPRDIIEKAIDRDMWMTANEA
KDFGLLDGILFSFNDL

CPn_0521   603803   602241
glyA-Serine Hydroxymethyltransferase
KSLLKVFEKFKKFAIVEIFTKVVAVVSLLHKFLENASGKKGQSLASTAYLAALDHLLNAF
PSIGERIIDELKSQRSHLKMIASENYSSLSVQLAMGNLLTDKYCEGSPFKRFYSCCENVD
AIEWECVETAKELFAADCACVQPHSGADANLLAVMAILTHKVCGPAVSKLGYKTVNELTE
EEYTLLKAEHSSCVCLGPSLNSGGHLTHGNVRLNVMSKLMRCFPYDVNPDTECFDYAEIS
RLAKEYKPKVLIAGYSSYSRRLNFAVLKQIAEDCGSVLWVDMAHFAGLVACGVFVDEENP
IPYADIVTTTTHKTLRGPRGGLVLATREYESTLNKACPLMMGGPLPHVIAAKTVALKEAL
SVDFKYAHQVNNARRLAERFLSHGLRLLTGGTDNHMMVIDLGSLGISGKIAEDILSSV
GIAVNRNSLPSDAIGKWDTSGIRLGTPALTTLGMGIDEMEEVADIIVKVLRNIRLSCHVE
GSSKKNKGELPEAIAQEARDRVRNLLLRFPLYPEIDLEALV

CPn_0522   603825   604655
CT433 hypothetical protein
REPLSPEKTSLAFKVKNVNQRMIKKNQGKKKNYFQYIPLKVQKLRQPSFYPKRLMTLYLG
LHQKTARKLYPILILTLFPYAKSTPQNKRALQFLPQATHVILTSPSSTHLFLSRMTSL
LSKATLKTKTYLCIGESTKERLLSFLGQVKYVVATQEIAEGIFPLLOALPSSARILYPHS
ILARPVIREFLYNRFTFFSYPHYTVKPRKLKKNILSKYKKIIFTSPSTVRAFAKIFPRFP
EYTYWCQGRMTLQEFQKFSSQKQVSLLETLGKSRTSP

CPn_0523   604720   605052
No robust homolog present in Genebank/EMBL as of 11/7/98
FMACGATFGFDCTAPSLFPPATRPRYNFKLALFVTIAIALVWIALIATTIAIGLCIHPLC
LFIFLTAIPLYFISRYICSHYARNVYIALDVVPDHSKLQDMRSHSPIFSDR

CPn_0524   605079   606179
No robust homolog present in Genebank/EMBL as of 11/7/98
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CPn_0525   6......   607293
CT394 hypothetical protein
GIIFMHIDALLSILAIQELD44MIRLMRVMKEHCKELAKVQSLKGDLARKKQEKELEMENL
KTQIRDGENRIQEISEQINKLENQQAAVKKMDEFNALTQEMTLANKERRSQEQLSDLMD
KQAGGEDLIVSLKESLASTENSSSVIEKEIFESIKKINEECKALLEQRTELKHATNPELL
SIYERLLNNKKDRVVPIEMRVCSGCHIVLTPQHENLVRKKDRLIFCEHCSRILYWQESQ
VNAQENSTAKPRRRRAAV

CPn_0526   526   ......
....
VFNLIEKSFPGVCYDJLKCISGKENRMFSFMISTDVCQDILJGKQNEAVDFFFQAFQPKEAM
QLAEKILGHSGWVFFSGVGKSGCVARKLVATLQSLSERALFFSPVDLLHGDLGLVSPGDI
VCLFSKSGETQELLDTVPHLKSRRAILVAITSMPYSNLAALSDLVVILPSVAELDPFNLI
PTNSTTCQHIFGDFLAMLLFHSRGVSLSTYGKNHPSGQVGHKANGKVKDFMFPKTEVPFC
HLGDKVSFSLEVFSAYGCCCVCIVDPQFRLMGIFTDGDLRRSLASYGGEVLSLSLEKVMT
ANPRCITEDSDIAIALQLMESSSPVAVLPVLDNEENRHVTGLLHMHTLAKAGLL

CPn_0527   609910   608726
sucB-Dihydrolipoamide Succinyltransferase
RYMIFEFRFPKIGETSSGGSIVRWLKNLGDHVARDEPLIEVSTDKIATELPSPKAGRLVR
FCVNEGDEVASGDVLGLIELEEISEADDESTSCPPTSCETKSEAGSSSSSVWFSPAVLSL
AQREGIGLDNLQKIAGTGKGGRVTRODLEAYISESQQVSIPEIFQGEVNRIPMSPLRRAI
ASSLSKSSDEVPHASLVVDVDVTDLMNLISGERORFLDTHGVKLTITSFIVQCLAQTLRQ
FPLLNGSLDGTTIVMKKSVNVGVAVNLNKEGVVVPVIHNCQDRGLVSIAKALADLSSRAR
LNKLDPSEVODGSVTVTNFGMTGALIGMPIIRYPEVAILGIGTIQKRVVVRDDDSLAIRK
MVYVTLTFDHRVLDGIYGSEFLTSLKNRLESVTMG

CPn_0528   611165   609921
gltT-Glutamate Symport
LMKLWMKIFIGLFVGVTLGLVLEDKAIFFKPIGDIFLNLLSMVVYPLVFCSMVLGIASIS
DHKKLGRIGIKSVGLYLGTTALAIVIGLCFAWIFSPGNGCDFAQAQSMDSAVTVIDSNKT
AAYFLSIIAQVFPSNPVRSFAEGNILQIIIFAIFLGLALRLSGERGRPVERFIDGFSEIM
LRMVMHIMSFAPYGVGANSHAWISGNHGLGVLWOLGKFIIAYYLACLFHATLVFGGLVRFG
CKMSFSKFLSSMMDAISCAVSTASSSATLPVTHRCVSKNLGVSAEVSGFVLPLGATVNMN
GTAIFQGMAAVFIAQAYNCPLSLSSSLLLLVVTATFSAVGSAGVPGGGMITLGSVLASVGL
PIQGIAILAGIDRLRDIVGTPMNILGDAVVATYVASGEGELSPYESIKQESVETT

CPn_0529   612298   611165
ycaH-ATPase
FSCKEIRAFKRGTMXKRFPSTLFLFYRRVTIAISLEGILGWGWLGSLLSKVFAFLVACWN
RFSWSTPYRARSTVISVGNIVVGGAGKTPTVLWLAEALRLRGYSCGVLSRGYKSQSSROK
KLTVVDSKVHSASYVGDEPLLMAEKLPEGSVMVHKDRRISAARAAEKFGILLLDDGLQYR
KLHKDVEIAVVNGQDPLGGRAFFPKGRLRDFPLRLKTVDAIIVNGGKEAGTVVKRVSNA
PQIFVKPTIASVVWTHNGERIPKEALRELRVGVFCGLGFPQGFLNMLREEGIHILGKYLL
PDHAAITKKELNYFCQQMAMRQGQGLLCTEKDSVKLPRLSGEVSLLPIAKVEMRLSVNQD
DTLSLLNMIEQIHKNRGN

CPn_0530   613323   612460
spoU-rRNA Methylase
SVVLWGKFLWRRCGSLAFWEFCSMDCIGKHNPLVKEALALKRSRCRKSSWFLVEGAREIQ
KALRTGYLCQHVFCSTHLSEXEKEFLYELKRNSTKILYCLDSTLAQLSFKEHHDSFVAVI
QKRVWNKEDFLIQRKNAQPFYLIIEQVEKPGNVGAILRIADGAGVDGVILCNPIVDLYNP
NVVRSSLGAVFSLPILSISREEGKELFKQEGWTVFVTSPRAETHYFSKNYLGPTALVFGS
EKDGLTEDWFSEDFSEIALPMLGESDSLNLATSVAAVAYEVVRQRWVN

CPn_0531   614198   613245
SAM dependent methyltransferase
DSSKDDFRKEKGRRKSQYRDRYVNKDTGRHSKTYFSLIRERLVMDYKLLDSGDGNKLECF
GPVTLIRPSSIAVWPKSRPELWSQAQLQYVREGERGAWKNFKRLPEEWEVAFSDVRCLLK
RTPFGHLGVFPEHMGFWPALKQAIEKHKERQVLNLFAYTGAGSIFAAKCGARVTHVDASQ
AAVRWAQRNVEKNAFPERRIFWVIEDVISFLKKEIRRNKKYQVILLDPPSYGRGPDGEVF
KIDKDLFPLLSLCSKLLADDASYFLLTSHTPGHTPEFLRAIARRSVPTLVSEAWSCGESF
CGEGVGALPSGSFVQWIA

CPn_0532   614716   614075
ribC/risA-Riboflavin Synthase
ESFCCKDSVVKWGGMFSGIIQELGEVCFFEAQGNGLSLGIKSTPLFVTPLVTGDSVAVDG
VCLTLTSCNESKIFFDVIPETLACTTLGEKRCSDQVNLEAALKMGDSIGGHLLSGHVFGT
AEIFLIKENRYYFRGSKELSQYLFEKGFIAIDGISLTLVSVDSDTFSVGLIPETLQRTTL
GKKREGERVNIEIDMSTKIQVDTVKRILASSGKD

CPn_0533   614918   615385
CT406 hypothetical protein
EVAPMQCPFCNHGELKVIDSRNAPEANAIKRRRECLKCSORFTTFETVELTLQVLKRDGR
YENFQESKLIHGLNAASSHTRIGQDQVHAIASNVKSELLGKQNREISTKEIGELVMKYLK
KADMIAYIRFACVYRRFKDVGELMEVLSATPDMEK

CPn_0534   615389   615784
dksA-DnaK Suppressor
LNFIRSKVVPLSDDEIEQFKKRLLEMKAKLSHTLEGNAQEVKKPNEATGYSQHQADQGTD
TFDRTISLEVTTKEYELLRQINRALEKINESSYGICDVSGEEIPLARLIAIPYATMTVKA
QEQFEKGLLSCN

CPn_0535   615763   616296
lspA-Lipoprotein Signal Peptidase
KRTPIWKLSSMATRFRSTLLVITLFVLIDWVTKLVVLLOYKDLQILTHIPTLYTHSWGRFS
FSIAPVFNEGAAFGLFSNYKYFLFLLRIFVILGLLAYLFFKKKSIOSTTOTALVLLCAGA
IGNVGDIIFYGHIVDFISFNYKQWAFPTFNVADVLISLGTLLLVYKFYFPTKQTEKKR

CPn_0536   616300   617601
dliqA-Di Ala/Gly Permease
YRCIGEPLRYFFKTVMNRLLSLLSVFDDFFWSYYAFILIIVLGVSFGWKSRFFQFTKFSQ
FCKLFPYCSGNFQERETKQAVHPLKVFFASAVXIIGIGINVGIVTAACIGSMSALFWWHI
NIIFGSVVKYSEVVTAIKFRKLDRDGVVGGGPHYFLIKAFKTPVVGVIAILLGIIYGVEI
YQPSVITDSLAWWWNLPKVVTMLVDLVFYAIRGGLOPIGKICSIVLDFFMHLLYCALGL
YIIVKFFIIFTLIHLLSTVFSSAPKSQSALIGFAGCTVATTIHOGISRAAYSADIGIGFDSI
IQSEKMAKDPITVAQLSIVGIAIDNLICTLSILLMVLASGSWSLGLENASQVVEHTLAGYF
IMVKFFLIFTFFVNSYYTTLIRYFLVGFYYCAKFLYGNTCAKIYTLYGLLLLPLFCFLSQNT
ALLIMSVSSALLJAFNLLAYFILHKEYFPARAACLTETSLGTE

CPn_0537   617615   618665

CT914 hypothetical protein
LIFLLFMDNYLCHLIFCCVLLIUMGTIFVHTICFLROLNKILKNIHRVTTILNFEAKI
LAPLHUIKKLLLYWLKKRKNRIGLJEDIDELLDEKKQRUWKKNLDQGIKWCAALVLIWKV
FPNKD

CPn_0538   618129   618511
CT914 hypothetical protein
TKEINGAQHWCFCFKCFYIKTKTLRDIYMFRNNHKPKKTKCKRFRWLRGVLFGGFIATLL
...

CPn_0539   618678   621545
pmp_19-polymorphic membrane protein
GYNLLGLRHMKQMRLWGFLFLSSFCQVSYLRANDVLLPLSGIHSGEDLELFTLRSSSPTK
TTYSLRKDFIVCDFAGNSIHKPGAAFLNLKGDLFFINSTPLAALTFKNIHLGARGAGLFS
ESNVTFKGLHSLVLENNESWGGVLTTSGDLSFINNTSVLCQNNISYGPGGALLLQGRKSK
ALFFRDNRGTILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILFQENEGELGG
AIYNDNGAITFENNFQTTSFFSNKASFGGAVSRYCNLYSQWGDTLFTKNAAAKVGGAIH
ADYVHIRDCKGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQAT
GSILRLHANQGDIEFCGNKVRSQFHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICF
YOPIISATENYNSLYINHQRLLEAGGAVIFSGARLSPEHKKENKNKTSIINQPVRLCSGV
LSIEGGAILAVRSFYQEGGLLALGPGSKLTTQGKNSEKDKIVITNLGFNLENLDSSDPAE
IRATEKASIEISGVPRVYGHTESFYENHYASKPYTTSIILSAKKLVTAPSRPEKDIQNL
IIAESEYMGYGYQGSWEFSWSPNDTKEKKTIIASWTPTGEFSLDPKRRGSFIPTTLWSTF
SGLNIASNIYNNNYLNNSEVIPLQHLCVFGGPVYQIMEQNPKQSSNNLLVQHAGHNVGAR
IPFSFNTILSAALTQLFSSSSQQNVADKSHAQILIGTVSLNKSWQALSLRSSFSYTEDSQ
VMKHVFPYKGTSRGSWRNYGWSGSVGMSYAYPKGIRYLKMTPFVDLQYTKLVQNPFVETG
YDPRYFSSSEMTNLSLPIGIALEMRFIGSRSSLFLQVSTSYIKDLRRVNPQSSASLVLNH
YTWDIQGVPLGKEALNITLNSTIKYKIVTAYMGISSTQREGSNLSANAHAGLSLSF

CPn_0540   621631   626862
pmp_20-polymorphic membrane protein
FIHLIYLSLIEFVNISDRFSSHKWLPATAVFAAVLPALTAFGDPASVEISTSHTGSGDPT
SDAALTGFTQSSTETDGTTYTIVGDITFSTFTNIPVPVVTPDANDSSSNSSKGGSSSSGA
TSLIRSSNLHSDFDFTKDSVLDLYHLFFPSASNTLNPALLSSSSGGGSSSSSSSSSGSA
SAVVAADPKGGAAFYSNEANGTLTFTTDSGNPGSLTLQNLKMTGDGAAIYSKGPLVFTGL
KNLTFTQNESQKSGGAAYTEGALTTQAIVEAVTFTGNTSAGQGGAIYVKEATLFNALDSL
KFEKNTSGQAGGGIYTESTLTISNITKSIEFISNKASVPAPAPEPTSPAPSSLINSTTID
TSTLQTRAASATPAVAPVAAVTPTPISTQETAGNGGAIYAKQGISISTFKDLTFKSNSAS
VDATLTVDSSTIGESGGAIFAADSIQIQQCTGTTLFSGNTANKSGGGIYTKNAKGGGGVYL
EDALILEKVITGSVSQNTATESGGGIYAKDIQLQALPGSFTITDNKVETSLTTSTNLYGG
GIYSSGAVTLTNISGTFGITGNSVINTATSGGAIYKNAAFSNLSSVTFDQNTSSENGGALL
SAATKKTSTTKQIAGGAIFSAAVTIENNSQPIIFLNNSAKSEATTAATAGNKDSCGGAIA
ANSVTLTNNPEITFKGNYAETGGAIGCIDLTNGSPPRKVSIADNGSVLFQDNSALNRGGA
IYGETIDISRTGATFIGNSSKHDGSAICCSTALTLAPNSQLIFENNKVTETTATTKASIN
NLGAAIYGNNETSDVTISLSAENGSIFFKNNLCTATNKYCSIAGNVKFTAIEASAGKAIS
FYDAVNVSTKETNAQELKLNEKATSTGTILFSGELHENKSYIPQKVTFAHGNLILGKNAE
LSVVSFTQSPGTTITMGPGSVLSNHSKEAGGIAINNVIIDFSEIVPTKDNATVAPPTLKL
VSRTNADSKDKIDITGTVTLLDPNGNLYQNSYLGEDRDITLFNIDNSASGAVTATNVTLQ
GNLGAKKGYLGTWNLDPNSSGSKIILKWTFDKYLRWPYIPRDNHFYINSIWGAQNSLVTV
KQGILGNMLNNARFEDPAFNNFWASAIGSFLRKEVSRNSDSFTYHGRGYTAAVDAKPRQE
FILGAAFSQVFGHAESEYHLDNYKHKGSGHSTQASLYAGNIFYFPAIRSRPILFQGVATY
GYHQHDTTTYYPSIEEKNMANWDSIAWLFDLRFSVDLKEPQPHSTARLTFYTEAEYTRIR
QEKFTELDYDPRSFSACSYGNLAIPTGFSVDGALAWREIILYNKVSAAYLPVILRNNPKA
TYEVLSTKEKGNVVNVLPTRNAARAEVSSQIYLGSYWTLYGTYTIDASMNTLVQMANGGI
RFVF

CPn_0541   627137   628003
Solute binding protein (-yebL-Synechocystis Adhesin Homolog)
NNRSSYQTAFVMHKVIVFIFLTLYSLKSYGNDVIDKPHVSVIAPYKFLVEQIAEETCFV
YAIVTNHYDPHTYELPPQQIKELRQGDLWFRIGEAFEKTCERNLTCQQVDLSQNVSLIQG
KPCCNQHTTNYDTHTWLSPKNLKVQVETIVTTLSKKYPQHATLYQSNQEKLLLALDQLNE
EILTITSKAKQRHILVSHGAFGYFCRDYNFSQHTIEKSSHVEPSPKDVARVFRDIEQYKI
SSVILLEYSGRRSSAMLADRFHMHTVNLDPYAENVLVNLKTIATTFSSL

CPn_0542   628000   628737
ABC Transporter ATPase
FMTIRILAEGLAFRYGSKGPNIIHDVSFSVYDGDFIGIIGPNCGGKSTLTMLILGLLTPT
FGSLKTFPSHSAGKQTHSMIGWVPQHFSYDPCFPISVKDVVLSGRLSQLSWHGKYKKKDF
EAVDHALDLVGLSDHHHHCFAHLSGGQIQRVLLARALASYPEILILDEPTTNIDPDNQQR
ILSILKKLNRTCTILMVTHDLHHTTNYFNKVFYMNKTLTSLADTSTLTDQFCCHPYKNQE
FSCSPH

CPn_0543   628710   629603
(Metal Transport Protein)
KSGIFMLSSLIRDSFPLLILLPTFLAALGASVAGGVMGTYIVVKRIVSISGSISHAILGG
IGLTLWIQYKLHLGFFPMYGAIVGAIFLALCIGKIHLKYQEREDSLIAMIWSVMAIGII
FISRLPTFHGELINFLFGNILWVTPSDLYSLGIFDLLVLGIVVLCHTRFLALCFDERYTA
LNHCSVOLWYFLLLVLTAITIVMLIYVMJTILHLSMLVLPVAIACRFSYKMTRIMFISVL
LNILCGFSGICIAYCLDFPVCGPTISLLMGLGYTASLCVKKRYNPSTPSPVSPEINTNV

CPn_0544   630598   629525
yhbZ-GTP binding protein
KLEVFCYJIKEJOFFCLKKDKNVIMFVIQITLELRAGKYGNGVVAWRKEKYLPKGGPYCGN
GJNYGGYILGATTCVVJFEAYRNIPFLKAFGGQJGATINRTGRCGKDLIVSVFPTTLRD
AHTHETLHDFTVDGERLLVGVJGKYZKGNTFFKTGVHRAPTKATGVKPGEIRQVELELKL
IADGLGVGFFNAGKGTLFNTLAHTEVKVGAYPFTTIAPSLGLVLGKDRLYQKFWIIADIP
GLIEVAIGNKGQGDFLRHTERTLCLLFNVIGVJKREPNSPEEDLETLIHELIIGHOPPDFEK
RIMLVAIRKIDLLGPPEQEEGLJGFQKRFPGYTFVGLIGGLNIGIVIGLYRFFTGRLAV

CPn_0545   630008   630638
rl27-L27 ribosomal protein
TEAHFRFMAHKFYGNSGROGRDGGKRLGVKVGNGQKVGTPGGILVHGRGTRWRIPAQNVG
HGRGVTLFALVGIGVMKKTHIGTYIGVVPEGL

CPn_0546   633012
rl21-L21 Ribosomal Protein
LSKQRLTLSIERRIRKKLMEPYAVIQTISGKQYQVRGGGVICVELLGEAWQKEVLFQGVL
FVFDGTKASLGSETIANAQVKAEYLSHVEGEKVVAVKTKRBKNYHRKHQHRQKYLRWGIR
EILI

CPn_0547   631589   632188
yqbB family
...
EALKSLKPNGKIJHVAITIEGJRPKFLCKLJALRQNIAQVMNLTPTGISITATSGEGLGG
FCCGDGVQCFCVLTVMEYCD

CPn_0548   633234   632191
cysJ-Sulfite Reductase
KHYLQEKFKAQQVPLVLRELLSCSDSINDSDPIYRMVFDSNDTTISYKVGDALGVLPENS
KEVSEHVLQLLGYSPTTLVNVKKTSEKVSAQKFIQGYVDLDKIPAKLNSFFPDKDPKITL
YDAIQEYRPOIPIELFAESVFPLLPRFYSIASSPDLHPKSIELLVKHVSYPGKYQKRFGV
CSSFLCSELQVNDSAYIFVQPTKHFTLSTQTEGKPLVNIGAGTGIAPYKAFLEERLFNKD
PGNNLLFFGERKEKVNFYYREFWNHAEEEGKLKLFLAFSRERDQKVYVODLLRIQKDEVR
KAYEEGGFFFVCGRKVLGIEVKHALEEILGKDTLASLRKEHRYVVDVY

CPn_0549   633662   633255
rs10-S10 Ribosomal Protein
PQDVQHQPWNQHSLLRFLKKFKKRLLRSKGCMKQQKQKIRIRLKGFDQGQLDRSTADIVE
TAKRTGARVVGPIPLPTKREVYTVLRSPHVDKKSREQFEIRTHKKRLVDILDPTGKTIDAL
KMLALPAGVDIKIKAA

CPn_0550   635688   633580
fusA-Elongation Factor G
LNYGENNKFMSNQEFDLSAIRNIGIMAHIDAGKTTTTERILFYAGRTHKIGEVHEGGATM
DWMAQEQRGIIITSAATTVFWLGAKINIIDTPGHVDFTIEVERSLRVLDGAVAVFDAVS
GVEPQSETVWRQADKYGVPRIAFVNKMDRMGADYFAAVESHKEKLGANAFPVHCPIGSES
QFVGMVDLISQKALYFLDDTLGAKWEEKEISEDLKERCAELRANLLEELATIDESNEAFM
MKVLEDPDSITEDEIHQVMRKGVIENKINPVLCGTAFKNKGVGQLLNVIVKWLPSPLDRG
NIRGINLKTDQEISLEPRRDGPLAALAFKIMTDPYVGRITFIRIYSGTLKKGSAILNSTK
DKKERISRLLEMHANERTDRDEFTVGDIGACVGLKFSVTGDTLCDRNQEIVLERIEFPDP
VIDMAIEPKSKGDREKLAQALSSLSEEDPTFRVSTNEETGQTIISGMGELHLDILRDRMI
REFKVEANVGKPQVSYKETITVSGNSETKYVKQSGGRGQYAHVCLEIEPNEPGKGNEVVS
KIVGGVIPKEYIPAVIKGIEEGLNTGVLAGYGLVDVKVSIVFGSYHEVDSSEMAFKICGS
MAVKDACRKAKPVILEPIMKVAVITPEDHLGDVIGDLNRRRGKILGQESSRGMAQVNAEV
PLSEMFGYTTSLRSLTSGRATSTMEPAFFAKVPQKIQEEIVKK

CPn_0551   636174   635698
rs7-S7 Ribosomal Protein
MYMSRRHSAEKRDIPGDPIYGSVILEKFINKVMMHGKKSVARKIVYSALERFGKKLNLEN
VLEGFGEALENAKPILEVRSRRVGGATYQVPVEVASERRNCLAMQWIIKHARSKPGKSME
VGLATELIDCFNKQGATIKKREDTHRMAEANKAFAHYKW

CPn_0552   636698   636219
rs12-S12 Ribosomal Protein
IQAGYVPSSSENKPLPTKRALLYISMLVVVRLKREEYMPTINQLIRKRRKSSLARKKSPA
LQKCPQKRGVCLVYTKTPKKPNSALRKVAWVRLSNGQEVIAYIGGEGHNLQEHSIVLIQ
GGRVKDLPGVRYHIVRGTLDCAAVKNRKQSRSRYGAKRPK

CPn_0553   637753   636812
No robust homolog present in Genebank/EMBL as of 11/7/98
GCMVRVVLRFLIIFILGRAVFPLRASESFSWETSTCLTVLGIFEISLTTNEDFVAQCG
LQIGTISSTNNAKIKEIFLIYKEKFPEASISFKRKEPLNLSQSHLSDLGILCMRNGETYA
EGMANKENGPALKQPKDLRLVLRCPNQPDTLLYSEKEAEKGIETNTCLCNQGYTLLDGQL
ILYGDSIEKFLKETKRKNNHTLVDLCDSQVVTTFLGRFWSLLNYVQVLFLSEDSAKILAG
IPDLAQATQLLSHTVPLLFIYTNDSIHIIEQGKESSFTYNQDLTEPILGFLFGYINRGSM
EYCFNCAQSSLGET

CPn_0554   637806   638141
CT440 hypothetical protein
VFSYLLLCIILVYVRFMYEGKSRMASPTPGQLHLQQKVESKAYDYSRSLAMIATALLFFI
VALILSGLSLLPQVFLPFSGAYFIIGSFLAFIALGILLINCVCDLKQYLTSS

CPn_0555   638298   640241
tsp-Tail-Specific Protease
MFVMKKLVRLCVVLLSLLPNVLFSSDLLREEGIKKMMDKLIEYHVDAQEVSTDILSRSLS
SYIQSFDPHKSYLSNQEVAVFLQSPETKKRLLKNYKAGNFAIYRNINQLIHESILRARQW
RNDWVKNPKELVLEASSYQISKQPMQWSKSLDEVKQRQRALLLSYLSLHLAGASSSRYEG
KEEQLAALCLRQIENHENVYLGINDHGVAMDRDEEAYQFHIRVVKALAHSLDAHTAYFSK
DEALAMRIQLEKGMCGIGVVLKEDIGVVVREIIPGGPAAKSGDLQLGDIIYRVDGKDIE
HLSFRGVLDCLRGGHGSTVVLDIHRGESDHTIALRREKILLEDRRVDVSYEPYGDGVIGK
VTLHSFYEGENQVSSEQDLRRAIQGLKEKNLLGLVLDIRENTGGFLSQAIKVSGLFMTNG
VVVVSRYADGTMKCYRTVSPKKFYDGPLAILVSKSSASAAEIVAQTLQDYGVALVVGDEQ
TYGKGTIQHCTITGDASQDDCFKVTVGKYYSPSGKSTQLQGVKSDILIPSLYAEDRLGER
FLEHPLPADCCDNVLHDPLTDLTOTRPWFQKYYLPNLQKQETLWREMLPQLTKNSEQRL
SENSNFQAFLSQIKSSEKTDLSYGSNDLQLEESINILKDMILLQQCRK

CPn_0556   640921   640325
crpA-15kD: Cysteine-Rich Protein
ENGMSSNLHPVGGTGTCAAAPESVLNIVEEIAASGSVTAGLQAITSSTGMVNLLIGWART
KFIQPIPESKLFQSRACQITLLVLGILLVVAGLACMFFHSQLGANAFWLIIPAAIGLIK
LLVTSLCFDEASTGEKLMVFQKWAGVLEDQOLDDGILNNGNKIFGHVKTEGNTGRATTPVL
NDGRGTPVLSFLVSKIARV

CPn_0557   642879   641194
omcB-60kD: Cysteine-Rich Protein
EIFMCKLIRRVVTVLACIFMAGCFAGYTIFAAAVAEGLITKIVASAETKPAPVMHTAKKVR
LVRRNKQIVEXLGGFKAFGGWPETGLIEQVFEAQQEGCYGRLYGVKVNDAXNVEICQS
VPEYATVRIIFPIEILAIGKKDFVDVVITQQLFGEAEFVGDIGFTTPVIDIKLVWKIGRL
CAUDKCKITAWVKPLKRIAVFTAATVIGACPELRCYTKICQPAICIKCHFCILCACLCFAN
YKIEVVRIYGIAIARMVTVINPVIFGYGGIAGYQQRVLGFNLGDMKPGDKKVFTVEFCPQROI
QITNVATGTVVAGHKGGANVEFGAIEFGVVHIDTIADWGYVCKPVEYGITVGNIVIDLVLI
LVVIQUFLGLSIVFVILFEAIYRGMGDTLCGXAHIKEKPKEMCPGETLQFKLVVKAQVIHMTNVVAV
TGESNKYTGTGCAETPFWNRILAATIMGVLITHDDPICVGENTVRILCVTNRGIARGTNVI
LILKPGYEIAQFIAGGAIFPKGTIGYRFFGVFDALPKUIGGKEGVEFGVTLKGIAIKIDAHGFAI

L:DOTF:F:V:DTENTHVV

CPn_0558   543305   543031
omcA-9kDa Cysteine-Rich Lipoprotein
KLMKKAVLIAAMFCGV:GL:DCCRIVDCCFEDPCAPSSCNPCEVIRKKERSCCGNACGSY
VPSCSNP:CGTE:NCOGPQVVKGCTSPDGRCKQ

CPn_0559   541700   541927
....
.:::PROT:LAQ:F:T:::NEAILLCL:
FFLARSVFHTCYNTNL

CPn_0560   645666   644098
gltX-Glutamyl-tRNA Synthetase
RNSRFCQMKSLWSKDKRIMMWENVRVRVAPSPTGDPHVGTAYMALFNEIFAKRFKGKMIL
RIEDTDRTRSRQDYEENIFSALRWCGIQWDEGPDVGGPYGPYRQSERTKIYQGYVETLLK
TDCAYKCFATPOELAEMRAVASTLGYRGGYDRRYRYLSPEEVASREAAGQPYTIRLKVPL
SGECVFEDYSKGRVVFPWADVDDQVLVKSDGFPTYHFANVIDDHLMGITHVLRGEEWLSS
TPKHLLLYEAFGWEPPVFLHMPLLLNPDGTKLSKRKNPTSIFYYRDSGYVKEAFVNFLTL
MGYSMEGDEEVYSLERIIETFNPRRIGKSGAVFDIQKLDMMNKHYLNHEGSPECLLKELQ
GWLLNDEFFLKILPLCQOSRITTLAEFINLTSFFFSGLLEYRVEELLPQALSPEKAAILLY
SYVKYLEKTDQWTKETCTLGSKWLAQAFNVHHKKAIIPLLYVAITGKKQGLPLFDSIEIL
GKPRARARLVYAEKLLGGVPKKLAATVDKFMQREDFEEATFDL

CPn_0561   646407   645871
euo-CHLPS Euo Protein
LMACEQHEGCYELEEREEIEDIKDSDTKWVSITQAAKLHNVTRQAIYVAIKQKKLKASKE
TRWEIDKLDLEEYKRNRYSRKKSLYQGELVFDNGKGCYSINQVAQILGIPVQKVYYATRT
GTIRGERKGAAWVIHVSEIERYKNEYLSKQAAKKLKGAEPKEHQAPNFEPPTEIFPESN

CPn_0562   648051   646918
*CHLPS 43 kDa protein homolog_1
NYKVIMSIAIAREQYAAILDMHPKPSIAMFSSEQARTSWEKRQAHPYLYRLLEIIWGVVK
FLLGLIFFIPLGLFWVLQKICONFILLGAGGWIFRPICRDSNLLRQAYAARLFSASFQDH
VSSVRRVCLQYDEVFIDGLELRLPNAKPDRWMLISNGNSDCLEYRTVLQGEKDWIFRIAE
ESQSNILIFNYPGVMKSQGNITRNNVVKSYQACVRYLRDEPAGPQARQIVAYGYSLGASV
QAEALSKEIADGSDSVRWFVVKDRGARSTGAVAKQFIGSLGVWLANLTHWNINSEKRSKD
LHCPELFIYGKDSQGNLIGDGLFKKETCFAAPFLDPKNLEECSGKKIPVAQTGLRHDHIL
SDDVIKEVAGHIQRHFDN

CPn_0564   654359   650145
secD&secF-Protein Export Proteins SecD/SecF (fusion)
SGAMKQKVKRNFAIIICVFALALYYVLPTCLYYAKPLDKKIDGNEAEHIIKSFTKQAQQV
RKDVIPRVSAILSSLHLRGHIQQHPAIPDIVSVRFKRGEDAEDFIGNLVHGEPNVPIKSA
RLHVVGYSREHDDHVIQVASSINTSLVESDFSFVSYSSENEQEMASSILQRVYSACTFPK
QKDCSCSYPSIWETAPKEQLLQYAKNLSSGFEVFSSRLSAFCQOSFSSNQDRLAFLSRLS
SLSNDAAIDVEDQKLLKSVYETLSQTACIRSLDCPYIEGLRLDCSESSLFFSSIEYCPKE
RKIFLTLHSDLLAQRTSLSKEORLDFDSRLAVEKQKLSKNLTVQVEDYNNGFSFQWMDKD
TQGKIILQGERLLQGIAEHLTALTLHRPAAESCDLIPENFPVFCRQPRESEAFGCYIFSP
NTDCKHFSKGSVYILLKGLRSIVAKYQQGGGKELQSFEKDLQNLYNCFSHTEAISWTLGE
QVLEIRHPLQQFLDVWGEGFVIGKEGCAFLEVKDIQDRLATVNQIEKNRQSDLVRWHEQ
YRHAKCSMDLQERLSAPIPYQNLFLENMKLAMRKFSRGENILRLGIDFVGGRQLLLSFKD
HQGKQLTDKEDILKVSDELCARLNKLGVSEIELRREGDYIHLSVPGSSTISSSEILGTSK
MSFHVVNERFSSYSASRYEVQRFLDYLWFTSQAQGKTSPEEINTFASALFNEEVQVPPSV
HEAITKLKSEGLAFSPSGCETPSTDLDTTFSMIAIGKDAEQKANPLVIVFRNYALDGASL
KDIRPEFAAGEGYVLNFSVKDTSPKKMAEKLSPTESFHTWTSAYCQEGISGTANGQYSAN
RGWRMAVVIDGYMVSSPILNVPLKNHASVSGKFTHREVSKLASDLKSGAMSFVPEVLSEE
TISSDLGKKQCTOGIISACCGLAMLIVLMSVVYFGGVIASGAVLNLLLVAVAALQYLDA
PLTLSGLAGIVLAMGHAVDANVLVFERIREEFLLSQSLKKSVEKGYTKAFGAIFDSNLTT
VLASALLFFLDTYSPIKGFALTLILGIFSSMFTALFMTKFFFMLWMNKTQHTQLHMMNKFV
GIKHDFLRGCKKLWAVSGSVFLLGCVALGFGAWNSVLGMDFKGGYAFTFNPKEHGISDVA
QMRGKVVHKLQEAGLSSRDFRIQTFGSSEKIKIYFSDKALSYTKADTSLSPKINDHELAL
AVGLLSETGLDFSTETLNETONFWSKVSSKLSKKMPYQATIGLLGALAIILLYVSLRFEW
GYAFSAVCALIHDLLATCAVLFIAHFFLKKIQIDLQAIGALMTVLGYSLNNTLIIFDRIR
EDRQANLFTPMHVLVNDALQKTFSRTVMTTATTLSVLLMLLFIGGSSVFNFAFIMTIGIL
UTTLSSLYIAPPLLLFMVRKENRSK

CPn_0565   655741   654533
CT449 hypothetical protein
HKLFCFLIFCFVNISAILFDSSFLLKIKRNSKRMLRSMKFPRISISDLIPTQMVIWWRGG
GNVHYVPNAQNLPKKILCGVLACFGLALLGCAAFAAGVCQTIFPCIGLMILGLVLLGFAY
LQYSKGWSRFERPLFRETKVFEKPINWLGCLSLLQSWKKIRPGCYYHPGCPQVEICEGSQ
EIVTKIFQKKSDRNTSIFLIQEMDQIALRQGIEKSSLSRKTFAIDPSVVSSLLSEIGNEE
CQYLDPKVISWGSEDQASDRTHPKSAIYVNISDAACEPQGRCYIDAYTKAFFTVLDQIGD
INIVKKIFTIYVLTPILGVPDALPKEEQENLKLLSQAAFLYSAEQVAKRMREEKQDSIRIK
FIFTDPTCPTCLYFSPHHSSTDHSVTPISLSGFYCGVGEQESYTFA

CPn_0566   654999   656890
yaeS family
GP:VTVAL:HDF:VDL:SLATHNNAE:KFP::LQRLFHHVAIIMDGNRRWYKKHREECCGHTHTS
SIVYGAKVLFHTTNAVLDLGIKVLTLYTFSTENFGPKKEEIGE:FNIFYTQLDKQLPYLH
FHEQLHR::GD::KLFRGTQTKINHV:RMTA:SF:SRLELVLAVNVYC:KDELVRAFKHLIVD
HLRKK:::GDLDGR:::VLGT:VLTDPDLL:RTYZ:EMRV:NFLLWQIAYTELY:TDTLW
FDFTIQDLFEA:HVVY:QRC:R:ICX:K

CPn_0567   656894   657817
::EA Phosphate Acetyl glylyl transferase

CPn_0568   543395   543031
... ...

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VLNSNKFKSKTTAYGDLFQP: .SLVLTFLVLLLYGSLFFLTTFALGIF:TATCCAVCTY
EYSSMAKAKHHYPLSTFGAICGSFLFLALSFLGIRWGHGLPGFFDAL.PWTLL:VMVVWSIF
RVRKSTIGALQL:ZXVTEFSITTVGIRIBWELHVLYSR:GITRQEPYLGM:WWAGFL.IZXTXGA
DIFGYFFGKAFGNKKIAPOISPNKTVVGFVAGCLCATLISFIFFLQ:FTRFASTFPHPA:
LIPLGLALG:TTGFFGDIIES:FKRDAHLKNSNKLKAVCOMLDTLDSLLLSTPIAYLFL:
TQSKEFIG

CPn_0569   557805   658464
... ...
.::AVAPL:::NAPL:L:TKFL
EEPPFSFTTFATCGPLESFFIGHLLTSELTTQEVANAASELSCLPEVRAFHQDLQRRYAQL
GNCVFEGRDMGSKVFPNADLKIFLTGSPEVRAQRRLKDLPEGTLSPEQLQAELVKRDAAD
AQRAHDPLVIPENGIVIDSSDLTIRQVLEKILALLFRNEL

CPn_0569   658398   659099
plsC-Glycerol-3-P Acyltransferase
LFGFDNKTSSGENFSFTISKRAMIFRICKFFTWVAFSLFYKLKVYGVKKNFIKGPAIIAV
NHNSFLDPIALHMCVHECTYHLARASLFNIPWLWKQWGCFPVRQDECNSAAFKIASRLFN
KRKKLVIYPEGARSPDCQLQPGKVGIGMMAAKSRVPIIPVYIRGTFEAFNRHQKIPHVWK
TITCVFGTPMYFDDIIQNPEIKNKETYQIITNQTMNKIAELKAWYESGCKGDVP

CPn_0570   659044   660789
argS-Arginyl tRNA Transferase
TKLPSSKHGMNRGAKETSPKLMSTLLSILSVICSQAIAKAFPNLEDWAPEITPSTKEHFG
HYQCNDAMKLARVLKKAPRAIAEAIVAELPQEPFSLIEIAGAGFINFTFSPKVFFLNQQLEH
FKDALKLGFQVSQPKKIIIDFSSPNIAKDMHVGHLRSTIICGDSLARIFSYVGHDVLRLNM
IGDWGTAFGMLITYLQENPCDYSDLEDLTSLYKKAYVCFTNDEEFKKRSQQNVVALQAKD
PQAIAIWEKICETSEKAFQKIYDILDIVVEKRGESFYNPFLPEIIEDLEKKGLLTVSRNDA
KCVFHEAFSIPFMVQKSDGGYNYATTDLAAMRYRIEEDHADKIIIVTDLGQSLHFQLLEA
TAIAAGYLQPGIFSHVGFGLVLDPQGKKLKTRSGENVKLRELLDTAIEKAEEALREHRPE
LTDEAIQERAPVIGINAIKYSDLSSHRTSDYVFSFEKMLRFEGNTAMFLLYAYVRIQGIK
RRLGISQLSLEGPPEIOEPAEELLALTLLRFPEALESTIKELCPHFLTDYLYNLTHKFNG
FFRDSHIQDSPYAKSRLFLCALAEQVLATGMHLLGLKTLERL

CPn_0571   662179   660749
murA-UDP-N-Acetylglucosamine Transferase
TFEKVNVSFSDFDAKGERRMQIAQVFGCGRLAGEVKVSGCAKNAATKLLVASLLSDQKCTL
RNVPDIGDVSLTVELCKSLGAHVSWDKETEVLEIYTPEIQCTRVPPTFSNVNRIPILLLG
ALLGRCPEGVYVPTVGGDAIGERTLNFHFEGLKQLGVQISSDSSGYYAKAPRGLKGNYIH
LPYPSVGATENLILAAIHAKGRTVIKNVALEAEILDLVLFLQKAGADITTTNDRTIDIFG
TGGLGSVDHTILPDKIEAASFGMAAVVSGGRVFVRNAKQELLIPFLKHLRSIGQGFLVSE
SGIEFFQERPLVGGVVLETDVHPGFLTDWQQPFAVLLSQAQGSSVIHETVHENRLGYLHG
LQHMGAECQLFHQCLSTKACRYAIGNFPHSAVIHGATPLWASHLVIPDLRAGFAYVMAAL
IAEGGSIIENTHLLDRGYTNWVGKLRSLGAKIQIFDMEQEELTTSPKSLALRDASL

CPn_0572   662349   664616
CT456 hypothetical protein
IMAAPINQPSTTQITQTGQTTTTTTVGSLGEHSVTTTGSGAAAQTSQTVTLIADHEMQE
IASQDGSAVSFSAEHSFSTLPPETGSVGATAQSAQSAGLFSLSGRTQRRDSEISSSSDGS
SISRTSSNASSGETSRAESSPDLGDLDSLSGSERAEGAEGPEGPGGLPESTIPHYDPTDK
ASILNFLKNPAVQOKMQTKGGHFVYVDEARSSFIFVRNGDWSTAESIKVSNAKTKENITK
PADLEMCIAKFCVGYETIHSDWTGRVKPTMEERSGATGNYNHLMLSMKFRTAVVYGPMNA
KESSSGYTPSAWRRGAKVETGPIWDDVGGLKGINWKTTPAPDFSFINETPGGGAHSTSHT
GPGTPVGATVVPNVNVNLGGIKVDLGGINLGGITTNVTTEEGGGTNITSTKSTSTDDRVS
ITSTGSQSTIEEDTIQFDDPGQGEDDNAIPGTNTPPPPGPPPNLSSSRLLTISNASLNQV
LQNVRQHLNTAYDSNGNSVSDLNQDLGQVVVKNSENGVNFPTVILPKTTGDTDPSGQATGG
VTEGGGHIRNIIQRNTQSTGQSEGATPTPQPTIAKIVTSLRKANVSSSSVLPQPQVATTI
TPQARTASTSTTSIGTGTESTSTTSTGTGTGSVSTQSTGVGTPTTTTRSTGTSATTTTSS
ASTQTPQAPLPSGTRHVATISLVRNAAGRSIVLQGGGRSQSFPIPPSGTGTQNMGAQLWA
AASQVASTLGQVVNQAATAGSQPSSRRSSPTSPRRK

CPn_0573   665413   664691
yebC family
VEDHAGHSKWANTKHRKERADHKKGKIFSRIIKELISAVKLGGADPKSNARLRMVIQKAK
ENNIPNENIERNLKKATSAEQKNFEEVTYELYGHGGVGIIVEAMTDNKNRTASDMRIAIN
KRGGSLVEPGSVLYNFARKGACTVAKSSIDEEVIFSYAIEAGAEDLDTEDEENFLVICAP
SELASVKEKLISQGATCSEDRLIYLPLRLVDCDEKDGEANLALIDWLEQIEDVDDVYHNM
S

CPn_0574   665978   665394
No robust homolog present in Genebank/EMBL as of 11/7/98
SAERGFRHPIVMVETVLHNFQRYLSKYLYRVFRFPCRKKTFLSSHRVLARPSFPVDYCPG
KIYDLQEIYEELNAQLFQGALRLOIGWFGRKATRKGKSVVLGLFHENEQLIRIHRSLDRQ
EIPRFFMEYLVYHEMVHSVVPREYSLSGRSIFHGKKFKEYEQRFPLYDRAVAWEKANAYL
LRGYKKRVCCGYGRA

CPn_0575   666524   665982
YhhY-Amino Group Acetyl Transferase
SIFGRVWRSFMTAEKQNTGILGLEIRYTLPSDATYMLKWLNDPKILRGFPIQTEAEIRET
VNFWVGFYRYHSSLTAVVNGNVAGVATLVLNPYVKVSHHALISIIVCEEFRNKGIGTALL
NNLIHLAKTRFKLEVLYLEVYEGNPALHLYQRFGFVEVGRQNRFYKDEIGYLAKTTMEKD
L

CPn_0576   667543   666494
prfB-Peptide Chain Release Factor 2 (natural UGA frame-shift)
MQENLDKRLEALRTEISLAARSL

CPn_0576.1   ...7593
prfB-(natural UGA frame-shift)
MQENLDKRLEALRTEISLAAR::L

CPn_0577   667666   667720   668155
SWIB (YM74) complex protein
EC:MCQKHKN:AFMIPVN:::DLAV:VV:KG:MPRTEIVF:VWKY:KKH:K:OPQKNKRNIL
PGANLAKVHS:GDF:DMFVMPFAL:KH:TVK

CPn_0578   668386   668538   669165
yaeT-phosphoryltolase
TTHGFIVLGSI:LATLF:LAF:WAGFIEFHWLPTFAIFWRLPKKHAHUHGLRIAU:HGIJI
FHKRVPEKFLNKVKSIKNFSFGLIVFCYGLLICHARLELKERLETFLITTLEAFLAVFALL
CRHDYSSYIGRNTKGECTC:IFEFP:OR:IOPA:IAVMYJGLF:GSI:YRYDFHLTIQRMFDDL

LKLLKNTPLTLLHNTTHVIPNTLNIVGLCDLFARL...PEQAFKNYDPSLPGLLLSHNPDG
ITRLUQYPGDFVLSGHSHGPQVTLSWPKFARKFFERLSGLENPYLARGYF/TKEGKQLYV
NRGLCULKRIPFCSPPEICYITCSYD

CPn_0579   669310   669993
yqDP/y-icM-Sugar Nucleotide Phosphorylase
KEFASAPLLKGATGHVPHIKSSLILLSGGGCTRFGSKIPKQYLPLNGTPL/LHSLKILSS
L.PGIAEVY//CDPGYDETFQEYPVSFAIPGERRQDSVFSGLQQVGYPW/IIHDGARPFIY
...

CPn_0580   669936   670793
truA-Pseudouridylate Synthase I
ASSNQNFLPRRSNDCPSPPMTKVALLIAYGGTAYSGWQQQPNDLSIQEVIESSLKKITKT
RTPLIASGRTDAGVHAYGQVAHFRAPDHPLFANANLTKKALNAILPKDIVIRDVALFDDN
FHARYLAIAKEYRYSLSRLAKPLPWQRHFCVTPRHPFSTELMQEGANLLIGTHDFASFAN
HGRDYNSTVRTIYTLDIVDKGDSLSIICRGNGFLYKMVRNLVGALLDVGKGAYPPEHLLD
ILEQKNRREGPSAAPAYGLSLHHVCYSSPYNNFCCEQCSVSTSNEG

CPn_0581   671533   670745
Phosphoglycolate Phosphatase
EGLRWRSVKSFLRQCWIYSMLVSDEFQLCLRSGMYLEDYDVFFFDLDGLLVDTEPCFYRA
FLQACAEFSLEVHWDFSTYYSHTTLGTEIFSKKFIEQYPQAQEYMAEIFAKRLQIYYKSL
EHAGPALMPGVEAFIELVLSLNKTFGVVTNSPRDATHTLRTHYPILNKFLFWVTRENYAR
PKPYGGSYDYAYRTFAREGMXVIGFEDSVKGLRALSKIPATLVCINSMAEITPEDYPELK
GKEFFSYPSFDVLTEHCSQQKLL

CPn_0582   671305   672177
CT465 hypothetical protein
KNPNALLKKIQHRLVKMHDKNKVLYLQANHLNQKRKRHNPLNTYHSSNTTETRRLPTYYK
SNIVLKMILRISTVSLLTSCSFSKNSRTCFVTPERITSQKDCPVLLHKPSTTISPPLYDW
ISPNREVITAYSFYCRGGQNSIITPEGVLYDCCGLHHSITKEEFRYIHPRLIEVVRLLQQ
DHPKVSIIEAFCCPKHFHFLEASGISLSQLHLQGTAATFALDPPLPMEKLLATIKKLYKK
NSDPSLSNFIVTEATLTNPELRLTQQDLGSHTEITVEILDNLQNKEALSSA

CPn_0583   672349   672717
CT466 hypothetical protein
IVLSFFLGKTKVTPRFLMNERTLLLLLKKKKGLFLAILDLTQTESSLTTPELEKVLKQKK
IFLSCIDRVDLQIKEFRHAFSSELPQDIQEELEEIRDVIIRILDTDKRNYAQKKKEFGIY
ERP

CPn_0584   672659   673798
atoS/ntrB-2-Component Sensor
IRINATMHRKKRNLVFMNVPDSKNLHPPAYELLEIKARITQSYKEASAILTAIPDGILLL
SETGHFLICNSQAREILGIDENLEILNRSFTDVLPDTCLGFSIQEALESLKVPKTLRLSL
CKESKEVELFIRKNEISGYLFIQIRDRSDYKQLENAIERYKNIAELGKMTATLAHEIR
NPLSGIVGFASILKKEISSPRHQRMLSSIISGTRSLNNLVSSMLEYTKSQPLNLKIINLQ
DFFSSLIPLLSVSFPNCKFVREGAQPLFRSIDPDRMNSVVWNLVKNAVETGNSPITLTLH
TSGDISVPNPGTIPSEIMDKLFTPFFTTKREGNGLGLAEAQKIIRLHGGDIQLKTSDSAV
SFFIIIPELLAALPKERAAS

CPn_0585   675880   673865
*similarity to Cps IncA_2
ISLRRKILRPNNFSIGDCSSNMATPAQKSPTFQDPSFVRELGSNHPVFSPLTLEERGEMA
IARVQQCGWNHTIVKVSLIILALLTILGGGLLVGLLPAVPMFIGTGLIALGAVIFALALI
LCLYDSQGLPEELPPVPEPQQIQIEDLRNETREVLEGTLLEVLLKDRDAKDPAVPQVVVD
CEKRLGMLDRKLRREEEILYRSTAHLKDEERYEFLLELLEMRSLVADRLEFNRRSYERFV
QGIMTVRSEEGEKEISRLQDLISLQQQTVQDLRSRIDDEQKRCWTALQRINQSQKDIQRA
HDREASQRACEGTEMDCAERQQLEXDLRRQLKSMQEWIEMRGTIHQQEXAWRKQNAKLER
LQEDLRLTGIAFDEOSLFYREYKEKYLSQKLDMQKILQEVNAEKSEKACLESLVHDYEKQ
LEQKDANLKKAAAVWEEELGKQQQEDYEQTQEIRRLSTFILEYQDSLREAEKVEKDFQEL
QORYSRLQEEKQVKEKILEESMNHFADLFEKAQKENMAYKKKLADLEGAAAPTEIGEDDD
WVLTDSASLSQKKIRELVEENQELLKALAFKSNELTQLVADAVEAEKEISKLREHIEEQK
EGLRALDKMHAQAIKDCEAAQRKCCDLESLLSPVREDAGHRFELEVELQRLQEENAQLRA
EVERLEQEQFQG

CPn_0586   675993   677183
acoC/ntrC-2-Component Regulator
KEKMNPSRGENMAIKNILVVDDEPLLRDFLSELLTSQGFIPDTAENLRNALQMIRSRDYD
LVISDMSMPDGSGLDLIKIIKQSSPHTPVLVVTAYGSIENAVEAMHQGAFNYLTKPFSSE
ALFAFISKAEELKNLVHENLFLHSQTTPDSHPLIAESKAMKDLLAIAKKAASSSANIFIH
GESGCGKEVLSFFIHHNSPRANHPYIKVNCAAIPETLLESELFGHEKGAFTGATTKKAGR
FELAHKGTLLLDEITEVPVNLQAKLLRAIQEKEIEHLGGTKTLSVDVRILATSNRKLKEA
IDDKSFRQDLYYRLNVIPLHLPPLRDRQDDILPLANYFLNKFCRMNNTPLKTLSPKAQEL
LLNYPWPGNIRELSNVLERVVILENTSLLTEDMLALA

CPn_0587   677378   678124
*yvyD_Bs conserved hypothetical protein
SYGELFILSTLLKHHVTLCDKMRPHRKHVSSKSLALKQSASTHVEITTKAFRLSMPLKQL
ILEKSDHLPPMETIRVVLTSHKDKLGTEVHVVASHGKEILQTKVHNANPYLINVINAFKKI
RTMANKHSNKRKDRTKHDLGLAAKEERIAIQEEQEDRLSNEWLPVEGLDAWDSLKTLGYV
PASAKKKISKKKMSIRMLSQDEAIRQLESAAENFLIFLNEQEHKIQCIYKKHDGNYVLIE
PSLKPGFCI

CPn_0588   678033   678626
CT469 hypothetical protein
TSKSIKSNAFIKNMTATMSLLNLPSSGDSASEDSTSQSQIFDPIRNRELVSTPEEKVROR
LLSFLMHKLNYPKKLIIIEKELKTLFPLLMRKGTLIPKRRPDILIITPPTYTDAQGNTHN
LGDPKPLLLIECKALAVNQNALKQLLCYNYSIGATCIAMACKHSQVSALFNPKTQTLDFY
IGLPEYSQLLNYFISLNL

CPn_0589   678634   679395
CT470 hypothetical protein
...CMJLCVTKVVLR::RPLCKNITLTTLFTPEGLFTFFAKQQUTLQCDYRETLVP:ISLGKYT
IJHNVI.RLPKLTIKIDILNAFEAIKUT/ALLEA:XIKMIQALLA:QWKEKFSHKLFSLFLNF
IJIKIPE::NPEFFAAIFVLKLLQYES1LDLTPACSLCKA:SLPYACYRY\:HKLCKKHQHK
GALIIIERKEEEQILQAIIHAKQFSELLAIAEFPIAIAEKIFYLFD:SLQEEKK::ERNSSEDP
YHELLFIS:KVVHPY

CPn_0590   680136   679516
CT471 hypothetical protein

LFLYGDHNLGFACRYLFFFI...JGISFJNQLLTVP.WL:ERE:FFTTHPFFFKIYPDME
NMEIQAORKKRVEFILTGEFPKLETLHYQ:SFGHLRAKEROVYPVLYALNFGCSSCKMDH
DFRGKWNRSSTITISNQKESTRLKLPKOVLVIVNTKR:TLKGMVCPGIEFFUKO:HGVRRKI
YIHNDLVGFSEVTUIFNVSSEGT:TPS

CPn_0591   680364   681020
yagE family
GL.IMRCTAYCTAGA/RLHVLFHLLKPPYFTILSREYVLANLDSTQASNOLAIFFPFGVAV
...
HSDILDEPOFFWDHPETQAIYRDVLSCLCIEARINVLIV

CPn_0592   681132   681461
yidD family
LYSKMFSMSFKRFLQQIPVRICLL:IYLYQWLISPLLGSCCRFFPSCSHYAEQALKSHGF
LHGCWLSIKRIGKCGPWHPCGICMVPKTALQEVLEPYQEIDGGDSSHFSE

CPn_0593   682494   681391
CT474 hypothetical protein
VLGAKCMAFKRKTRWLHQVLILSVGLNMLFLLLFYSAIFRKDIYKLHLFSGPLIAKSSRK
VYLSEDFLNEISQASLDDLISLFKDERYHYGRPIKLWALSVA:ASHHIDTPVLSKPLTY
TELKGSSVRWLLPNIDLKDFPVILDYCRCHKYPYTSKGLFLLIEKMVQEGWVDEDCLYHF
CSTPEFLYLRTLLVGADVQASSVASLARHVIRCGSERFFHFCNEESRTSMISATQRQKVL
KSYLDCEESLAALLLLVHDSDVVLHEFCDEDLEKVIRLMPQESPYSQNFFSRLQHSPRRE
LACHSTQRVEAPRVQEDQDEEYVVQDGDSLWLIAKRFGIPMDKIIQKNGLNHHRLFPGKV.
LKLPAKQS

CPn_0594   682517   684958
pheT-phenylalanyl tRNA Synthetase Beta
NTCHYTQVIVKSLVKTSLRLSSMRIPITLLQTYFSEPLSTKEILEACDHIGIEAEIENTT
LYSFASVITAKILHTIPHPNADKLRVATLTDGEKEHQVVCGAPNCEAGLIVALALPGAKL
FDSEGQAYTIKKSKLRGVESQGMCCGADELGLDELQIQERALLELPEATPLGEDLATVLG
NTSLEISLTPNLGHCASFLGLAREICHVTQANLVIPKEFSFENLPTTALDMGNDPDICPF
FSYVVTGISAQPSPIKLQESLQALKOKPINAIVDITNYIMLSLGQPLHAYDASHVALDS
LRVEKLSTPESLTLLNGETVLLPSGVPVVRDDHSLLGLGGVMGAKAPSFQETTTTTVIKA
AYFLPEALRASQKLLPIPSESAYRFTRGIDPQNVVPALQAAIHYILEIFPEATISPIYSS
GEICRELKEVALRPKTLQRILGKSFSIEILSQKLQSLGFSTTPQETSLLVKVPSYRHDIN
EEIDLVEEICRTESWNIETQNPVSCYTPIYKLKRETAGFLANAGLQEFFTPDLLDPETVA
LTRKEKEEISLQGSKHTTVLRSSLLPGLLKSAATNLNRQAPSVQAFEIGTVYAKHGEQYQ
ETQTLAILLTEDGESRSWLPKPSLSFYSLKGWVERLLYHHHLSIDALTLESSALCEFHPY
QQGVLRIHKQSFATLGOVHPELAKKAQIKHPVFFAELNLDLLCKMLKKTTTKLYKPYAIYP
SSFRDLTLTVPEDIPANLLRQKLLHEGSKWLESVTIISIYQDKSLETRNKNVSLRLVFQD
YERTLSNQDIEEEYCRLVALLNELLTDTKGTINS

CPn_0595   684943   685926
CT476 hypothetical protein
RDYQFMKQLLTVCVFAMSCSAYSPRRQDPSVMKETFRNNYGIIVSGQEWVKRGSDGTI
TKVLKNGATLHEVYSGGLLHGEITLTFPHTTALDVVQIYDQGRLVSRKTFFVNGLPSQEE
LFNEDGTFVLTRWPDNNDSDTITKPYFIETTYQGHVIEGSYTSFNGKYSSSIHNGEGVRS
VFSSNNILLSEETFNEGVMVKYTTFYPNRDPESITHYQNGOPHGLRLTYLQGGIPNTIEE
WRYGFQDGTTIVFKNGCKTSEIAYVKGVKEGLELRYNEQEIVAEEVSWRNDFLHGERKIY
AGGIQKHEWYYRGRSVSKAKFERLNAAG

CPn_0596   685930   686457
ada-methyltransferase
FAVMADDTLIPKLMXNSLSQACSEGLLIAKYPPLQVIVHFDNNLVVKTHLSVAPVFSCLF
LGPAAHKAMQEIVLWCSRYANKEHPPFSSHFAKDLIPSOYLEILNCVAEIPFGEQQTYAE
IAKKTDTHPRTVGAACKQNPFLLFFPCHRVVGSHGERNYVLGPVIHEILLKFENSY

CPn_0597   688215   686479
oppC-Oligopeptide Permease
MQKHPSFYQRFLSAYVKNFFISVALIGIYAPLFASSKPLLVTWHGEIFFPLL
RYLFFPGYYTKPVDLFFNVLMVTFPFFILSFKLTRGWLRRWLLGLCIISQCMIFAWAYSG
KVQDPALAENLKKMRAEKVRENISKVNSEMVMLLPKDTRTWEMERRYMSTYEQLGILIKA
KYRKKQEASVKKYOVAFEEKRQSPMPTLRHLEMKNEGICLKRLQQRVDKMORPYEMAQQA
WNRATDNYRPFLMALTRIEHELRLADYNMWGOPEDLCIAYANVEKRAEPYKKSLLEIRQV
LEDYAKLRSAISFIQDKRLWIEKESEDLRILINPFFSSFHWEDDAGGSREMNKYVPWWQL
SRVTRKDLLAALVFGIRIALVVAGIGITIALAIGIMIGLVSGYFGGTVDMILSRFTEIWE
THPVLFILMLVISITQQKSLLLNTVLLGCFSWTGFSRYVRIEVLKQRDRGYVLAATNLGY
SHYYIMVHQILPNAIVPVISLVPFAMMAMISCEAGLTFLGLGEESSASWGNLMREGVTGF
PAESAVLWPPAIILTMLLIAIALIGDGVRDALDPRLQDS

CPn_0598   689712   688219
oppB-Oligopeptide Permease
EEGGSVLKYLKRLVLIPLTLFAIVSINFVILNAAPGDVLEEKSRDALGEAGKSDKMRSY
KGPDRYLQFREHYGLTLPIFFNTRPPKITHKKIQTALQELANANNTTPSAKNAAKSLVYWG
DCAKFVMPALLFEADDASRDDK'RHIAADLFIRGGVLQGFVGPNLSPEDRAQNKEIAESN
AFLVRQLNEEDLDTKVEALKGWFQDHGGTKVCFCYSSKOFWKTFFLETRFARYMSRVLRLD
FGTLRNDAHKTVISEVIKRLRCSLVLSILPMIVGFVLCQIFGMIMALKRNRWIDHSLNFI
FLILFSIPVFVAVWILDNFVINKTIPFTTIPHPYSGLRSPPEVFNELSTLCRIFDLVSH
GFLPFCAVSYGALAAQSRLSRSIFLEVLSQDFICAAKARGLRWFDILYKHVGKNAAVSIV
TSLASSLGTLLGGALVVETLFIIDGFGHFFYQAILNRDHHNVVLFSVLVGSALSLVGYLLG
DICYVLLDPRVQLEGRRI

CPn_0599   691823   689682
oppA-oligopeptide Binding Lipoprotein
KRRESGHMYKRCVLDKILKGYVAGSLILLLYWSSDLLERDIKSIKGNVRDIQEDIREISRV
VKQXX/TSQAIPAADGVMLAPKL/RDEAFALLFGDPSYPNLLSLDPYKQQTLPELLGTNFH
PHGILRTAHVCKPENLSPFNGFGYVVGFYDLCIPGLA:PHVGKYEEFSPDLAVKIEEHLV
EDGXXIDKEFHIYLRFNVFWRPILPKALPFHVQLDEVFORPHPVTAIIDIKFFYDAVMNPYV
ATMRAVALR:XYET/V:VVSVEHLCLKLVPWKAIHT/INEDTKEERKVLY::AFSNTLSLQPL
PRFVYGYFANGEKIIEDENIDT/PTN:THVMQNFTMHWANNY/IVX:XGAYYFACHDDEKIVF
SRNIUFYDFLAAL:IDGKFRKFVYFFE:TTDSLFQDFPFIKIDI:GYLDPNQRDNFYSFMKGSAYN
KQVAP/ZZAVRFTV:SADRAYTY:I?MK:FSLLFFCLPOVRCAMHMALGHRPRIIEKXLDXXYT
1GGPPAXCGSFYNKQIELXWHY:SPEFAAPIIEERDSWIDTIX/X:IREKVIDSVIVPPRFRLC
YYVKX77TANFTADYVATA:KEICTEX:IE:CLLFGIEMADLCQAFTAPHPDALLM3KT/GIPPED
PRALMIGE:AMKAGSANVVSFHHEADF!IDGL:XYEYDLKEPURLYHRFUEIHEFAPYA
FLFGRHICSLLYKDVVKNIFVFTHPTDLTIEA:GETVRNVTMVWLEKKEDIXTET:SI

CPn_0600   681150   681967   691827
No evident homolog present in GenBank/EMBL as of 11/7/98

HGYMKIKKGFQYSLCQAKRFQMMLPNHFDPCLOP. JLKQDRLAYGELIILLSKYQQKT
FGSLLKEETCGLNRAKQHLLYKILRDFHTMQHLRGLGLNGWGEIPMSPCL

CPn_0601   693092   692736
CT49J hypothetical protein
QFPRIHADDIINSMDEITPNYPLLRQDSLWHR'R'/SWRADLSVSSRYEIASAIAILGLLV
AFCASAAVSIIFTANPLAQVFIDCCLALGLLPIPLVIGLLIIGIIVLLYGIYLFPQQRE

_ . . . 602   64YuT   . . . 643104

DSGFMKPLGFQENLEALCNKTSRGLLKYLIKQILFVCGASLLIALEFSFFLYFFLFSGKT
VIPAFCLACFFLTLFVCLVTRLYLLSGKGDFFEDLASEYLQGAVPPNKRSQNIVEEQSHL
AAAATKLSINLQNQEYSLLSEIFKFLPKHDLIRKFSCFCFWKDYFLFRECLLQKAIEAYI
KVVQAIPVDLSAHVSLADAYVALSGLYADPRKYPEFDANYWIPSGRYSAEIQEKFFATAR
RAIEEFQILNEYAPGNAWVHAQLAYSYHDLQMPMEEIQEYEIVLKLKPNDVETHSKLGIL
YFQQGMNAKGLRIYEEIKKRDYKKSQKLIKFYGVEYKY

CPn_0603   694136   695185
hemZ-Ferrochetalase
WKIMRLIVLMQCLVSLFLAKKVTVTTPAYLLANFGGPRHAKDLQEFLISLLTDRDVTGTF
LPRVLHRHLFTFIAKKRVPKVLPQYQSLQMWSPIYFDTETLAKTLSEILRAPVIPFHRYL
PSTHEKTLLALRTLHTRHVIGIPLFPHFTYSVTGSIVRFFMKHVPEIPISWIPQFGSDSK
FVSLITCHIRDFLQKLGILEKECCFLFSVHGLPVRYISQGDPYSKQCYESFSAITTNFKQ
SENFLCFQSKFGPGKWLSPSTAQLCQNIDTDKPNVIVVPFGFISDHLETLYEIERDYLPL
LRSRGYRALRIPAIYSSPLWVSTLVDIVKENSTVVAEELIKSGKKHTGIR

CPn_0604   695981   695196
fliY-Glutamine Binding Protein
CKKRQNSEAQLNVKIKFSWKVNFLICLLAVGLIFFGCSRVKREVLVGRDATWFPKQFGIY
TSDTNAFLNDLVSEINYKENLNINIVNQDWVHLFENLDDKKTQGAFTSVLPTLEMLEHYQ
FSDPILLTGPYLLVCVNDSPYQSIEDLKGRLIGVYKFDSSVLVAQNIPDAVISLYQHVPIA
LEALTSNCYDALLAPVIEVTALIETAYKGRLKIISKPLNADGLRLAILKGTNGDLLEGFN
AGLVKTRRSGKYDAIKQRYRLP

CPn_0605   696737   696150
yhhF-Methylase
LRKLCSSRGDVRILAGKYKGKSLKTFSNPHIRPTSGLVKEAFFSICREDIEGAAFLDLFA
GMGAIGFEALSRGAASVVFVDISIKAIQLIHTNSALLGEQLPVVIFRQDAQSAIQRLIKQ
KRSFDLIYIDPPYELCNCYVETLLQKIVSGNILNPEGTLFLENASDEEIACEGLTLRRRR
KLGKTYLAEYIVEKDP

CPn_0606   697492   696707
CT488 hypothetical protein
SSYSRRQLRFYTGSLQMHIYGLADLHLALGVPEKTMEVFGDPWIGYHQKICSEXQAVVHP
EDIVLLPGDISWAMNLSEAHKDFAFIGDLPGTKYMIRGNHDYWSSASTSKILQALPPSLY
YLNQGFALLTPHLAVVGVRLWDSPTICVKKENFLTPSTQEQSYTEQDEKIFLRELGRLKR
AFAALPKEVTEVIVMTHYPPISSDGTPGPISEFLEADGRVSLCLFGHIHKVQRPIDGFGN
IRGIHYILVAADYVNFVPQEVM

CPn_0607   698910   697573
glgC-Glucose-1-P Adenyltransferase
NRRIQMIENDFPEASNFESSHFYRDKVGVIILCGGEGKRLSPLTNCRCKPTVSFGGRYKL
IDIPISHAISAGFSKIFVIGQYLTYTLQQHLFKTYFYHGVLQDQIHLLAPEARQGDQIWY
QGTADAIRKNLLYFEDTEIEYFLILSGDQLYNMDFRSIVDTAIRTHVDMVKAAYQNPIPEKD
AYRMGVLDIDSEGKLIDFYEKPQEKEVLKRFQLSSEDRRIHKLTEDSGDFLGSMGIYLFR
RDSLFSLLREEEGNDFGKHLIQAQMKRGQVQTLLYNGYWADIGTIESYYEANIALTKPH
AEKRGLNCYDDNGMIYSKNHHLPGAIITDSMISSSLLCEGCVINTSHVSRSVLGIRSKIG
ENSVVDQSIIMGNARYGPSPMPSLGIGKDCEIRKAIIDENCCIGNGVKLQNLKGYIKYDS
PDKKLFVRDNIIIVPQGTHIPDNYIF

CPn_0608   699690   699016
*Uridine 5'-Monophosphate Synthase (Ump Synthase)-truncated?
VSFLYFVKNGRRLHRMMNYEDAKLRGQAVAILYQIGAIKFGKHILASGEETPLYVDMRLV
ISSPEVLQTVATLIWRLRPSFNSSLLCGVPYTALTLATSISLKYNIPMVLRRKELQNVDP
SDAIKVEGLFTPGQTCLVINDMVSSGKSIIETAVALEENGLVVREALVFLDRRKEACQPL
GPQGIKVSSVFTVPTLIKALIAYGKLSSGDLTLANKISEILEIES

CPn_0609   699672   699986
CT490 hypothetical protein
QNTKNSLIRENMLIRLFLGISLPKGFPLYLEPPLVLATFQGTQFVGTYSEATNPLYIDNL
NLNYHYTQELLYKAVPCNYKSIYREIPLIIFPEVLIGSTPTQSTE

CPn_0610   701450   700029
rho-Transcription Termination Factor
RIFLRFKGSIMKEERSSEILPRVKETKKHAYVSMQEKSCVGECAVVASESEEAESVTVTK
IAKLQRMGIEELNILARQYGVKNIGSLTKSQVVFEIVKAKSERPDELLIGEGVLEVLPDG
FGFLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGDTIIGTIRSPKEKEKYFALLKVDKING
STPDKAKERVLFENLTPLYPNQRIVMEMGKDHLAERVLDLTAPIGKGQRGLIVAPPRSGK
TVILQSIAHAIAVNNPDIVLIVLLIDERPEEVTDMIRQVRGEVVASTFDEQPERNIQVAE
MVIEKAARLVEHGNDVVILLDSITRLARAYNTVQPHSGKILTGGVDASALHKPKRFFGAA
RNIEGGGSLTILATALIDTGSRMDEVIFEEFKGTGNMELVLDRRLSDRRTYPAIDLIKSG
TRKEELLYHPSELERVVYLFRQAIADLTTIDAMHLLLGRLKKTNSNAEFLLSLKE

CPn_0611   702133   701420
yacE-predicted phosphatase/kinase
RRNRRDAKTSEREDGISYDFIRSYSCEYLNWKKLGPMLKLLKVSITGDLSCGKTEACQVF
QELGAYVVCADEISHSFLIPHTRIGRRVIDLLGSDVVVDGAFDAQAIAAKVFYNSVLLQG
LEAILHPEVCRIIEEQYHQSIQDCGNYPLFVAEVPLLYEIHYAKWFDSVILVMANEDIRRE
RFMKKTGRSCEDFDQRCSRFLNVEEKLAQADVVVENNGTKKKELHQKIEEYFYALKGAL

CPn_0612   704688   702022
polA-DNA Polymerase I
RCHFTCLLCTVERFRREYAMKKLFVLDASCFIFRAYFALPEMKNHQGQATQAVFGFIRSL
HKLIKEFCPEYMLSVFDIPNNKQIRQAIYADYKSNPUKKFEDIPFQIALVKFYCSLIGLA
YLFYECVEALDDVIASIAKKAREENYKVVCTAVRHDLLQLVNDVVAWNFWADQGVIQGL
VIERVHIPFUNIPDYLALVDSSDNIFCLRCGPKKAAALLKQFCSVEGLLENLDAVKGL
JLTMLCERQETLKLLIKHLALLDSNIPIFVPIESLTFPQHPVDEEKLIHFYICQGFKTLVP
RKJTEAATVDVDIIKDAFCLTNILNLWAXXRDIAFAVAYYTGHILLCLKLEGLALTQCSCVF
PIALEEEITKILIILKOFFLREDLTFFVCVNLKRDCHALLNACIVIREICYGLALAEHLTN
+YYXICPQILLVNBKIFFTANHRFAKEWENSCLPICHRLPEQPRQYFCGEFVAYLPIIKDAIL
RFIHPFNIMHILLCDIFMPLEKVLFCMERAAVFLDVERLAILHLALFETELAVLTEEIYDLS

CRPFNIKSPPFCLSDILYHEL   PIDKAKJTPAEYLEALRJEHFIIEKLLAFRTIEKLLS
TYVKALPKOVDSHTORIHPCFDCTGAVTURLACRDFNLSNFFPCERGICLLRKAFRLSEK
NSYFLGADYSQIEERRCAHCSODKILARAFECGECGHARIAJCVTLIIDYLFCGVSREOROCA
KTVNFGIVVYGQQAFCGEAKVIKISICEACEICAYFSRYPEIAHFVEETFICQAAKDLAVTT
HLGRERIIDSWNEFPGSRAASGRFAVNTRIQYSAAELIKLAMLDSQAIKQQOMKSRMLL
QIHDELLFEVPEEEIEEMQRLVREKMESAMTLSVPIVVNILIGKHWAEC

CPn_0613   705662   704653

VVMKTISEREFFAPIANFPTFELCREGSRTMERDVNSTRNVTRNDKIUDHTIAAHYCKLIR
KTAPIIAVIEMKDVIASSKNTAKTIUNILEUFEKAPLKDHVKGIVIDMDCPGGEVFEIDR
IYSMLRFWKERKGFPIYIYVNGLCASCGYVVSCAATKIYATSSSLICSIGVRSGPFFNVK
EGLNRYGVESDLLTACKDKAPHNPYTPWTSHDREERQATLDFLYCQFVDIVTQNRPLLTX
EKLVHTLGARIFSPEKAKQEQYIDVVGATKEQVLQDIVAVCKIEDNYRVIGSCGDGHWKR
VASAAASSPLVTGMIKHDILPLSHDAAYIPPYLAL

CPn_0614   707435   705793
adc-ADP/ATP Translocase
VFIRHKVGKEFMOSSEVKVPFSRLRAYLCPIYKSEFSKFVPLFLLAFFVGFNYCLLKNMKD
TLVIVGSDAGAEVIPFLKVWGIVPGAVIVTMVYGWLGSRYPRDTVFYCFHAAFLGFFFLF
AVIIYPVGDSLHLNSLADKLQELLPOGLRGFIVMVRYWSYSIYYVMSELWSSVVLSHLFW
GLANQITTITEAGRFYALINTGLNLSSICAGEISYWMGKQTFVAYSFACDSWHSVMLNLT
MLITCSGLIMIWLYRRIHHLTIDTSIPPSRRVLAEEGAATANLKEKKKPKAKARNLFLHL
IQSRYLLGLAIIVLSYNLVIHLFEVVWKDQVSQIYSSHVEFNGYMSRITTLIGVVSVLAA
VLLTGQCIRKWGWTVGALVTPLVMLVSGLLFFGTIFAAKRDSIFGGVLQMTPLALAAWT
GGMQNVLSRGTKFTFFDQTKEMAFIPLSPEDKNHGKAAIDGVVSRIGKSGGSLIYQGLLV
IFSSVAASLNVIALVLLIIMVVWIAVVAYIGKEYYSRAADAVATLKQPKEPSSSIVREAQ
ESVEQEEMAVL

CPn_0615   708149   707634
pgsA-Glycerol-3-P Phosphatidyltransferase
LAKIMRQFCNLLSLSRLMLALYFCQEKLHIRLLAIVGAMLSDVLDGYLARRYKATSRLGS
ILDPITDKVFVFVCITVLYMEGSLSIAHLFFICARDLFLIIFVCYLSLVKGWKGYDYGSL
FWGKIFTVVQFIILLGVTAGGEIPWTGLVPLVALGFLYFLERIHDYKKQFLR

CPn_0616   708704   710137
dnaB-Replicative DNA Helicase
TLTNYESSLLMDKSTGVPLPSPPHSKESEMIVLGCMLTGVHYLNLAANQLYEEDFYYLEH
KIIFRVLQDAFKQDKPIDVHLAGEELKRHNQITVIGGPSYLITLAEFAGTAAYLEEYVDI
IRSKSILRKMISTAKEIEKRALEQPKNVAEALDEAQNSFRKISQSTSVSQYTLVADKLRG
LTTTTDKPYLVLQLQERQELFLQNAQGDNKSFFTGIPTHFIDLDQLIHGFSPSNLMILAAR
PAMGKTALALNIAENLCFQNRLPIGIFSLEMTVDQLIHRMICSRSEVDSKKISIGDLSGH
DFQRIVSVINEMQEHTLLIDDQPGLKVSDLRARARRMKESYDIQFLIIDYLQLLSGSGTL
RATESRQTEISEISRMLKTLARELNIPILCLSQLSRKVEDRANHRPMMSDLRESGSIEQD
SDLVMFLLRREYYDPNDKPGTAELIIAKNRHGSIGSVPLVFEKELARFRNYSAFECIS

CPn_0617   710481   712316
gidA-FAD-dependent oxidoreductase
LMWTHPIAYDVIVVGAGHAGCEAAYCSAKMGVSVLMLTSNLDTIAKLSCNPAVGGIGKGH
IVREIDALGGIMAEVTDQSGIQFRILNQTKGPAVRAPRAQVDKQLYHIHMKRLLENTPGL
HIMQATVESLLDKEGVISGVTTKEGWMFSGKTVVLSSGTFHRGLIHIGDRNFSGGRLGDP
SSQGLSEDLKKRGFPISRLKTGTPPRLLASSINFSCMEEQPGDLGVGFVHRTEPFQPPLP
QLSCFITHTMKTKAIISANLHRSALYGGCIEGVGPRYCPSIEDKIVKFSDKERHHVFLE
PEGLHTQEIYANGLSTSMHPFDVQYDMIRSVLGLENAIITRPAYAIEYDYIHGNVIHPTLE
SKLIEGLFLCGQINGTTGYEEAAAQGLIAGINAVNKVFNRPPFIPSRQESYIGVMLDDLT
TQILDEPYRMFTGRAEHRLLLRQDNACARLSHYGYELGLLSEERYELVKKQNQLLEEEKV
RLQKTFROYGQSVVSLAKALSRPEVSYDMLREAFPNDIRDLGAVLNASLEMEIKYSGYID
RQKILIQSLEKAESLLIPEDLDYKQITALSLEAQEKLAKFTPRTLGSASRISGIASADIQ
VLMIALKKHAHH

CPn_0618   712300   713010
lplA-Lipoate-Protein Ligase A
KNMPTTNCIFLDLRGHSILHQLQIEEALLRVANQNFCIINSGAKDSIVLGISRNLNQDVH
ISRAQADHIPIIRRYSGGGTVFIDSNTLMVSWIMNSSEASAQPOELLAWTYGIYSPLLPN
TFSIRENDYVLGHKKIIGGNAQYIQRHRWVHHTTFLWDIDLDKLSYYLPIPQQQPTYRNQR
SHEEFLTTLRPWFPSRDDFLERIKASGSLLFTWEEFLDNELEEIILAQPHRKATTVLN

CPn_0619   713462   713013
ndk-Nucleoside-2-P Kinase
RRYVYTMEQTLSIIKPDSVSKAHIGEILSIFEQSGLRIAAMKMMHLSQTEAEGFYFVHRE
RPFFQELVDFHVSGPVVVLVLEGANAVSRNRELMGATNPAEAASGTIRAKFGESIGVNAV
HGSDTLENAAVEIAYFFSKIEVVNASKPLV —

CPn_0620   714145   713519
ruvA-Holliday Junction Helicase
DKMYDYIRGTLTYVHTGAIVIECQGICYHIAITERWAIECIRALHQDFLVFTHVIFRETE
HLLYGFHSREERECFRILISFSCIGPKLALAILNALPLKVLCSVVRSEDIRALASVSGIG
KKTAEKLMVELKQKLPDLLFLDSRVETSQTHTTSSCLEEGIQALAALGYSKIAAERMIAE
AIKDLPEGSSLTDILPIALKKNFSGVNKD

CPn_0621   714707   714144
ruvC-Crossover Junction Endonuclease
LSRLGSSFKDNKFKVFQESIVSELIIGVDPCTIVAGYAIIAVEQRYQLRPSYGAIRLSS
DMPLPMRYKTLFEQLSGVLDDTOPNAMVLETQFVNKNPQSTMKLAMARGIVLLAAAQRDI
LIFEYAPNVAKKAVVGKGHASKRQVQVMVSKILNVPEVLHPSNEDIADAFALAICHTHVA
RSPLCGVR

CPn_0622   715761   714791
CT494 hypothetical protein
RYCSVPLLSILKLHLFSLRSSSCLSHHFYCHSCSRCMLHILLCRWKDADIHEWQQICNILSGV
CSPMCFIKLVSLQFETQDSAINEHERIHLQYREQLCALEEEYRRREEAKHQDLEKLQQENT
WLJAIRLAEKLXUFRIRQSDIIDEIFKKELLQCVVRTEICEFERPLCYEHIKIKQLEEQLQRYVS
QHFAISIIEIEEDKSCAAYAEINPLKKCLIDLAQEKDIYIKTYIISEIAKLREKLQRQECAQ
TCCISVCIIEKLFIVQTDLAEKKFYATALLQDIVEDYCCLPFDLIHKEKCHAMPCNTKLDHLK
HLUIFEFESEVIAVVFSESKSIIJ

CPn_0623   717011   716164
CT404 hypothetical protein
IFCFHIYVIFTRDIVIFFVFITLFFFYFKLCVRNTKHFCQDPFMVPALEVICLCRNIFFRNCD
HLIYEFLVTACYEFMFVROTHIHLKAFIJLBSVKIAVJHREALIKLTFCSTPLFVIDEKPLA
IZDEFFTFCFCSFCKKEKHFEARFLCFFVCEKWKERKFFLCPRPFHIIKEIAFYTYACUOEILOTVK

FEELWEEKQRNEIVEQKKFFLLPPPAKLISEVISO. .JPVVTSADLNESLQALVRESSDL
INALLSADDAIHFPETEEEPTSASFEESSAMFFPETSSATEEE

CPn_0624   718018   717011
gapA-Glyceraldehyde-3-P Dehydrogenase
AMKVVINGFGRIGRLVLRQILKRNGSVEVLAINDLVPGDALTYLFKFDSTHGRFPEDVRC
EADHLIVGKRKIQFLSERNVQNLPWKDLGVDLIVECTGLFTKKEDAEKHIQAGAKRVLIS
APGKGDIPTFVVCANHKTFNPEKDFVIGNASCTTNCLAPIAKVLLDNFGITEGLMTTVHA
...........FFIWRYDIPVSLSLIIAACDWAVZAVTOLICISLFVFVLTTMAFRVEIDCT
..........FRULIVTTTVELIDVPFEAMPVUSIFLSILVTTOENVVCVGGRFVEFCSTFDALAS
IALNDRFFKLVAWYDNETGYATRIVDLLEYVEKNSK

CPn_0625   718488   718060
rl17-L17 Ribosomal Protein
VMQHARKKFRVGRTSSHNRCMLANMLKSLIHYERIETTLPKAKELRRHADKMITLAKKNS
LAARRIAIGRLMVRYNKLTSKEARQAKGGDTSVYNVDRLVVNKLFDELGNRFVERKGGYT
RILKLQNRIGDNAQKCIIEFLAS

CPn_0626   719670   718495
rpoA-RNA Polymerase Alpha
WLPAKKKAQSVVLGKEKGMSDNAHNLLYDKFELPEAVKMLPVEGLPIDKHARFIAEPLER
GMGHTLGNALRRALLIGLEAPAIISFAMTGVLHEYMAIEGVIEDVTNIILNLKGALLKKY
PHQDSSLGRTTOVLKASISIDASDLAAANGQKEVTLQDLLQEGDFEAVNPDQVIFTVTQP
IQLEVVLRIAFGRGYTPSERIVLEDKGVYEIVLDAAFSPVTLVNYFVEDTRVGQDTDFDR
LVLIVETDGRVTPKEALAFSTQILTKHFSIFENMDEKKIVFEEAISIEKENKDDILHKLI
LGINEIELSVRSTNCLSNANIETIGELVIMPEPRLLQFRNFGKKSLCEIKNKLKEMKLEL
GMDLTQFGVGLDNVKEKMKWYAEKIRAKNTKG

CPn_0627   720059   719640
rs11-S11 Ribosomal Protein
FLIRSRVLVKNQAQAKKSVKRKQLKNIPSGVVHVKATFNNTIVSITDPAGNVISWASAGK
VGYSGSRKSSAFAATVAAQDAAKTAMNSGLKEVEVCLKGTGAGRESAVRALISAGLVVSV
IRDETPVPHNGCRPRKRRRV

CPn_0628   720461   720063
rs13-S13 Ribosomal Protein
DAYTILREAQRMPRIIGIDIPAKKKKLKISLTYIYGIGSARSDEIIKKLKLKLDPEARASELT
EEEVGRLNSLLQSEYTVEGDLRRRVQSDIKRLIAIHSYRGQRHRLSLPVRGQRTKTNSRT
RKGKRKTVAGKKK

CPn_0629   721881   720487
secY-Translocase
KIRLFRPYMTTLRQFFLITELRQKLFYTFALLTACRVGVFIPVPGINGELAVAYFKQLLG
SGQNLFQLADIFSGGAFAQMTVIALGVVPYISASIIVQLFLVFMPALQREMRESSDQGKR
RIGRLTRLFTVALAVIQSLLFAKFALRMNLTIPGIVLPTLLSSKLFGVPWIFYITTVVVH
TTGTLLLMWIGEQISDKGIGNGISLIIALGILSSFPSVLGSIVNKLNLGSQODSSDLGLIS
ILILALVFVFVLITTILIIEGVRKIPVQYARRVIGRREVPGGGSYLPLKVNYAGVIPVIF
ASSLLMFPATIGQFIASESSWMKRIAALLAPGSLVYSICYVLLIIFFTYFWTATQFHPEQ
IASEMKKNNAFIPGIRQGKPTQHYLEYTMNRVTLLGALFLAAIAILPSLLGCLLRVDSNV
SYFLGGTAMLIVVGVVLDTMKQVDAFLLMRRYDSVLKTDRTKGRH

CPn_0630   722316   721885
rl15-L15 Ribosomal Protein
HIKLESLFDISERKRRKKLLGRGPSSGHGKTSGRGHKGDGSRSGYKRRFGYEGGGVPLYR
RVPTRGFSHKRFDKCVEEITTGRLAELFQEGEAITLDALKAKKAIARQAVRVKVILKGDL
EKTFVWQDTAVVLSQGVQNLLGIT

CPn_0631   722812   722312
rs5-S5 Ribosomal Protein
EEMSLSKNSHKEDQLEEKVLVVNRCSKVVKGGRKFSFSALILVGDGKGRLGYGFAKANEL
TDAIRKGGEAAKKNLMKIEALEDGSIPHEVLVHHDGAQLLLKPAKPGTGIVAGSRIRLIL
EMAGIKDIVAKSFGSNNPMNQVKAAFKALTGLSPRKDLLRRGAAIND

CPn_0632   723354   722827
rl18-L18 Ribosomal Protein
KGLISSWLVNLLQVFAPNVLLNLIKVREFVMKMNMSVVKLVKLRKQAKNRSRVMESSLCK
KSLMKRRALRVRKVLKGSPTKPRLSVVKTNKHIYVQLIDDSIGKTLASVSTLSKLNKSQ
GLTKKNQEVAKVLGTQIAELGKNLQLDRVVFDRGPFKYHGIVSMVADGAREGGLQF

CPn_0633   723760   723209
rl6-L6 Ribosomal Protein
SMSRKAREPILLPQGVEVSIGDDKIIVKGPKGSLTQKSVKEVEITLKDNSIFVHAAPHVV
DRPSCMQGLYWALISNMVQGVHLGFEKRLEMIGVGFRASVQGAFLDLSIGVSHPTKIPIP
STLQVSVEKNTLISVKGLDKQLVGEFAASIRAKRPPEPYKGKGIRYENEYVRRKAGKAAK
TGKK

CPn_0634   724215   723787
rsH-S8 Ribosomal Protein
ESSIKRKRIYMGMTSDSIADLLTRIRNNALMAEHLYVDVEHSKMREAIVKILKHKGFVAHY
LVKEENRKRAMRVFLQYSDDRKPVIHQLKRVSKPSRRVYVSAAKIPYVFGNMGISVLSTS
QGVMEGSLARSKNIGGELLCLVW

CPn_0635   724763   724206
rl5-L5 Ribosomal Protein
GERKANMSRLKKFYTEEIRKSLFEKFGYANKMQIPVLKKIVLSMGLAEAAKDKNLFQAHL
EELTMISCQKPLVTKARNSIAGFKLRECQGIGAKVTLRGIRMYDFMDRFCNIVSPRIRDF
PGFSNKGDGRCCYSVGLDDQQIFPEINLDRVKRTQCLNITWVTTAQTDDECTTLLELMGL
RFKKAQ

CPn_0636   725100   724750
rl24-L24 Ribosomal Protein
FKEKEVMKKQNIRVGDKVFIILACNDKGKEGKVLSLTEDKVVVEIVNVRIKNIKRSQQNPK
GVRGISIEAPIIIISNVRLTIACIEPAKLSVKVTEQGRELWQRRPFITSQLYRLVRGKKG

CPn_0637   725473   725099
rl14-L14 Ribosomal Protein
IEIMLQUEQOLKVATATNOAKKVKCFKVLGCGRRRYATVGDVIVGNVRDVEFREGIKKGDV
IYAVIVKTHRHIITPKDSGTLKFDTNSIVIIDDKGNDPKGTRLIPGIPVARELRDRGFIKISSL
AIFVI

CPn_0638   725773   725490

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rs17-S17 Ribosomal Protein
NKKEKVKSHASEPPGGRKVKIGVVVSAKMEKTVVVRVERIFGHPQYLKVVRSGKKYYAHT
ELKVSEGDKVKICETRPLSELKRWRVIERVGVVSI

CPn_0639   725979   725743
rl29-L29 Ribosomal Protein
ASGKGINMAAKKDLLTQLRGKSDDDLDAYVHENKKALFALRAENLLQNKVVKVHMFSTHK
KNIARALTVKQEPYGKVHG

rl16-L16 Ribosomal Protein
IIHLMPKRTKFRKQQKGQFAGLSKGATFVDFGEYAMQTLERGWVTSRQIEACRVAINRYL
KRRGKVWIRIFPDKSVTKKPAETRMGKGKGAPDHWVAVVRPGRILFEVANVSKEDAQDAL
RRAAAKLGIKTRFVKRVERV

CPn_0641   727092   726409
rs3-S3 Ribosomal Protein
KGRRIMGQKGCPIGFRTGVTKRWRSLWYGNKQEFGKFLIEDVRIRQFLRKKPSCQGAAGF
VVRRMSGKIEVTIQTARPGLVIGKKGAEVDLLKEELRALTGKEVWLEIAEIKRPELNAKL
VADNIARQIERRVSFRRAMKKAMQSVMDAGAVGVKIQVSGRLAGAEIARSEWYKNGRVPL
HTLRADIDYATACAETTYGIIGIKVWINLGENSSSTTPNNPAAPSAAA

CPn_0642   727440   727096
rl22-L22 Ribosomal Protein
RRHSMFKATARYIRVQPRKARLAAGLMRNLSVQEAEEQLGFSQLKAGRCLKKVLNSAVAN
AELHENIKRENLSVTEVRVDAGPVYKRSKSKSRCGRSPILKRTSHLTVIVGEKER

CPn_0643   727725   727450
rs19-S19 Ribosomal Protein
EIRIMGRSLRKGPFVDHHLLKKVRAMNIEEKKTPIKTWSRRSMITPEMIGHTFEVHNGKK
FLTVFVSETMVGHKLGEFSPTRIFKSHPVKKG

CPn_0644   728594   727722
rl2-L2 Ribosomal Protein
FIREINSMFKKFKPVTPGTRQLVLPAFDELTTRGELRGTKSKRSLRPNKKLSFFKKSSGG
RDNLGHISCRHRGGGAKQLYRVVDFKRNKDGITAKVVTVEYDPNRSAYIALLSYEDGEKR
YILAPKGIQRGDVVVSGEGSPFKPGCCMTLKSIPLGLSVHNIEMRPSSGGKLVRSAGLAA
QVIARSPGYVTLKMPSGEFRMLNEGCRATIGEVSNADHNLRVDGKAGRRRMGVRPTVRG
TAMNPVDHPHGGGEGRHNGYIPRTPWGKVTKGLKTRDKNKSNKWIVKDRRK

CPn_0645   728933   728598
rl23-L23 Ribosomal Protein
DMKDPYDVIKRHYVTEKAKMLEHLSAGTGEGKKKGSFCKDPKFVFIVSHDATKPLIAQAL
EAIYVDKNVKVKSVNTINVKPQPARMFRGRRRGKTSGFKKAIVTFYQGHSVG

CPn_0646   729636   728950
rl4-L4 Ribosomal Protein
YREDLMVLLSKFDTSGNKIGEVEVADSLFADEGDGLQLIKDYIVAIRANKRQWSACTRNR
SEVSHSTKKPFKQKGTGNARQGCLASPQFRGGGIVFGPKPKFNQHVRINRKERKAAIRLL
LAQKIQTNKLTVVDDTVFVDALTAPKTQSALRFLKDCNVECRSILFIDHLDHVEKNENLR
LSLRNLTAVKGFVYGININGYDLASAHNIVISKKALQELVERLVSETKD

CPn_0647   730490   729657
rl3-L3 Ribosomal Protein
YLEYFSYCKNLPPLITCPFIFLRENFLFFLENSISKILSRFVSLFLQEESKSLLLMDKFM
RSHISVMGKKEGHIHIFDKDGSLVACSVIRVEPNVVTQIKTKESDGYFSLQIGAEEMNAP
AHTITTKRVSKPKLGHLRKAGGRVFRFLKEVRGSEEALNGVSLGDAFGLEVFEDVSSVDVR
GISKGKGFQGVMKKFGFRGGPGSHGSGFHRHAGSIGMRSTPGRCFPGSKRPSHMGAENVT
VKNLEVIKVDLEKKVLLVKGAIPGARGSIVIVKHSSRT

CPn_0648   731636   730605
CT529 hypothetical protein
FFFKKPCKEVKMATNAIRSAGSAASKMLLPVAKEPAAVSSFAQKGIYCIQQFFTNPGNKL
AKFVGATKSLDKCFKLSKAVSDCVVGSLEEAGCTGDALTSARNAQGMLKTTREVVALANV
LNGAVPSIVNSTORCYQYTRQAFELGSKTKERKTPGEYSKMLLTRGDYLLAASREACTAV
GATTYSSATLVNLLQVFAPNVLINKLTAKPFLDKATVGNFGTAVAGIMTINHMAGVAGAVGGIAL
EQKLFKRAKESLYNERCALENQQSQLSGDVILSAERALRKEHVATLKRNVLTLLEKALEL
VVDGVKLIPLPITVACSAAISGALTAASAGIGLYSIWQKTKSGK

CPn_0649   732672   731710
fmt-Methionyl tRNA Formyltransferase
LNLKVVYFGTPTFAATVLQDLLHHKIQITAVVTRVDKPQKRSAQLIPSPVKTIALTHGLP
LLQPSKASDPQFIEELRAFNADVFIVVAYGAILRQIVLDIPRYGCYNLHAGLLPAYRGAA
PIQRCIMEGATESGNTVIRMDAGMDTGDMANITRVPIGPDMTSGELADALASQGAEVLIK
TLQQIESGQLQLVSQDAALATIAPKLSKEEGQVPWDKPAKEAYAHIRGVTPAPGAWTLFS
FSEKAPKRLMIRKASLLAEAGRYGAPGTVVVTDRQELAIACSEGAICLHEVQVEGKGSTN
SKSFLNGYPAKKLKIVFTLNN

CPn_0650   733513   732665
lpxA-Acyl-Carrier UDP-GlcNAc O-Acyltransferase
SRRNMASIHPTAIIEPGAKIGKDVVIEPYVVIKATVTLCDNVVVKSYAYIDGNTTIGKGT
TIWPSAMIGNKPQCLKYQGEKTYVTIGENCEIREFAIITSSTFEGTTVSIGNNCLIMPWA
HVAHNCTIGNNVTLSNHAQLAGHVQVGDYAILQGHVGVHQFVRIGAHAMVGALSGIRRDV
PPYTIGSGNPYQLAGINKVGLQRRQVPFATRLALIKAFKKIYRADGCFFESLEETLEEYC
DIPEVKNFIEFCQSPSKRGIERSIDKQALEEESADKEGVLIES

CPn_0651   733975   733517
fabZ-Myristoyl-Acyl Carrier Dehydratase
MNQPSVIKLRELLDLLPHRYPFLLVDKVLSYDIEARSITAQKNVTINEPFFMGHFPNAPI
MPGVLILEALAQAAJVLICLVLENDRNKRIALFLGIQKAKFRQAVRFGDVLTLQADFSLI
GGKVVIKAWAQARVTVSQLVTEAELSFALVDKESI

CPn_0652   734880   733990
lpxC-Myristoyl GlcNAc Deacetylase
KKNGIIYGGDLAVFYMLERTQRTLKREVRYGFVGIHUGKGSTLHLQPACTNTVIVFQRQG
AGCGDNVFVRLIGVAGICEVEDKVGIARLTPPVYYQHGQIFLAAFPGDELKISYTLHYPQ
GGTTITQYKSLVINEECFRQEIAGCRTFALVHELCFLHEKGLIGGGCLLDNAVVVFKDIGII
SRVJLRFADEIVRHKILGLGIDLGIVGRPFVAHVLAVGGGHSSNIAFGKKILEALEL

CPn_0653   734549   734868

curE-ApolLipoprotein N-Acetyltranst...ase
GEPVLRIFCFVIGWCLIAFAQPDLSGFVSILGAACGYGFFWYSLEPLKKPSLPLRTLFVS
CFFWIFTIEGIHFGWMLSDQYIGKLIYLVWLTLITILSVLFSGFSCLLVAIVROKRTAFL
WSLPGVWVAIGMLRFYGIFSGMSFDYLGWPMTASAYGRQFGGFLGWAGQSFAVIAVNMSF
YCLLLKKPHAKMLWVLTLLLPYTFGAIHYEYLKHAFQQDKRALRVAVVQPAHPPIRPKLK
SPIVVWEQLLQLVGPIQQPIDLLIFPEVVVPFGKHRQVYPYESCAHLLSSFAPLPEGKAF
LSNSDCATALSQHFQCPVIIGLERWVKKENVLYWYNSAEVISHKGISVGYDKRILVPGGE
...VFIKFTCLICPQLPPCYALGCKRLPGRRGTYCVRGLPRIGITCYEETFGYRLQSYK
...GARLLICPPLRIFCWLEGSGFVIFLPMLPLPP IMY VMAMCTTCAAWVLGURTLR
...LYDTRETKAILGIVLLTLGLLFNYKTLGRTGIGTTNILIAPCAVGYGGGIFLGYRLLAK
KEIR

CPn_0654   737051   736503
vdlD/yciA-acyl-CoA Thioesterase
KKIIDFLSVDRYYRNQEYPIKILSVESTMLKKKPVSFSCIDGHIYKIFPNDLNANNTVFG
GLLMSLLDRLALVVAERHTESVCVTAFVDALRFYAPAYMGENLICKAAVNRTWRTSLEVG
VKVWAENIYKQERRHITSAYFTFVAVNEDNQPIPVHQIVPETPEEKRRYNEADRRRQARL
ELK

CPn_0655   737856   737101
dnaQ-DNA Pol III Epsilon Chain
KEIMSLLKDTVFTCLDCEMTGLDVKKDRIIEIAAVRFTFDSVISSIEFLINPERVVSAES
QRVHHISNAMLRDQPKIAEVFPQIKAFFKEGDYIVGHSVGFDLQVLAQEMERIGETFLSK
YTIIDTLRLAKEYGDSPNNSLESLAVHFNVPYDGNHRAMKDVEININIFKHLCKRFRTLE
QLKQVLAKPIKMKYMPLGKHKGRCFSEIPLAYLQWASKMDFDSDLLFSIRHEIKHROKGT
GFSQVNNPFMEL

CPn_0656   737842   738048
No robust homolog present in Genebank/EMBL as of 11/7/98
THNFLLLPLSLFDILLTVEGFLCLTLYFASVQRMPCEQKRVPGNLYYYYIAAHSSLCLSV
CKDTMENKD

CPn_0657   738476   738051
yjeE (ATPase or Kinase)
PMGRYRRVSHSSQETLLLGTELGQVLVPGAVLLLFGDYGAGKTEFVRGIVSGYLGDTIAE
EVASPSFSILHVYGNEPKRLCHYDLYRIDQKNQEYIFQDAEEDDVLCIEWADRLPKPRFC
DTINIYITMQTNMEREIIIEKR

CPn_0658   739180   738455
CT538 hypothetical protein
KRVGMDISGAVKQKLLQFLGKQKKPELLATYLFYLEQALSLRPVVFVRDKIIFKTPEDAV
RILEQDKKIWRETEIOISSEKPQVNENTKRIYICPFTGKVFADNVYANPQDAIYDWLSSC
PQNMEKQGGVRIKRFLVSEDPDVIKEYAVPPKEPIIKTVFASAITGKLFHSLPPLLEDFI
SSYLRPMTLEEVQNQTKFQLESSFLSLLQDALVEDKIAAFIESLADDTAFHVYISQWVDT
EE

CPn_0659   739482   739838
trxA-Thioredoxin
LQENNRDSNSIFREGKLMVKIISSENFDSFIASGLVLVDFFAEWCGPCRMLTPILENLAA
ELPHVTIGKINIDENSKPAETYEVSSIPTLILFKDGNEVARVVGLKDKEFLTNLINKHA

CPn_0660   740327   739860
spoU-rRNA Methylase
MRVVLHCPDIPQNTGNIGRTCVALGAELILVRPLGFSLADKFVKRAGMDYWDKLQLTVVD
SIEEALHDVPEDQIFCLSTKGSASYTEFSLPSSGTYVFGSESKGLPKEILKKYYKNCLRI
PMQQDIRSLNLATSVGIVLYEVVRQKTVALQKNPTV

CPn_0661   741139   740327
mip-FKBP-type peptidyl-prolyl cis-trans isomerase
HSRCLKIKDRRRKMNRRWNLVLATVALALSVASCDVRSKDKDQGSLVEYKDNKDTNDI
ELSDNQKLSRTFGHLLARQLRKSEDMFFDIAEVAKGLQAELVCKSAPLTETEYEEKMAEV
QKLVFEKKSKENLSLAEKFLKENSKNAGVVEVOPSKLQYKIIKEGAGKAISGKPSALLHY
KGSFINGQVFSSSEGNNEPILLPLGQTIPGFALGMQGMKEGETRVLYIHPDLAYGTAGQL
PPNSLLIFEINLIQASADEVAAVPOEGNQGE

CPn_0662   742938   741172
aspS-Aspartyl tRNA Synthetase
SKGCYMKYRTHRCNELTSNHIGENVQLAGWVHRYRNHGGVVFIDLRDRFGITQIVCREDE
QPELHQRLDAVRSEWVLSVRGKVCPRLAGMENPNLATGHIEVEVASFEVLSKSQNLPFSI
ADDHINVNEELRLEYRYLDHRRGDIIEKLLCRHQVMLACRNFMDAQGFTETVTPVLGKST
PEGARDYLVPSRIYPGKFYALPQSPQLFKQLLMVGGLDRYFQIATCFRDEDLRADRQPEF
AQIDIEMSFGDTQDLLPIIEQLVATLFATQGIEIPLPLAKMTYQEAKDSYGTDKPDLRFD
LKLKDCRDYAKRSSFSIFLDQLAHGGTIKGFCVPGGATMSRKQLDGYTEFVKRYGAMGLV
WIKNQEGKVASNIAKFMDEEVFHELFAYFDAKDQDILLLIAAPESVANOSLDHLRRLIAK
ERELYSDNOYNFVWITDFPLFSLEDGKIVAEHHPFTAPLEEDIPLLETDPLAVRSSSYDL
VLNGYEIASGSQRIHNPDLQSQIFTILKISPESIQEKFGFFIKALSFGTPPHLGIALGLD
RLVMVLTAAESIREVIAFPKTQKASDLMMNAPSEIMSSQLKELSIKVAF

CPn_0663   744220   742901
hisS-Histidyl tRNA Synthetase
KSNHFERRHHVTVTLPKGVFDIFPYLADAKQLWRHTSLWHSVEKAIHTVCMLYGFCEIRT
PIFEKSEVFLHVGEESDVVKKEVSIFLDRKGRSHTLRPEGTAAVVRSFLEHGASHRSDNK
FYCILPMFRYERQOAGRYRQHHQFGVEAIGVHRPLRDAEVLLFIGLDYYSDLVFEATTTPVLGKNH
NFLCGSETRFRYDKVLRAYLKESMGELSALSQQRFSTNVLRILDSKEPEDOEIIRQAPPI
LQYVSDEDLKYFNEILDALRVLEIPYAINPRLVRGLDYYSDLVFEATTTFQEVSYALGGG
GRYDGLICAFCGASLPACCFGVGLERAIQTLLAQKRIEPQFPHKLRLIPMEPDADQFCLE
WCQHLRRLIIIPTEVDWSHKKVKGALKAASTEQVSFYCLIGERELISCQLVIKNMSLRKEF
FYTKEEVEQRLLYEIQNTFL

CPn_0664   744775   744557
No robust homolog present in Genebank/EMBL as of 11/7/98
LWFAHAMKKLIALIGIFLVPIKGNTNKEHDAHATVLYAARAKYNLFFVQDVFPVHEVIEP
ICPDCLVHYEIWV

CPn_0665   744998   744365
nhaC-Hexophosphate Transport
FMNVWTKFPQPPKHLKEIEDQEVVKKKYKYWRIRIFYCMPIGYIFYYFTRKSFTFAMPTL
IAUGIDRKAQIICIGSTLVPDYCICGKFVGCVMSDQGHPRYFMAICLHITGLTNIFFGMSS
GIVLFAIWWSLXKWFQWAWPFCARLLTHWYAKGEFGTWWIVWITGHNICGALIPILTGF
IIFYGWIAIAMYVYIICICIGMGLVLINRRLRDTFQGICILPPIEKYKRDPHHAHHEGKSASE
GFFEEIEKGLGTRELLFTVVLTNQWLWFLAAAGFFIYIVRMAVNDWGALFLIETKHYAAVK

ANFCVSLFEIGGLFGMLVAC___GKISGKGNPGPHNVLFGLGLLFAILGHWFGRSHHDWWV
DGTLLFVIGFFLYGPQHMIGLAAAELSHKKAAGTASGFTGWFAYFGATFAGYPLCKVTDV
WGWKGFFIALLACASEALLLFLPTWNATEKDTRSKX|

CPn_0666   746370   750107
dnaE-DNA Pol III Alpha
GFFLTWIPLHCHSQYSVLCAMSSIKDFVAKCQEFGIPALALTDHGNLYGAVDFYKECTQK
GIQPIIGCECYIAPGSPFDFKKKEKRSRAAHHLILLCKNEGGYPHLCILTSLAFTEGFYYF
FRIGKELPLVGEIGIGLIL AGIGDPCYIVSG WFGLLFFCVYTFEGLIIR
MGEEJIAGFKEEWLRGEWTIGDGGGGTIITAENGGGHIANIAQAH
EILLNVQSGETVRIAKQNTHIPNPKRKVYRSREYYFKSPAQMAELFKDIPEVISNTLEVA
KRCDFTFDFSKKHYPIYVPESLKTLNSYTEEDRYQASAVFLKQLAEEALPKKYSSEVLAH
IAKKFPHRDPIDIVKERMDMEMAIIIPKGMCDYLLIVWDIIHWAKANGIPVGPGRGSGAG
SVLLFLLGITEIEPIRFDLFFERFINPERLSYPDIDIDICMAGRERVINYAIERHGKDNV
AQIITFGTMKAKHAVKDVGRTLDMALSKVNHIAKHIPDLNTTLSKALETDPDLHQLYIND
AESAQVIDMALCLEGSIRNTGVHAAGYIICGDQLTNHIPICISKDSTMITTQYSHKPVES
VGMLKVDLLGLKTLTSINIAMSAIEKKTGQSLAMATLPLDDATTFSLLHQGKTHGIFQME
SKGMQELAKNLRPDLFEEIIAMGALYRPGPMDMIPSFINRKHGKEIIEYDHPLMESILKE
TYGIMVYQEQVMQIAGALASYSLGEGDVLRRANGKKDFQOMEQEREKFCKRACNNGIDPE
LATVIFDKMEKFAAYGFNKSHAAAYGLITYTTAYLKANYPKEWLAALLTCDSDDIEKIGK
LIREAQSMGIPILPPHINVSSNHFVATDEGIRFAMGAIKGIRGLIESIVEERDHHGPYE
SIRDFIQRSDLKKVSKKSIESLIDAGCFDCFDSNRDLLLASVEPLYEAIAKDKKEAASGV
MTFFTTLGAMDRKNEVPICLPKDIPTRSKKELLKKEKELLGIYLTEHPHDTVRDHLSRLSV
VLAGEFENLPHGSVVRTVFIIDKVTTKISSKAQKKFAVLRVSDGIDSYELPIWPDMYEEQ
QELLEEDRLIYAILVLDKRSDSLRISCRWMKDLSIVNENIIYECDQAFDRIKNQVQKMSF
TMSTSGKETKAKGNKPNENGHTQALAPVTLSLDLNELRHSHLCILKKIVQKHPGSRTLVL
VFTQDNERVASMSPDDAYFVCEDIEELRQELVTADLPVRVITV

CPn_0667   751097   750177
No robust homolog present in Genebank/EMBL as of 11/7/98
NISLLCKIQKRYFMKKLILYFAAFVASLFCGVFLWDRVPCAQKIMRLAADHSSEVFSKSC
RFVRKISGFEELQVFERHVSPEQALALFPEYRDGKSFVELAFIPHTLMHVRFSKEEPVKK
HIISQEGEILWSLVNGEMVLHTGTWTCSKGFRECLLLHAGKQDMRVIQTLATLGGTTSRE
SLAQALALKNIRAERVIKECQKKKLIFASGNQIGTHFQQFQPIRGCTTTLNNNPVWLQKP
RHAAVFPAQYSEDRVRHLVKHIFGDNFLIVRSSMVYVPVYKISLVSADNSVRVEYINAVT
GKSFQDL

CPn_0668   751176   752162
CT547 hypothetical protein
WRFVVVSPRLIMKFLLYVPLLLVLVSTGCDAKPVSFEPFSGKLSTORFEPQHSAEEYFSQ
GQEFLKKGNFRKALLCFGIITHHFPRDILRNQAQYLIGVCYFTQDHPDLADKAFASYLQL
PDAEYSEELFQMKYAIAQRFAQGKRKRICRLEGFPKLMNADEDALRIYDEILTAFPSKDL
GAQALYSKAALLIVKNDLTEATKTLKKLTLQFPLHILSSEAFVRLSEIYLQQAKKEPHNL
QYLHFAKLNEEAMKKQHPNHPLNEVVSANVGAMREHYARGLYATGRFYEKKKKAEAANIY
YRTAITNYPDTLLVAKCQKRLDRISKHTS

CPn_0669   752140   752775
CT548 hypothetical protein
IEYLSILPKIEINMRLFSLGTIYLFFSLALSSCCGYSILNSPYHLSSLGKSLLQERIFIA
PIKEDPHGQLCSALTYELSKRSFAISGRSSCAGYTLKVELLNGIDKNIGFTYAPNKLGDK
THRHFIVSNEGRLSLSAKVQLINNDTQEVLIDQCVARESVDFDFEPDLGTANAHEFALGQ
FEMHSEAIKSARRILSIRLAETIAQQVYYDLF

CPn_0670   752738   753196
rsbW-sigma regulatory factor-histidine kinase
PRRLLNRYTMTFFEGETVFPAVLSELHSMLDLIKRAGKQSKCPQEKLLKLELACEELLVN
IISYAYQGENSPGTIAISCISHRGDLEVVIKDHGPSFNPLAVSINIQEDLPLEQRKLGGL
GIFLAKSSVDEFLYAREDHCNIVHLKMLNGQHS

CPn_0671   753660   753205
CT550 hypothetical protein
RITINQRKYTMSLDFFEEFYHQSILNTGTSFPEGYLNIAEILSYPHCTDANTDFLCSQSD
NDFIIAESKDKLTLFNADFAIWLVPELVQGQOAVTRGYIAVSQGEGNYEPEMAFEASGQYN
QSSLILEALQLYLKDIKDTENALRSFRFNNDH

CPn_0672   753723   755048
dacF(pbp5)-D-Ala-D-Ala Caroxypeptidase
TIKSPKHMKRPFVTYLCIIFYGSCASLSLHAGLSFPEVRGATAAVVHADSGKVFYDKDIDA
VIYPASMTKIATALFILKHYPTVLDTLIKVKQDAIASITPQAKKQSGYRSPPHWLETDGS
TIQLHLAEELQNVSFLLTEAPITIRVRTDKISVKELQEKLEYPSSPGELPEALHFSKRHPLQST
FNNPHGLHHPNHYTTTRDLISIMRCALKEPPFRGVISTTSYKIGATNLHGERILSPTNKL
LLPGSTYHYPPALGGKTGTTKTAGKNLIMAAEKNNRLLVTIATGYSGPVSDLYQDVIALC
ETVFNEPLLRAKCLVPPSDCLQLEIANLGKLSCPLPEGLYYDFYASEDREPLSVSFIAHAD
AFPIEQGDLLGHWVFYDOEGKKISSQPFYAPCRFERTIKPWKLYMKRVFTSYRTYMSITM
LLMYFRIRKHRKYKNLKHYSKI

CPn_0673   755242   755463
CT552 hypothetical protein
GKSTEGKAYHCFLKQVSIALNREEVWDNPHHLMFILMQFQQFSGEQDRFGSFLEATIRDR
VSFLVLQEKIATLK

CPn_0674   756689   755577
fmu-RNA Methyltransferase
RGILYVTMVPFRQHHAYQLLKQLHTSAISEADRVSYYFKQNRSLGSKDROWIQNIIFNIL
RHRRLLETLILDSGEOVTPEALVAKVNEGVLENLDSYSAIPWPVRYSISDDLAHFLVQDY
GEEQAEEIAKIWLTEAPITIRVRTDKISVKELQEKLEYPSSPGELPEALHFSKRHPLQST
EAFRRGFFEIQDENSQRISQGIGLTDKDIVLDFCAGAGGKSLIFAQKAKHVVINDSRKAI
LQTAKHRLLRAGARNFSLADQLPLGSFGVVIVDAPCSGTGVFRRHPEHKWQFSKKLLLNY
VRVQKSILKQASAYVGPRGRLVYITCGLLKEENEAHVAYMHSLGWKEVHRKTLPLQVGKG
DAFFTSIIFQKI

CPn_0675   757931   756768
CT595 hypothetical protein
VPLGMILDFQFSIGYYLRVLELAIRIZTRILAYIARKRILLDAWIVHUPLPFNYDTSVGTI
RQVIHELFGWGAIGYGIISSRLLAIIELPLIIEEKFGYHWLYBLFFCVYHIKKAIVDKLLM
FKGLILIFECSKRPVDKIVQAANKYFGYFGPGNPGSWEDFTHEITEVEVJOTLAIEVONRLAA
DAGLQHIIEALTTLLEGIFAIYLPLIGELLINGFIGEKAQILKTLCEKCVVILRELIQLFSL
SAEDFQTIINSIIGDGLIEVLAIGLPIPLPLPFIGKTFVPLHQPTALAGPEDIKIALCFL
AEVLRKVIVEKKLHVGKGIWNTFPEEVGIIYLIRDANFALMDKMITHLLMIGWLJAYDRDIG
IALRKAAEYYNPHPSFWRQFLPLPDPPP

CPn_0676   759220   758051
homologous to CT695
DMVTPISCNDGDRNTISDPLEESAAEECDSDLEDRVSESATQVIETIADTGIPEATPSEG
TNSDLNSDLVDRVEYEARGSLLTTMLARIRKAVSQIWMHVKTKRHPKEQGVRSLGDIPCD
LLKATRLPKETAEPPYFYALETALASCRSFFFHVFLRLFTLLRRQHPEAPLDLCGTDPIS
PEAAVAFALILRSCCKWVATDAVQECLPLEVIEEAGMYNAFSLEATTTVEEVSKRLSELL
YSDKRIDGLANVRGITKIITSPYLCAGQCVSVVDNLKTYDLGRNYTQVLACASQIDEFAD
YGFNFALVMKDILYLVRQDRCKFIGDFLMMWSEEHASEVNYDVVLAILEVNLPILEEDYR
... ...

CPn_0677   760410   759256
No robust homolog present in Genebank/EMBL as of 11/7/98
RIAMGINPSGNRSPDDVVVRGAQGDSSSTQGTGATNSNLGAHNVTTSTSQPQVASKAKQL
WQTVREFFLGKKSPDSSQGASGPAMQSPSGPTIRPTRPAPPPPTTGGANAKRPATHGKGR
APQPPTAGSSSGSEQPTAMSSEVAKLVSELKQKDAVHSHAESQKVLKKVSQELQTKNTDWEN
NRGPDYLLHGYRVIARALQQTYTEQSMLIEGTSSTGPVPQAVTVAKDAVTQTVRGAIKNL
ENPKPGNDPDGVLMQVVISLGIEGPTLDPGESIQNFLETRVSDFGGDDSDIDYTSDIARL
GSALDRVRENHPNEMPRIWIALARELGAAVHSHATSVRIANAGKNHTRDVVRMANESSRL
LQGMKVLSVGAWANTMTVLIGDLFE

CPn_0678   761329   760682
No robust homolog present in Genebank/EMBL as of 11/7/98
KIIMSVNPSGNSKNDLWITGAHDQHPDVKESGVTSANLGSHRVTASGGRQGLLARIKEAV
TGFFSRMSFFRSGAPRGSQQPSAPSADTVRSPLPGGDARATEGAGRNLIKKGYQPGMKVT
IPQVPGGGAQRSSGSTTLKPTRPAPPPPKTGGTNAKRPATHGKGPAPQPPKTGGTNAKRA
ATHGKGPAPQPPKGILKQPQGSGTSGKKRVSWSDED

CPn_0679   762936   761725
pgk-Phosphoglycerate Kinase
GYMDKLTVQDLSPEEKKVLVRVDFNVPMQDGKILDDIRIRSAMPTINYLLKKHAAVILMS
HLGRPKGQGFQEEYSLQPVVDVLEGYLGHHVPLAPDCVGEVARQAVAQLSPGRVLLLENL
RFHIGEEHPEKDPTFAAELSSYGDFYVNDAFGTSHRKHASVYVVPQAFPGRAAAGLLHEK
ELEFLGRHLLTSPKRPFTAILCGAKISSKIGVIEALLNQVDYLLLAGGMGFTFLQALGKS
LGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAENLQSKEYSVISIDQGIPPHLOG
FDIGPRTTEEFIRIINQSATVFWNGPVGVYEVPPFDSGSIAIANALGNHPSAVTVVGGGD
AAAVVALAGCSTKVSHVSTGGGASLEFLEQGFLPGTEVLSPSKS

CPn_0680   764254   762971
ygo4-Phosphate Permease
YSMLPLIIFVLLCGFYTSWNIGANDVANAVGPSVGSGVLTLRQAVVIAAIFEFFGALLLG
DRVAGTIESSIVSVTNPMIASGDYMYGMTAALLATGVWLQLASFFGWPVSTTHSIVGAVI
GFGLVLGKGTIIYWNSVGIILISWILSPFMGGCVAYLIFSFIRRHIFYKNDPVLAMVRVA
PFLAALVIMTLGTVMISGGVILKVSSTPWAVSGVLVCGLLSYIITFYYVHTKHCSYISDT
PKKGSLTYRLKERGGNYGRKYLVVERIFAYLQIIVACFMAFAHGSNDVANAIAPVAGVLR
QAYPASYTSYTLIRLMAFGGIGLVIGLAIWGWRVIETVGCKITELTPSRGFSVGMGSALT
IALASILGLPISTTHVVVGAVLGIGLARGIRAINLNIIKDIVLSWFITTLPAGALLSILFF
FALRALFH

CPn_0681   765001   764258
CT691 hypothetical protein
NGIRSHKSFTRSFRQVIIAKKAILMQTLARLFGQSPFAPLQAHLEMVVSCVEYMLPIFTA
LRDGRYEELLEMAKLVSDKEYQADCIKNDMRNHLPAGLFMPISRAGILEIISIQDSIADT
AEDVAILLTIRRLNFYPSMETLFFRFLEKNLEAFELTMTLLHEFNQLLESSFGGRKADKA
RLLVGRVAKSEHESDVLQRELMQIFFSDDFIIPEKEFYLWLQVIRRTAGISDSSEKLAHR
INMTLEEK

CPn_0682   764912   765955
dppD-ABC ATPase Dipeptide Transport
TSKGLHKNSLFRNNNLPKRSCKRLMASNPILQIEDLSITLAKQRQQYPIVQSLSFTINEG
QTLAIIGESGSGKSVSAHAILRLLPCPPFSVSGQVNFQGHNLLTASRSIQKKIIGTEISM
IFQNPQASLNPVFTIEQFREIIHTHLALTAEVAKEKMLYALEETGFHDPRLCLNLYPHQ
LSGGMLQRICIAMALLCSPKLLIADEPTTALDVSVQYQILQLLKTLQKKTGMSLLIITHN
MGVVAETADDVLVLYAGRMVEACPVQMFHNPHSPYTRDLLASRPSLQPQQLGSFNPIPG
QPPHYTAFPSGCRYHPRCSKILNRCSAEAPEIYPVRGHKVRCWLYDD

CPn_0683   765936   766919
dppF-ABC ATPase Dipeptide Transport
GVGCMTTNFPOPLIQATSLTKHYYKRSFWFQGKTIASRPVDDVSFSLYSRRAVGLIGESG
SGKSTLALALAGLLPLTSGFLTFNGTPIKLHSKHGRHQLRSQVRLVFQNPQASLNPRKTI
LDSLGHSLLYHKLVPKEKVLATVREYLELVGLSEEYFYRYPHQLSGGQQQRVSIARALLG
VPQLIICDEIVSALDLSIQAQILNMLAELQKKLSLTYLFISHDLAVVRSFCTEVFIMAYG
QIVEKGNTKRIFSDPQHPYTRMLLNAQLPETPDQRQSKPIFQEYHKDSEESCSTGCYFYN
RCPQKQEACKSEIIPNQGDAHHTYRCIH

CPn_0684   768056   767181
spoJ/parB-Chromosome Partitioning Protein
EKSGDIVTEEISKDTIIEVAIDDIRVSPFQPRRVFSNEELQELIASIKAVGLIHPPVVRE
ICTGDRVLYYELIAGERRWRAMQLAGATTIPVILKHVIADGTAAEATLIENIQRVNLNPI
EMAEAFKRLIHVFGLTQDKVAYKVGKKRSTVANYLRLLALSKTIQESLLQGQITLGHAKV
ILTLEDPILREKLNEIIIQEHLAVREAELIAKQLISEEGSSIELKPTPLDMAESSKQHEE
LQQRLSDLCGYKVQIKTRGSKATVSFHLQNTQDLQKLEAWLSSHGTLSESLS

CPn_0685   768026   768217
No robust homolog present in Genebank/EMBL as of 11/7/98
FPQSOYLLIFPNRILDLQAFEILDVQGMLTDQRKHIQMLHKHNSIEIFLSNMVVEVKLFF
KTLK

CPn_0686   768373   768176
No robust homolog present in Genebank/EMBL as of 11/7/98
AKDSMMPQLRLFRVYQELFFFSSVYVCEQRRPRKLYPSLQHLNFPIEKPRFLLKGFKKEL
HFYHHV

CPn_0687   768501   769214
CT482 hypothetical protein
RKIHKHLHHAYRFSTPNCRGFMCKLVHNIWKKFYCFCSAIAICIVLASFLCLKIVSNTYK
HXQAKPHSILLLTRAAEVAVSQXIFLPSKSALGSLEQAYHUGGESMKPYACFLASCCYIHN
KFLRIAYYNSLAYHRICQALQLCHPIQKLLKEISEAQADQLYDVALSKGYOLLQTANSGPE
YHTLSIFLTLLKVIELKELLIIQDVSQDFAALKGSSPLFHQFEPMYSSDGEWTLCKRFGKKG

CPn_0688   769176   770137
CT481 hypothetical protein

GLMLIVLAFRQVFFGHSRSQ... LKNYLRLLKQNFAITLFKERTRKRHLHMLTFCFASFD
FYTNIFPFLEEQKIPAVVTVASRYIFSNAAQDLIFSHRLKDIETLAFSDEIFSNYMPFCC
QNELIEMAKGPYIGLASGGFATRNLHNNDIYLTTEIGDSRHILECDDEFKPHAFDFFEEK
SDPTSRKLAADHYPYSFELGNTINRKLKTHNIYRLDTKPHQYVCPSLPTSGRYEKNWRKE
KSKQLYLKKQLPKR

CPn_0689   771407   770197
vfhO-NifS-related Aminotransferase
...
...
HHANVLSWEIACRRRGSLVKKIRVHDSULIDLDDLEKLLNEGAQFVSIPHVSNVCQP
LQQVAELVHRYDAYLAVDGAQGAPHLPIDVQLWDVDFYVFSSHKIYGPTGIGVLYGKKDL
LDDOLPPVEGGGDMVAIYDHQNPEYLPAPMKFEACTPNIAGVLGLGAALDYLDGLSAKFIY
DKEIALTTYLHKELLEIPGVEILGPSIEEPRGALIGMTIDGAHPLDLGFLLDLRGIAVRT
GHQCAQPAMERWNVGHVLRVSLGIYNDEDDIDQFILVLCQDSLDKIRR

CPn_0690   772704   771436
ABC Transporter Membrane Protein
LSVLRGDKVLVSIETFSSIASGSPVQKAAEACYTQYSKQPSSKEVLSSFSWIQELSLFPD
RYNLATGASELIKQHWLHNNHSLAFECILINGKYEPSLSQLPEGVIVCGIDEARGSLSSF
MQGFDVNKHPLAFLNAVCSEDRGVVIYIPEEMQTSDPIFVRHISFPTVSDHDVIFSPRIV
VILGQRASAQIQISHDVDLEMVGSSKTIVNGVTELFVGEGADLTVFMVPGYSEEDTLSWS
TIATVEKDAICRMTQNLLESCQGFGWFDNTSYIVGKKGHAESLVLVQSPRKTWVNNLMSH
DAEETVSRQNIKSILYSGHFLFEGTISISSQGDLSDANQKHDTLLLSSEARVSTFPRLEI
ETDEVKASHGATVGPLDPQQIFYMRSRGMTEAEAQEKLIHGFLKQGLVSDTFLGSSFQLN
QTS

CPn_0691   773467   772685
CT691 hypothetical protein
RGLGSMLKIKHLHASCNDVKILDDFNLNIQPGTMHVIMGPNGAGKSTLAKILAGDESVLV
SSGEIALQEQNLLSMLPEERSRAGLFVGFQMPPEIPGVNNKMFLRDAYNARRRANQEGDI
SIDEFNTLLSTVLETYEYNATTDLFLDRNVNEGFSGGERKRNEICQMLVLEPEMVLLDEP
DSGLDVDALRLICRVLEKYRELHPTSSLCIVTHNPKLGNLIRPDVVHLLLDGRVALSGDV
SLMHELEAKSYQEVTKRVAWR

CPn_0692   774945   773461
ABC Transporter
IQEFCATGLKVMGESVKVFLEEREDYPYGFVTPIESQGLTRGLSEETIEEIAALRNEPQF
IIDFRLQAYRYWKQLHEPAWARLHYGPIAYDDIVYFSSPKQKKPLGRLEDADPEILDTFK
KLGIPLDEQKRLLVENVAVDLVFDSVSIGTTFKEALEKAGVIFCSLGEAIQEHPNLVKK
YLGSVVSHRDNFFAALNAAVFSDGSFVYVPKGVKCPMDISTYFRINNKEAGQFERTLIVV
EDGGYASYLEGCTAPAYSSNQLHAAVVELVAHEHAVIRYSTVQNMVAGDKKTGKGGIYNF
VTKRGLCAGYRSKISWSQVEVGAAITWKYPSCILKGDESVGEFYSVALTSGIMQADTGTK
MLHVGKRTTSTVISKGISSDESKNTFRSLVSLGKKAEHSSNYTQCDSMLIGKASGAYTDP
KIVVENSTSSIEHEATTSKLREDQLLYLRSRGLSPEEAVSLVIHGFCREIIEQLPLEFAQ
EASKLLLIKLENSVG

CPn_0693   776292   775240
TPR Repeats (O-Linked GlcNAc Transferase homolog)
LRSTNHVLGEISMEEAAKHLAKEFLCSGINLFLSGEYEQAEKRLKETLEDSTAALAYCY
LGIIALETGRVSEALNWCSKGLASEPGDSYLRYCYGVALDRGNQYEAAIEQYSAYVALHP
DDVECWFSLGSVYHRLKRLQEALDCFDKILALDPWNPQSLYNKAVILSEMDDEAESIRLL
EVAVAKNPLYWKAWVKLGFLLSRKRWDKATEAYERVVQLRPDLSDGHYNLGLCYLTLDK
TRLALKAFQEALFLNAEDADAHFYVGLAHLDLKQMREAYEAFNSALSINLEHERAHYLLG
YLHHMQGETDKATKELLFLQKKDSTFAPLLQKTVVSDPSSMQFERRLDTIS

CPn_0694   779635   776330
pbpD-PBP2-transglycolase/transpeptidase
FSDESEAHNIHSHKRPKKFPIYLSIAQKTNRLLSGIVIAFAVIALRLWYLAVVEHEQKLE
EAYKPQIRVLPQYVERATICDRFGKTLAVNQLQYDVSVAYGAIRDLPTRAWRVDEHGHKQ
LIPVRKHYIMCLSELLSQELHLDREAIEDAIHAKASVLGSVPYLVAANVSERTYLKLKML
SKDWPGLHVEAVVRRHYPOESVASDILGYVGPISLQEYKRVTQELSQLRECVRAYEEGED
PKLPEGLASIDQVRALLESVESNAYSLNALVGKMGVEACWDSKLRGKIGKKPILVDRRGN
FIQEMEGAVPEAPGTKLQLTLSAELQAYADALLLEYEKTETFRSAKSLKKREKLPPLFPW
IKGGAIIALDPMNGEILAMASSPRYRNNDFVNAKVAEDSKAVRSSIYRWLENKEHIAEIY
DRKVPLIRERRNPLTGLCYEEILPLTFDCFLDFLFPENSVIKLQLKRNSFVGQAIEVQNL
VTRLLSLFPYEEGTCPCSAIFDAVFPNEEGHILIQEVISLQEQKWIMECLNQHKADIEEL
KEALDQVFNELPANYDKILYTDILRLIVDPERFSPVLPSEVHRLSLSEFTELQGRYVVLR
SAFSTILEDAFIEVHFKSWRKSEFLQYLAAKRQEEALRKQRYPTPYVDYLEEEKTROYKM
FCQEHLDTFLAYLFSKTPYKEGLEPYYDILDLWINELDNGAHRALSWHEHYLFLKERVSH
LSEHLPALFSTFREFNELQRPLLGKYPISIVRNKRQTEQDLAASFYPVYGYGYLRPHAYG
QAATLGSIFKLVSAYSVLSQRILWGHNEEPANPLVIIDKNSFGYRSSKPHVGFFKDGTPI
PTFFRGGSLPGNFMGRGFIDLVSALEMSSNPYFSLLVGEGLGDPEDLADLAASFSPKKEK
TGLGLPGEYAGRVPHDLAYNRSGLYATAIGQHTLVVTPLQTAVMLASLVNGGVVYVPKLL
LGEWEGEHVSYLSSKKKRTIFMPDAVVEVLKTGMRNVIWGQYGTARAICSQQFPPOLLSRI
IGKTSTAESIMRVGLDREYGTMKMKDIWFAAVGFSDQDLSLPTIVVIVYLRLGEFGRDAA
PMAVKMIDMWEKIQORESFLRG

CPn_0695   780201   781382
homologous to CT695
SLEVSMKKLLKSALLSAAFACSVGSLQALPVGNPSDPSLLIDGTIWEGAAGDPCDPCATW
CDAISLRAGFYGPYVFDRILKVDAPKTFSMGAKPTGSAAANYTTAVDRPNPAYNKHLHDA
EWFTNAGFIALNIWDRFDVFCTLGASNGYIRCNSTAFNLVGLFGVKGTTVNANELPNVSL
SNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNK
PKGYKGVAFPLFTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFD
ADNIRIAQPKLFTAVLNLTAWNPSLLGNATALSTTDSFSGDFMQIVSGQINKFKGRKACGV
TVGATLVDADKWSLTAEARLINERAAIVSGQFRF

CPn_0696   781703   782599
CT696 hypothetical protein
NGGFYVRMPLLTYSNFEIEVQSLECQQSKLTIKDLMSAIAIIFHIQTRIWNPKMKLYIFEE
KNFLYIINLAKTLSQLPHALMHIIRKVIQDNKTVLFVITKKQAKCVIREAAIEAGEFFIAE
RWLSCMLTNMTTIRNSIKTLDKIERDIISMQAYLITKKEAALLAKHHQKLLHNLESIRYMK
KAFSLLVVVDPSYEKIAVAEAKFUSIIVLALVVDTNKDIFTFDNIVISINDIELKSITRLLIN
VIFENIIEAKIIKLSIEIFSINVEGLEVPILSAIESQDLIESDEENKFPDLLAKKFDSKAN

CPn_0697   782687   784447
fst-Elongation Factor TS
WMGFIMCDFSMETLKTLRGVTDYSCIFFCKEALEAVYYRHLEEAVVYLHKLSLASAKKFHR
ETFFSIILAAKTDANATALIEVRHPSTDFANNHAVPRGEVHILLHDILEKYKVIFVEAISQAA
CSQDFSLSVDELRAVTMJTVSHIIRISDPVAYFFKATTFTMSGIYSINKSKTVALTMLSPQSI

TADSLAKDIAMHVVAAQPQFLGKESVPAEAIAKL   IASQIQGKPQE/IEKIVTGKLNT
FFQEACLLEGPFIKNADLSIQSLIDDFSKTSGSSVAIEQFILWKIGA

CPn_0648   783443   784201
pyrH-UMP Kinase
EPNKNMAKQTRRVLFKISGEALSKDSSNRIDEMRLSRLVSELRAVRNNDIEIALVIGGGN
ILRGLAEQKELQINRVGADOMCMLATLINGMAVADALKAEDIPCLLTSTLSCPQLADLYT
PQKSIEALDGSKILICTTAGSPYLTTDTGAALPACELNVDVLIVATMHVDGVYDKDPRL
...

CPn_0699   784172   784721
rrf-Ribosome Releasing Factor
TMSVLQDTEKKMAAALDFFHKEVKSFRTGKAHPALVETVVVDVYGTTMRLSDIASISVAD
LRQLVISPYDGNNASAIAKGIIAANLNLQPEVEGSIIRIKVPEPTADYRQEMIKQLRRKC
EEAKINVRNIRREANDKLKKDSALTEDVVKGNEKKIQELTDKFCKQLDELTKQKEAEIAS
:

CPn_0700   785094   785609
CT676 hypothetical protein
LMVHSPTHQCYHCQQPATICYTEIDKDKVIRSYVCATCPCPSHYYNNEHLSLSKGVGVLT
LECGNCKTVWHSKQDDEQLLGCHQCYTNFKNQITSKLKSERVVSSSFTMEKGQGSLHIGR
APGEASNTNPLLKLIALNEALQDTLEREDYEQAAVIRDQINHLKTKNPDDPS

CPn_0701   785584   786672
karG-Arginine Kinase
KPKIQMTLPNDLLETLVRKESPQANKVWPVTTFSLARNLSVSKFLPCLSKEQKLEILQF
ITSHFNHIEGFGEFIVLPLKDTPLWQKEFLLEHFLLPYDLVGNPEGEALVVSRSGDFLAA
INFQDHLVLHGIDFQGNVEKTLDQLVQLDSYLHSKLSFAFSSEFGFLTTNPKNCGTGLKS
QCFLHIPALLYSKEFTNLIDEEVEIITSSLLLQVYVFPGNVIVVSNRCSLGLTEELLLSS
LRITASKLSVAEVAAKKRLSEENSGDLKNLILRSLGLLTHSCQLELKETLDALSWIQLGI
DLGLIKVTENHPLWNPLFWQIRRAHLALQKQAEDSRDLQKDTISHLRASVLKELTKGLSP
ESF

CPn_0702   789700   786929
yscC/gspD-Yop C/Gen Secretion Protein D
LKKNPVKTVILNIGRKILQGIKKKKKKIGILSGLFFLDLVLLGVSSQRPTETSANVKHNL
RDEKLAACPKNSAASLSAKKSHTKKTTPGSIPSKVFSKFDATODKTFQKTSGSAFPAKPT
TLKELEERKKPRPERRTTADVKRSPRFLPTQEVEEPVPAASKEQLDSIQVWEEKQNYARR
AVNAINLSIKKQLEEQTSTVTEKDVQPKTQATPHASKQNVASPSTSMPGIEKAATTVAVP
QDKSEEEKVKERLTKRELTCEDLKDNGYTVNFEDISILELLQFVSKISGTNFVFDSNDLQ
FNVTIVSHDPTSVDDLSTILLQVLKMHDLKVVEQGNNVLIYRNPHLSKLSTVVTDSSLKE
TCEAVVVTRVFRLYSVSPSAAVNIIQPLLSHDAIVSASEATRHVIISDIAGNVDKVSDLL
AALDCPGTSVDHTEYEVKYANPAALVSYCQDVLGTLAEDDAFQMFIQPGTNKIFVVSSPR
LANKAEQLLKSLDVPEMAHTLDDPASTALALGGTGTTSPKSLRFFMYKLKYQNGEVIANA
LQDIGYNLYVTTAMDEDFINTLNSIQWLEVNNSIVIIGNQGNVDRVIGLLNGLDLPPKQV
YIEVLILDTSLEKSWDFGVQWVALGDEQSKVAYASGLLNNTGIATPTKATVPPGTPNPGS
IPLPTPGQLTGFSDMLNSSSAFGLGIIGNVLSHKGKSFLTLGGLLSALDQDGDTVIVLNP
RIMAQDTQQASFFVGQTVPYQTTNTIIQETGTVTQNIDYEDIGVNLVVTSTVAPNNVVTL
QIEQTISELHSASGSLTPVTDKTYAATRLQIPDGCFLVMSGHIRDKTTKVVSGVPLLNSI
PLIRGLFSRTIDQRQKRNIKMFIKPKVISSFEEGTRVTNKEGYRYNWEADEGSMQVAPRH
APECQGPRSLQAESDFKIIEIEAQ

CPn_0703   791205   789685
pkn5-S/T Protein Kinase
RKIGFMDCRGGIPLPEPQVIGGYHVKKILSKKLRSRVVHGLHPETRHSTVIKVFSPSPSF
TSRSVVYNFLKEAQSLHQITHPNIVKFHRYGKWQDCLYIAMEYIEGISLREYILAQFISLP
QAIDIIFDIAQALEHLHSRNILHKDIKPENILITPQGKIKLIDFGLADWDTEIQRAHPSV
IGTPYYMSPEQRQGESHSPASDIYALGLLAYELILGHLSLGRVFLSLVPERISKILAKAL
QPSPNNRYSSTREFIQDIHHYRMSGDMQEDLRIKDHTVALYEQLQTQRFWLAPETLRFPD
FISGVLYHQGYPLYPHAYDTLLEGDVFNLWLGYSPISNATIALSVVKSLVCQQDLQRPLL
DRVCEINECLIRMKIPIDEMGISILCLEISKENKELSWIACGKTVFWIKROGRVVQDFES
FSPGLGKITSLQIRETKVAWEIGGDAAVVCTLELEESVASLKTLSLAELQDRRQKAIFCPI
ESIHGGIQSRQHGSNSPSTLISLKRIR

CPn_0704   792330   791209
fliN- Flagellar Motor Switch Domain/YscQ family
RYFMAVAADSSASWLKSRNNFLSSLGKTEEQVAAPEFPKELCQHKIREKFRLEDVQVSIK
FRGSITAVEATKEFGVHLLIQPMVVQPWEVENLLFLTSEEDLQELMVAVFDDASLASYFY
EKDKLLGFHYYFVAEACKLFEELQWVPSLSAKVGGDAIFTATSLQGSFQVVDISLRLDGK
NVRCRLLLPEDTFQSCKFFSGLMHDIQTQQISLSVEVGYSQLTQEKWHQVVPG
SFIMLDSCLYDPETEESGALLTVQKHQFFGGRFLTPSSGEFKITSYPNLTHEDPPLPENP
QASAAPLPGYSRLVVEVARYSLAVSEFIKLNLGSILSLGNHPAYGVDIILDGAKVGRGEI
IALGDVLGIRVLEV

CPn_0705   793176   792334
CT671 hypothetical protein
FMELKKTAESLYSAKTDHTVYQNSPEPRDSRDVKVFSLEGKQTRQEKTTSSKGNTRTES
RKFADEEKRVDDEIAEVGSKEEEQESQEFCLAENAFAGMSLIDIAAAGSAEAVVEVAPIA
VSSIDTQWIENIILSTVESMVISEINGEQLVELVLDASSSVPEAFVGANLTLVQSGQDLS
VKFSSFVDATOMAEAADLVTNNPSQLSSLVSALKGHQLTLKEFSVGNLLVQLPKIEEVQT
PLHMIASTIRHREEKDQRDQNQKQKQDDKEQDSYKIEEARL

CPn_0706   793689   793180
CT670 hypothetical protein
YAVAKYPLEPVLAIKDKDRVDRAEKVVKEKRRLLEIEQEKLREKEAERDKVKNHYMQKIQQ
LRDLLDEGTTCDAVLQIKSYIKVVAVQLSEEEEKVNKQKEVVLAASKELEKAEVNLAKRR
KEEEKTRLHKEEWMKEALKEEARAEEKEQDEMGQLLFQLRQKKKRESGGS

yscN-Yop N (Flagellar-Type ATPase)
VNMDQLTTDFGTIMSQLADVNLITTVVGRITEVVQHLIKAVVPNVRVGEVCLVKRNGMEPL
VTEVVGFTGIFAFLSPLAELSGVSPSSEVIPTGLPLHIRAGIKILLAVRVLNGLGCEPIDVET
...
...
...
...
...

CPn_0648 hypothetical L ...
AFKTVKRFFCFNIDPVECFPHLGGDAEAQGITTCNGTTFLAUGLKKDIFFALASYAAPKD
TTLVCGFKPNPHMSMQDQRHLIQRELQERALEGEELIER INNUKGREWQFRQTEEDSQTT
AQFADEHFQAVGVIIDUNEDLVTPAEHTQQDARKEDKEECSVTRKT FDWVSSGEEVLNR
ALLYFSDRDGNREGLANFLKPQYAVQRATQRAELFASIVGTJVSGSVKTIMTTCLG

CPn_0709   796203   795742
CT667 hypothetical protein
...
...
QVIANCKIESTRALAQSVLGWHDTLVAKSALPLG

CPn_0710   796482   796210
CT666 hypothetical protein
RSRGEKSMATNKSCTAFDFNKMLDGVCTYVKGVQQYLTELETSTQGTVDLGTMFNLQFRM
QILSQYMESVSNILTAVNTEMITHARAVKGS

CPn_0711   796791   796486
CT665 hypothetical protein
TTINNQVLGFINYLYLGRYSMFNMENTAKEEKNSQPLLDLEQDMQDHDRAQELKASVQDK
VHKLHALLREGSDKESFGQQQSLLAGYVALQKVLGRINRKMI

CPn_0712   799315   796781
FHA domain: homology to adenylate cyclase)
MAVRLIVDEGPLSG/IFVLEDGISWSIGRDSSANDIPIEDPKLGASQAIINKTDGSYYIT
NLDDTIPIVVNGVAIQETTQLKNEDTILLGSNQYSFLSDEFDPQDLVVDFDIPEENFSND
SGDLSDSNEQGKDLEPRQTSETNHSPKPKEKLTKDQGSSDPITSGDQELADAFLASAKAE
KNQPRAKVAKKGLKESSNESLNPKEQNAKDSPKGEERTNKPQNAIMEDNGASPRQDPQPK
SAEPSLKNTARDETPLKENKPVEEKANKKATPDSPEKKDQPEEGSKKEGSKIEATPLDSQ
KESEDKEAEEAFVQEEEENLTEDNKEDSDSAADANDDTASDHTAEDNKETPKKVENEKSA
VLSPFHVQDLFRFDQTIFPAEIDDIAKNISVDLTQPSRFLLKVLAGANIGAEFHLDSGK
TYILGTDPTTCDIVFNDLSVSHQHAKITVGNDGGILIEDLDSKNGVIVEGRKIDKTSTLS
SNQVVALGTTLFLLIDHHAPADTIVASLSPDDYSLFGRQQDAEEALERQEAQEEEERQKRA
TLPAGSFILTLFVGGLAILFGIGTASLFTHKEVVPLENIDYQEDLAQVINQFPTVRYTFN
KTNSQLFLIGHVKNSTDKSELLYKVDALSFVKSVDDNVIDDEAVWQEMNILLSKRPEFKG
ISMHSPEPGKFIITGYVKTEEQAACLVDYLNIHFNYLSLLENKVVVETQMLKAIAGHLLQ
GGFANIHVAFVNGEVILTGYVNNDDAEKFRAVVQELSGIPGVRLVKNFAVLLPAEEGIID
LNLRYPNRYRVTGYSRYGEISINVVVNGRILTRGDVIDGMTVTSIQPNAIFLEKEGLKYK
IDYNK

CPn_0713   799817   799332
CT663 hypothetical protein
LDLKEEKAGFRNEIVSIPQGTKTTIAALENTSMLEKLIKNFATYMGITSTLELDADGAYV
LPISEVVKVRAQQNADNEIVLSASLGALPPSADTAKLYLQMMIGNLFGRETGGSALGLDS
EGNVVMVRRFSGDTTYDDFVRHVESFMNFSETWLSDLGLGKQ

CPn_0714   801125   800091
hemA-Glutamyl tRNA Reductase
NYRIVLMVLGVVGISYREAALKERERAIQYLQSFEKNLFLAQRFLGKGAFIPLLTCHRA
ELYYYSESPEIAQAALLSELTSQGIRPYRHRGLSCFTHLFQVTSGIDSLIFGETEIQGGV
KRAYLKGSKERELPFDLHFLFQKALKEGKEYRSRIGFPDHQVTIESVVQEILLSYDKSIY
TNFLFVGYSDINRKVAAYLYQHGYHRITFCSRQQVTAPYRTLSRETLSFROPYDVIFFGS
SESASQFSDLSCESLASIPKRIVFDFNVPRTFLWKETPTGFVYLDIDFISECVQKRLQCT
KEGVNKAKLLLTCAAKKQWEIYEKKSSHITORQISSPRIPSVLSY

CPn_0715   801636   803462
gyrB-DNA Gyrase Subunit B
KFNKISHMAAYTEASILSLASLDHIRLRAGMYIGRLGKGSQKEDGIYTLFKEVVDNGIDE
FIMGHGKSLKISASDKQISIQDQGRGIPLGKLIDCVSKINTGAKYTQDVFHFSVGLNGVG
LKAVNALSEIFSVRSVRKKKYHLATFHRGVLQESKQGSTKDPDGTFVSFTPDPSIFPEFT
FNHDFLKDKIROYTYLHSGLEIRFNDEVFISHNGLKDLFDAEITEPPLYSPLFFQNEDLT
FIFSHLEGNTERYFSFWGOETLDGGTHLTAFKEAIVKGVNEFFGKTHSNDIREGIVGC
IAIKIASPIFESQTKNKLGNTQIRSSLIKDVKEAIVQALRKDKVAPELLLEKIKFNEKTR
KNIQFIKODLKSKQKKVHYKIPKLRDCKFHYNDRSLYGEASSIFLTEGESASASILASRN
PLTQAVFSGFKPMNVFSLEETKMYKNDELFYLATALGITQNEIQHLRYNKVILATDADV
DGMHIRNLLITTFFLKTLLPLVENNHLFILETPLFKVRNKTTTLYYYSEQEKMOALQQFGK
KDSSLEITRFKGLGEISPKEFAAFIGPEIRLTPVTITSLESISSILQFYMGKNTKERKQF
IMDNLITDF

CPn_0716   803466   804902
gyrA-DNA Gyrase Subunit A
FMRDVSELFRTHFMHYASYVILERAIPHILDGLKPVQRRLLWTLFLMDDGKMHKVANIAG
RTMALHPHGDAPIVEALVVLANKGYLIDTQGNFGNPLTGDPHAAARYIEARLSPLARETL
FNTDLIAFHDSYDGREKEPDILPAKLPVLLLLHGVDGIAVGMTTKIFPHNFAELLKAQIAI
LNDKKFTVFPDFPSGGLMDPSEYQDGLGSITLRASIDIINDKTLVVKQICPOSTTETLIR
SIERAAKRGTIKIDTIQDFSTDVPHIEIKLPKGSRAKEMLPLLFEHTECOVILYSKPTVI
YENKPVECSISEILKLHTTALQGYLEKELLLLQEOLTLDHYHKTLEYIFIKHKLYDSVRE
VLAINKKISADDLHQVHLAHALEPWLHELATPVTKQDTSQLASLTIKKILCFNEEACTKEL
LAIEKKQAAIQKDLJRIKEVTVKYLKGLLERHGHLGEPKTQITNFKTAKTSILKQQTLI

CPn_0717   804968   805306
CT656 hypothetical protein
IRIKFIDTITIVVRMEPRHIYIRKPETPKAPDVEKPGVPEYMTMANTTTFECPVKTLDQL
RRALIEORGAEEGJKMYDNFIQSILISTFGLVHKDMDPAQKASKRMRSVYKEQ

CPn_0718   805300   805626
CT657 hypothetical protein
RA/MGFTYFLALFVTRLMOERFLCSPKRWAPFINSPLYLTLIADHDTPYLAKNLDKFPLP
VEGWEKTVLIIVGGLLKSIFLGDLSSLRLLACTKFEILTLIIDLYCAQNI

glnS (Glutamine tRNA Synthetase)
FDIFLVKKVIKISMKTVTSFTVCKENKGRLDKYLTE/HPPYSRAFYQEHILGYLVQINGQ
HTTP/TATRGTGIGTIDIDIQEKEELLELLDFAIIGLQPTIEDGMTLVINKIRDMVVHPAPG
HFIPTTLVHALLJIELGERLKEEFPEEIWRNGIVDHLGDVIATYGLITAKTRQAKVVFSELFS
TYPLPFGTVLAVGGKIRTTIHTHIQDIUNKRFKEMTPOOKIKEAVTIHQVLAFNGKLGFV
ALAIHDPDTNLRVDMPMLATTTEII/DPIYDIPGMNGGCSLDPQQLIATJYUFTHPETROF
QGLYNGLPEMMGCLLKPEFRNETTIINKNLGESTLKEG

CT655 hypothetical protein

LR:TMKEFLAY::KNLVDRPEEVR:KE/QCTHT:....LLVAKPDIGY::GKEGRTIKAIR
TLLVVVA:IPNHVRVGLEIMEEK

CPn_0721   807671   808489
kdsA-KDO Synthetase
KRMVMPNNKM:L:AGPCV:EGEG:TTLEIAGKLQS:ILAPYSDRIQWFFY3STYDKANRSSLN
:JFRGPGLTEGLRILAKVKETF7VG:LTCVHTPCDAYAAAEVCN:LCVPAFLCRQTOLLVA
TAE77GAIVNLXYCGELGPWTMEGDIHIC/L:7T7HHK:LLTEPGCGFT7GRIL/GDMRSIPVL
:.:
GAVXHHLLGGELLAGLLHWL/L:TF7L:LLHLL:MVLA

CPn_0722   808477   808974
CT654 hypothetical protein
YGLSMTKFLYCGLFYSLGGLLVLAFGTMVAIIQVDQICDVSCMNKHFQESPPFLKIKKVNV
SKQICSPEERFFHCKIDKSCMELHFPQSSYSCKEYLTRISGHILTQNFEKQMQFRGNSGL
LNYQDCSLHVYDCRFQVDPVPGYGSPDKEDSSSGGMKTLYLSLFRN

CPn_0723   808978   809703
yhbG-ABC Transporter ATPase
ASMPILSVCNLVKKYNKKPVTNDVSFQINPGEIVGLLGPNGAGKTTAFYLTVGLIRPDSG
KIIFKNVDVTKKTMDHRARLGIGYLAQEPTIFKELTVQDNLICILEIIYKARKQQSHLLN
TLVDDLQLGSCLHKKAGTLSGGERRRLEIACVLALNPSVLLLDEPFANVDPLVIQNVKYL
IKILAGRGIGILITDHNAKELLSIADRCYLIIDGKIFFEGSSSQMISNPMVKQHYLGDSF
SY

CPn_0724   810602   809706
No robust homolog present in Genebank/EMBL as of 11/7/98
RTSTRLDYRSGCILSKILPFPELWKMLLGFLCDCPCASWQCAAVANCYDSVFMSRPEHKP
NIPYITKATRRGLRMKTLAYLASLKDARQLAYDFLKDPGSLARLAKALIAPKEALQEGNL
FFYGCSNIEDILEEMRRPHRILLLGFSYCQKPKACPEGRFNDACRYDPSHPTCASCSIGT
MMRLNARRYTTVIIPTFIDIAKHLHTLKKRYPGYQILFAVTACELSLKMFGDYASVMNLK
GVGIRLTGRICNTFKAFKLAERGVKPGVTILEEDGFEVLARILTEYSSAPFPRDFCEIH

CPn_0725   810829   810587
CT552.1 hypothetical protein
SCGDVGMFFAPLLYESLRRGLMHPTSHMQQOLARLEFINDQLTTELEHVNELLCSLGFPE
GLTTIKAIAEEVLSDDEPLLD

CPn_0726   813384   810880
CT620 hypothetical protein
ADIDMIYSTSISTFYKKLSLVSSMHSFAQRHRESLEHIANYEKTTAERDILKRLIEVLDQ
RASERYRSAVEKLHKYEVERATVAKSIPVAAIHEKPLSSTHASVQVTASTPAATGSGVGA
YYNAVKQKWAQDLIVELNTVMTTIMASVNSKNPANKDVFDKLNTELQALVAAGNNLTEEN
FQTLYNFPEEIFTAIQRADTFTGGMKTDFTNQLAGKYGNQATLTQTFADGRVEGFKDILT
AVQGVLTPEQFTIFAEIATELQALADHVGNFDEAGLQRIEDAGEKLAAVINSSDLTRNDK
IMFCQHITDLYSDQVAALGSFDTVLDASIYVNQHQGTMFSNLSSFVGSLIGTFAPIDLSS
SQGDISSAALAGALQTARGLNSRFNELTAEQQKLINECIKSLVTFKCGEHLGAIWAYFTA
STVVALNPTATMDHVKAAILEEAKELDNSSFQLASSIKSAMTSIVNSSGSFSVTVNSSTL
QYTIYSEKNGKVEINQILLNYGSTGFLPEITKLAKTNAESTARSYFRFKALAAVESENVQ
NKIEDLQSQLQQFTNMKTELFDGQLLSQASELRALPLPSAVASVLIDRYMPKEVDYLNEI
YKKLYYSNLGSSIGNSIIDAISQYVNGATYFNFASYVGQQPAVGAGGANAFPGSQESAQA
KLDQERKQAALYLQETRGALTVIEEQRAVRLKKDPETTNEQRSTILDSLRNYEDNINSISG
SLVLLQNYLQPLSIAGGSVAGTFEVKEGQEQWQARLQILEEALVSGLVGNMINGGHFPLQ
STIQSDQQSFADMGQNFQLDLQMHLTSMQQEWTVVATSLQLLNQMYLSLARSLTG

CPn_0727   813559   816192
CT619 hypothetical protein
KYYLFSMSTFSIQNRLRTISGESTRIIKLDHKYSGFDPRSVPAINLEELNSGIYALRHLM
NALQSENTNVAALLNPNNTIFPTTSWTDYKHSRPQASSPRAPSSQTPTDIVSAAALALVL
VIDGGLAELVASVTEIDLGALSTISTVRQLMASYLGLTTLTAEQEKVVFSSSYVPSEKNL
LEHVKQEKAAEIQAKQEEIKAVLEAKGVSTEEIEAILKEYPDIYAADFFKEFIEEPLHTY
RAKVGAPIQEMNENAIQLLPTPPAITPDNVNEVNGMNTLSTILQAIDNALGDYKTOAQTAY
EIITILQTLVPLVDKTTFTKAEFDLIYTATQLPNTASLKLYLTDRQIAEYRGKITKVYQN
SIQNLSETKRVVENNRSMLETOLSHFQQAQNCFVTWISQANALNIAITNKYISAVLTTSH
EMYGGLLCLSYMYERLADDEKAIFDKSVNEYLPIHIVVGGSWVNGWIAKMAAYQELAEYS
LGTAVTSQDQIKAYLQTRGNEFKATRHFFHNIGDQMYQFANETVFGNCLTTANGAIQPDL
GGFIREAMTNVGTVEADYVSNAQRILNEFNTAATAHVLQLQLQIAELQKKADDLDPGKAS
FTENRKFAVAAWITSESLGDALISHILNSQLPKQEAFLKPLIEEINFNNLAANALNSLLQ
ITNEFSTTSVVYSLSSYLVQSKTGQNLFAGDYYETLLAAAREREYIYRDTARCKQAINLV
NGLLQKINSLPGATSAQKQEMLNATTYYQYSLSVTVLNQLTVLESLLAGLKMTLQTTSNNK
YDKSVFKIESFDDWIPTLAALESFLTSGFPNISATGGLGPLFTQVQSDQQTYTSQGCTQQ
LNLQNQMTTIQQEWTLVSTSMQVLNGILSQLAGAIYSN

CPn_0728   818483   816525
CHLPN 76kDa Homolog (CT622)
VFMVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERW
SILRSAVNALMSLADKLGISASSNSSSSTSRSADVDSTTATAPTPPPPTFDDYKTOAQTAY
DTIFTGTGLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAVKVGAQITELA
KYASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMODNPVVPGKTPAIAQSL
VDQTDATATGIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAE
AQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVCGSKQQGSSIGSIRVSM
LLDDAENETASILMSGFRQMIHMFNTENPDSQAAQGELAAQARAKAAGDDSAAAALADA
QKALEAALGKACGQQGILNALGQIASAAVVSAGVPPAAASSIGSSVKQLYKTSKSTGSDY
KTQISAGYDAYKSINDAYGRARNDATRDVINNVSTPALTRSVPRARTEARGPEKTDQALA
RVISGNSRTLGDVYSQVSALQSVNQIIQSNPQANNEEIROKLTGAVTKPPOFGVPYVOLS
NDSTQKFIAKLESLFAEGSRTAAEIKALSFETNSLFIQQVLVNIGSLYSGYLQ

CPn_0729   819905   818592
CHLPN 76kDa Homolog (CT623)
PAWSSV:TLN:DTKDTMKKQVYQWLA:GVVLLALT:SGYAELF:L:EQKVKSHTYTTLDEVR
DYL:KRGFVETHKQDGVLR:AGDVRARWL/FREDIKHP:DKDKYNFLPVNRYK:GEFYLYI
DYRAEPNML:GKMNWTAIA:XENTAA/VDINRAFLGYRFYKNPETRTDFFME:GRGGLCD
:JFE:EVUFQ:NFLX:LH:IYWTREL:KDYPYQV1VHCG:PYVMEAIIIO:IFGK1:PFLEI
QFFVKH:VVLWNTFVFGEH:TTEKAATNAMKYKTGVK/WLVF3HE:QVIW:INFJKKPLYLY
GAPLMFHLAKAYKTFLGKENLAWF:GYTLG7:LRFA/IIA:SAT/HGYEVVEALC7VPEIDVG:
HIRGNLLEKFWFAQA:AANYDPKEAN:FTNYKIGF:AL/MY/G1TI:LL/FRAYGAYGKPANDK
LLGGDFTFDGFDLLI:GAF

CPn_0730   821616   819664
mviN Integral Membrane Protein
GGFRQ22ENGIMQRRKIHEV:IARG:IFNLL/X7PPV:GF:FY:IFRGIAHATYFGADPIVAAFW

U:FRTVFFLPK:LG:IL:LEL.....PHFEFLRAQGLDRAAFFFRF:IRLIY7GT:IFTLLIE
AVLVVVLQY/EEGTYCM:LLTM:LLFGG1FLMMYNVNGALLHGENKFF7/GLAPVVVNII
WIFFVVAARHSDPBER:7TGLVALMIGFPFFEWL:STMNGWKFLLEAKFYQEHUSVRALL
APLGLUGILTSG:IFCLUL:LGGICLARYVHETGPLYLMYSLKIYQCFFTRCF7GFGVFFVLLPA
ISPCVOREDHERGLKLMFVFVLTLTMSVMIIMTAGLLLLALPGVRVLYEHGLFPQSAVYA:
VRVLRGYGASI:PHALAPLVGVLFYAQRQYAVPLF:1:1GTALANIVLSLVLGRWVLKDVS
7I:GYATS:TTAW/QLYFLWTYGSKRLPMYSKLLWESIRRSIKVMGTTMLACHITLGLNILT
7TT7VVIFLNFLTPIAWPL::TAQATAFL:TEGCIFLAFLFGFAKLLRVEDLINLASFEYW
:.:.:.:.:.:.:.:.:.:.:.:.:.:.:

CPn_0731   921494   921760
No robust homolog present in Genebank/EMBL as of 11/7/98
VAIAISRNIPVIRLCY:/PONILKIERAKETSLSFLLIKPFSPPPLKQDYLFDISPYTSSE
ITIGGSYFKLNKASLGSSTLRLRSISIIS

CPn_0732   822092   822976
nfo-Endonuclease IV
NFMKVLPPPSIPLLGAHTSTAGGLKNAIYEGRDIGASTVQIFTANQRQWQRRALKEEVIE
DFKAALKETDLSYIMSHAGYLINPGAPDPVILEKSRIGIYQEILDCITLGISFVNFHPGA
ALKSSKEDCMNKIVSSFSQSAPLFDSSPPLVVLLETTAGQGTLIGSNFEELGYLVQNLKN
QIPIGVCVDTCHIFAAGYDITSPQGWEDVLNEFDEYVGLSYLRAFHLNDSMFPLGANKDR
HAPLGEGYIGKESFKFLMTDERTRKIPKYLETPGGPENWQKEIGELLKFSKNRDS

CPn_0733   823739   823101
rs4-S4 Ribosomal Protein
GLKYMARYCGPKNRVARRFGANIFGRSRNPLLKKPHPPGQHGMQRKKKSDYGLCLEEKQK
LKACYGMIMEKQLVKAFKEVIHKQGNVAQHFLERFCRLDNMVYRMGFAKTIFAAQQLVA
HGHILVNGRRVDRRSFFLRPGMQISLKEKSKRLQSVKDALESKDESSLPSYISLDKTGFK
GELLVSPEQDQIEAQLPLPINISVVCEFLSHRT

CPn_0734   823863   824915
yceA
QNTKEHFSSNGNFLQCNYFQDYVRVFIMEKKYYALAYYYITRVDNPHEEIALHKKFLEDL
DVSCRIYISEQGINGQFSGYEPHAELYMQWLKERPNFSKIKFKIHHIKENIFPRITVKYR
KELAALGCEVDLSKQAKHISPQEWHEKLQENRCLILDVRNNYEWKIGHFDNATLPDIQTF
REFPEYAEKLAQECDPETTPVMMYCTGGIRCELYSPVLLEKGFKEVYQLDGGVIAYGQQV
GTGKWLGKLFVFDDRLAIPIDESDPDVAPIAECCHCQTPSDAYYNCANTDCNALFLCCDE
CIHQHQGCCGEECSQSPRVRKFDSSRGNKPFRRAHLCEISENSESASCCLI

CPn_0735   825680   825003
*Uridine Kinase (Uridine Monophosphokinase) (Pyrimidine
Ribonucleoside Kinase).
GEKFHLMMLMMIIGITGGSGAGKTTLTQNIKEIFGEDVSVICQDNYYKDRSHYTPEERAN
LIWDHPDAFDNDLLISDIKRLKNNEIVQAPVFDFVLGNRSKTEIETIYPSKVILVEGILV
FENQELRDLMDIRIFVDTDADERILRRMVRDVQEQGDSVDCIMSRYLSMVKPMHEKFIEP
TRKYADIIVHGNYRQNVVTNILSQKIKNHLENALESDETYYMVNSK

CPn_0736   827731   825992
ygeD-Efflux Protein
RGELLKLARQCLVAFMTVSVKKKSFRALVTTHFLTIINDNLYKFLLAFFLLEGKTLTENA
KILSCVSFFFALPFLLLAPLAGSLADRFQKRNIILATRFIEILCTILGTYFFFIQSVVGG
YVVLILMACHTTIFGPAKLGILPEHLPSEQLSOANGIMTAATYTGSILGSCLAFFLLYDVT
HRLGVNSYVWPTLMCVIVSIISTLISFCIRPSNVKNVKQKITLVSFKDLMKVLKDTRMIH
YLTVSIFLGSFFLLIGAYTQLEIIPPVEFTLKYPKHYGAYLFPIVALGVGTSGYITGKIS
GKDIKIGYVPLAAIGLALVFMGLYAFACSILFVLFFLLALGFLGGVYQVPLHAYVQYASP
EHKRGQILAANNFLDFFGVLVAAGVIRVLGSNLGSLPETSFFYIGWFVLAVSIWTLWIWR
EHVYRLLLGIILRROLGYYLKIHQSSSPKCYFVAVQSYREIRRVLAALTKTVRSRVIILD
QKLVPGWRAWLLSWCVPTVVSSVRDNDSEAQDAWAVLQANHLKTSLKKFPDVSVVCLGLP
KNVERFTSILQEQGIDLHPIQLVQKEGKKRVIYTLVFPHA

CPn_0737   827469   830756
recC-Exodeoxyribonuclease V. Gamma
KRSAKLPASGASKRKGRAKKKLTQERIFAFSVRVLPSNRKNAKRNLYKLSFIIVRKCVVT
SALNDFFLTETVMNATKHCRASFSNSPRHLLAQLAEDITSTHQKPFTKRWILVANATTGH
WIKNQLVHLSDHIFMGSTIFTASDSIVKHLFLGSGCSOPNIPDYLTLPLLINNILEEIS
KASKFENGREFLSPPTYETTKKLAAAFKQFHTFSQRPTKNASHYQELFQILESHFSSYEE
MFTTILNRTOEEDCSLHIFGVAHLPKHLAEFFINLSTYFPVYFYCFSPCREYFGDLLSD
RAIDFFWNOLPDSPIKNAWEHYVLSDRQALLANLAHKSQSSQNFFLDREIDYQEMFLPSK
HDSSLGVIQNSILDLKPTSPODFSQTKQTICIYRALNIPREVQEVFCKVTELLHRGVSPE
EIFILSSHIESYKVHLNAIFHPVPLVFFDEVDPRAEDLRNKILLLSSILQTQGDLHYIL
QLLTHPQLQOPIDQNKVPYLIKKLSSEWGKISSKDRASGQQMKALGDLILEEYPFHQEGG
RVSQVEWETTVPLIYFIQERINLYLSSQHSYEDLFQNVFSCLEKIFVLSPEETSFITT
LRNSLFPTFATSSCSLLFFTDFCLDFLLHFHKPSPLYDKPGPYIGSLSSLSLIPKGYVFI
LGANKTTSSDIFDLLNRTTTHEELAFSSTEDEENFHFLQILVSTKHELHISYISSAAQFN
LPSPFLMHIKETLDLPVETLPTQPYLSAFFKNKACLHTSOEYNYSLAHAFYSKKALLPSL
FIPTVKQVNLPQHLSLNEIIKGIFSPLDLFLKTNYNLRISYPEHLKKQQKLFPTKHQIED
FWNECFVDKEHDLIFSISPHAEELFTYYREKTILLRNGLDKDPKHSPYTVTFSSSIFEER
PYHESYLFPPLSLSFQGNPVQIHGTIHGVCNEGLYLCSIDPRDSLKXTTRTLGSLPETSS
EQKQLLERYVALAVL MSQHLSSDSALIKLTSFHTKENHHPPFSDPEGYLRKVLEVYHLM
SSQPIPLLSPLCWKTLDDEEKFHQAVLSAIGEEAKNPSLPIFWQFHNRNIEEILNHVGAS
ERLKILSLFRGPCEAV

CPn_0738   830719   833895
recB-Exodeoxyribonuclease V. Beta
KFYLFCEVPVKPFNIFDSNSSIQGKFFLEASAGTGKTFTIEQIVLRALIEGSLTHVEHAL
AITFTNASTNELKVRIKDNLAQTLRELKAVLNCOPASLPTVLDINCNVKQIYHQVRNALA
TLDQMSLFTIHGFCNFVLEOYFPKTPLIHKNPALTHSQLVLHHITNYLKQDLWQNVLFQE
QFHLLAVRYNITUKIT:SLVDKLLAG7TOPICS7FGGRVERLEOIGLWHCQIYNSLLEIP
KQVFLDOLTAH:GFKKQPF:SILDCLHHFVDLL/TGSETHGGLFSFFKIAETFNFKHRLAR
YKICAAFTVLENMSWERTLEFCHLDRIFNTLL/DLQEYLKONYTPWLSPDESVFALEKL
LSGGEAQPVVQALRE/NQLVLIDFFQTDOKUJWGIFSGLFISPKFTGSLFLIGDPKQSIY
EWRSADLPTYLTAKS:SF:EQKQLSLVIRMYRITFYLMEAIIIQ:IFGKI:PFLEIPGYLPIEY
HALNI:QSJETFENPFHAPIHFFFYET:IKQJALHIFSEALPLOKEQKIFLAMWVVLVGDSN
QAFELI:YAT:PV:FPKNK:IFHL:TETHIL:TTALLEAILHIPENYEK:ISKILFSSLFGLGL
DEVTTKREDFT:IYFGSILICY:LHHIL:LIATFYP/MFFV/FJLFSSPHGDL:FQEMEKLCGY
LIFT:IGGYPYHQLLILKNFJED:PWEEIELA/F:/7EDLETLKITTTIH:J:HL:LEYDIVFCPG
IEKGKKNKGSGELLIRHMVA:TPAF7QL/LF:I:TQPPGGLG7IT:ALTNYVKLEYTQGSAYD
LAIIILIQEHIPDLF5Y:LFKDMIHIAFT/IILGLLCETFALK/7MFFD:IIKKH:LEYDIVFCPG
IKQU:IPY:7KLF:IGKQ/LLPHJEKT:IH:I1K:ILEGI:QFLIL/DJFEYLM:T:IMRFIKHTHILEG
FEET:ILKLL:IKTFF:IPL7FFGUTF:GI:GJVFLHIF:IFRGT:IPLFLEGWHJKMXXV:DLFFEHE
GKYY:I:LDWKT7FLU:TNGDYGKGIIL:IJI7IKOEYLDYG7ZG17CVVKAVRKFLNQFEIDDWEL

'VIFIP'H'UT'ANGFFA'.:'ED IPNFNPKA'UF   /H

CPn_0739   834392   833861
'T 164 hypothetical protein
CKVLFKLMCYGLRNKFTKICVTIIALGILSFRSIFQEVYDKIRSSFVSLHVKFFPKIKQ
APGSILANLELENLTLKERVASLEEKLKLYEVSNHTPPLFPEILTPYFHKLVECKVVYRD
YTHWSSSCWMVGKTIGIKKNGPVLSGNVLVGLYDYVGEHQSRIRLITDVGMKPSVVAMR
GSIOGWWIKHGLRELIPOVEOIGHAYILEKDKYEKISCLOELDGLIQGEGENQALLRGIL
...

CPn_0740   836054   834864
tyrB-Aromatic AA Aminotransferase
SYMSFFNHIPTFSPDAILGLONVFFADKRPEKVNLVIGVYEHPQKRYGGLSCIRKAQTVI
LEEEQNKSYLPISGLQIFLDEMRELVFGAVDPSAIVGFQSLGGTGALHLGARLLSVAKGS
GKVYVPEQTWSNHIRIFSQEGLEVIRYPYYSKEQKQLLFEPLIAFLKEVEKNSVILLHGC
CHNPTGVDFTEDMWKELAILMKERELIPFFDTAYQGFAHGIELDRKPIEIFISEQNTVLV
AASSSKNFALYGERVGYFAVHSTFTDELVKIHSFLEEKIRGEYSSPORWCVEIVSTILSN
PYLKEEWQSELNFIRESLGKMRTRFVQALRKVAGHTFDFLLSQHGFFAYPGFSDKQVLFL
REQHAVYTTAGGRMNLNGITEKNIDHVVQSFIQAYEL

CPn_0741   838383   836185
greA-Transcription Elongation Factor
EYIFRLKTGCIVDYLEKLQVLIEEGQSANFLSLWEEYCFNDVVRGRELVEILEKVKSSSL
ASLFGKIVDTVVPLWKIPEGKDKDRVLQLIDLQTSNSQMFFDIATEYVNKKYSGEENF
NEALRVVGLRDGRDFQFSLSRFDFLMHMHKGNFVFHOGGWGVGEVMGVSFLQQKVLIEFE
GIMSAKDISFETAFKSLTPLSGDHFLSRRFGDPDGFEAFAKENPIEVVEILLRDLGPKTA
KEIKDELVDLVIPEADWNRWWQSAKTKIKKGTRIISPDNPKEPYVLSDAGCSHMGQLERK
LGLSLSNSAEKISLIYHFIRDLHSELKNIEIRKSLVKALQDLDVEEGNKSLILORELLLSE
YLGIKDASIDKEYITSLSEDDTSRLLENMPIVALQKSFLSLVRKYSSFWQQVFMQILLYT
TSPTMRDFVYKTIKNDPSSVEVLKKRLLDSAHQPMHFPELFVWFFLKLQNHEDGLFDPED
KEVLRLFLESALNFMYQVASTPHKELGKKLHHYLVGQRYLAVRQMIEGASLPFLKELLLL
STKCPOFSSSDLVKLSLAEVVQPTLKKHKSNVEEENVLWSTSESFSRMKAKLQSLVGKE
MVDNAKEIEDARSLGDLRENSEYKFALEKRARLQEEIRVLSEEINRARILTKDLVFTDKV
GVGCKVTLKGDAGEVVEYTILGPWDADPDSCILSLQSKLAQNMLGKKLNDVVILQGKEYK
ISRIQSIWEEHGA

CPn_0742   938442   838888
CT635 hypothetical protein
TKMMVIVMNSKSAQKIIDSIKQILTIYNIDFDPSFGSSLSSDSDADYEYLITKTQEKIQE
LDKRAQEILTGTGMSKEQMEVFANNPDNFSPEEWLALEKVRSSCDEYRKETENLINEITL
DLHPTKESKRPKQKLSSTKKNKKKNWIPL

CPn_0743   838956   840362
'nqrA-Ubiquinone Oxidoreductase, Alpha'
IFMKITVNRGLDLSLQGSPKESGFYNKIDPEFVSIDLRPFQPLSLKLKVEQGDAVCSGAP
IAEYKHFPNTYITSHVSGVVTAIRRGNKRSLLDVIIKKTPGPTSTEYTYDLQTLSRSDLS
EIFKENGLFALIKQRPFDIPAIPTQTPRDVFINLADNRPFTPSPEXHLALFSSREEGFYV
FVVGVRAIAKLFGLRPHIVFRDRLTLPTQELKTIAHLHTVSGPFYLQEYAYRRYNSIDVHIHSVAPIT
NEKEVVFTLSFQDVLTIGHLFLKGRILHEQVTALAGTALKSSLRRYVITTKGASFSSLIN
LNDISDNDTLISGDPLTGRLCKKEEEPFLGFRDHSIISVLHNPTKRELFSFLRIGFNKPTF
TKTYLSGFFKKKRTYTNPDTNLHGETRPIIDTDIYDKVMPHRIPVVPLIKAVITKNFDLA
NELGFLEVCGEDFALPTLIDPSKTEMLTIVKESLIEYAKESGILTPHQD

CPn_0744   841387   840389
hemB-Porphobilinogen Synthase
EMSSLTLSRRPRRNRKTAAIRDLLAETHLSPKDLIAPFFVKYGNNIKEEIPSLPGVFRWS
LDLLLKEIERLCTYGLRAVMLFPIIPDDLKDAYGSYSSNPKNILCHSIHEIKNAFPHLCL
ISDIALDPYTTHGHDGIFLNGEVLNDESVTDIAPSDMMDGRIGYI
RSKLDQSGYSKTSIMSYSVKYASCLYSPFRDALSSHVTSGDKKQYQMNPKNVLEALLESS
LDEEEGADILMVKPAGLYLDVIYRIRQNTCLPLAAYQVSGEYAMILSAFQQGWLDKETLF
HESLIAIKRAGADHIISYSAPFILELLHQGFEF

CPn_0745   841903   841742
No robust homolog present in Genebank/EMBL as of 11/7/98
VDSCFDDWRASSLQGSTTYNVAYDPKHTLAYGFCNQVSVKKFHLKPPKSQEKFL

CPn_0746   841939   843567
CT632 hypothetical protein
FSGRCPFSFEVFMLGKEEEFTCKCKQCLSHFVTNLTSDVFALKNLPEVVKGALFSKYSRS
VLGLRALLLKEFLSNEEDGDVCDEAYDFETDVQKAADFYQRVLDNFGDDSVGELGGAHLA
MENVSILAAKVLEDARIGGSPLEKSTRYVGEYLYYRDPILMTSAFKDMFLGTC
OFLFDTYSALIPQVRAYFEKLYPKDSKTPASAYATSLRAKVLDCIRGLLPAATLTNLGFF
GNGRFWONLIHKLGDNLAELRRLGDESLTELMKVIPSFVSRAEPHHHHHHQAMMQYRRAL
KEQLKGLAEQATFSEEMSSSPSVQLVYGDPDGIYKVAAGFLFPYSNRSLTDLIDYCKKMP
HEDLVQILESSVSARENRRHKSPRGLECVEFGFDILADFGAYRDLQRHRTLTQERQLLST
HHGYNFPVELLDTPMEKSYREAMERANETYNEIVQEFPEEAQYMVPMAYNIRWFFHVNAR
ALQWICELRSQPQGHQNYRTIATGLVREVVKFNPMYELFFKFVDYSDIDLGRLNQEMRKE
PTT

CPn_0747   843949   844053
CT631 hypothetical protein
RTCMGCKGAEVQILSSRSLSGMKILSGSLFYKKFC

CPn_0748   844096   844121
ispA-Geranyl Transtransferase
CTLVLHALDTYRPSIESAIEKALECFGPIGHPIRSPYEYALQGGCKRLRPGLVCMMAQGL
GLNIIDVMDSALAVEFVIHTSTLIADDLPCMDNDDERPGRPTVHKAFDEATALLAGYALIPA
AYSHLRLNAKKLKEQGGDPREIDIAYNIIGDITDKIIGGSGVLGGGQYDDMFFSNRGQEHV
QSIMIKKNSSLFEIACLGGWLFGCGDFQFAPIITFFCFNNFGLLFQIKDDFSDLQKDSQOI
GINYALLFCGKAALELLARGONNCLELLDRLSAGGLFNSSEFETIIGGLGSF

CPn_0749   844634   845006
glmU-UDP-GlcNAc Pyrophosphorylase
VCYMTYILAGSIFGSPEDFLYFELISKAHYIWDILGKANIYWDILDLMUQMLENIIVFXSIIGTVEGGVTLKN
IEKIEIAEDPAYVEISAYIVGNITGLAGUTEVRIIGAYLPGNVIRGSRCVVGHCTEIKNSYLG
HIITKAAIIFAYIGGVLGGEVNLIGAGVRCAANFRLDGFHIIYVREFSDKCKKKIDTGRRKLGAF
LGKGVAIGANVVIENGAGVIGDITRIRDGQVI

CPn_0750   845065   845702
...

CPn_0761　　　857494　858375
CT410 hypothetical protein
GIMTSWIELLDKQIEDQHMLKHEFYQRWSECKLEKQQLQAYAKDYYLHIKAFPCYLSALH
ARCDDLQIRRQILENLMDEEAGNPNHIDLWRQFALSLGVSEEELANHEFSQAAQDMVATF
RRLCDMFQLAVLGALYTYEIQIPQVCVEKIRGLKEYFGVSARGYAYFTVHQEADIKHAS
EEKEMLQTLVVGRENPDAVLQGSQEVLDTLWNFLSSFINSTEPCSCK

EELLYFSRFSEKQNYSLGNMETKRSIYMNLPDRKKALEAAVAYIEKQFGAGSIMSLGRHS
ATHEISTIKTGALSLDLALGIHGVPKGRVIEIFGPESSGKTTLATHIVANAQKMGGVAAY
IDAEHALDPSYASLIGVNIDDLMISQPDCGEDALSIAELLARSGAVDVIVIDSVAALVPK
SELEGDIGDVHVGLQARMMSQALRKLTATLSRSQTCAVFINQIREKIGVSFGNPETTTGG
RALKFYGSIRLDIRRIGSIKGSDNSDIGNRIKVKVAKNKLAPPFRIAEFDILFNEGISSA
GCILDLAVEYNIIEKKGSWFNYQEKKLGQGREFVREELKRNRKLFEEIEKRIYDVIAANK
TPSVHANETPQEVPAQTVEA

CPn_0763　　　860520　859972
ygfA-Formyltetrahydrofolate Cycloligase
HFPMTDPKIEKSALRKLFISIRRDLSEERKHEASSAVASFVRSFSKESVVLSFVSFNHEI
DMQEANRILIQKCTLALPKIDQENLYPVLIPSIDDLISVVHPKDPFSKQTPISSDKITHV
LVPGLAFDQQGYRLGYGHGFYDRWLAQHPYPSIRTIGIGYCEQKIDRLPQESHDIPLSQI
YLC

CPn_0764　　　861819　860524
CT648 hypothetical protein
GYKSMDIKKLFCLFLCSSLIAMSPIYGKTGDYEKLTLTGINIIDRNGLSETICSKEKLKK
YTKVDFLAPQPYQKVMRMYKNKRGDNVSCLTAYHTNGQIKOYLECLNNRAYGRYREWHVN
GNIKIQAEVIGGIADLHPSAESGWLFDQTTFAYNDEGILEAAIVYEKGLLEGSSVYYHTN
GNIWKECPYHKGVPQGKFLTYTSSGKLLKEQNYQQGKRHGLSIRYSEDSEEDVLAWEEYH
EGRLLKAEYLDPQTHEIYATIHEGNGIQAIYGKYAVIETRAFYRGEPYGKVTRFDNSGTQ
IVQTYNLLQGAKHGEEFFFYPETGKPKLLLMWHEGILNGIVKTWYPGGTLESCKELVNNK
KSGLLTIYYPEGQIMATEEYDNDLLIKGEYFRPGDRHPYSKIDRGCGTAVFFSSAGTITK
KIPYQDGKPLLN

CPn_0765　　　862415　861801
CT647 hypothetical protein
TTIYIKLLGRLMKKWISILILSFLSLLSILPVLAITINHVKISQRWSDLNSQILTLKVIR
DHEDQVIKHNARISKDRNNLSIESLNASCKQLRPLSKERERLNKLNSNSLLAQSKEVWER
KRALEKSNHQLVWNCEQMHNDFAFVRLEQATEMDNEDIESLFSLFNPENPVAPLVFFTCW
KMTKQTTPLGNEVWLTHAEAISRWI

CPn_0766　　　863785　862394
CT646 hypothetical protein
AMNFKLPVYHIGLTKAENNTIKIAILQKTCKGWIVCHCEQIPEGKTWSLPKKYFAAPTTF
SLQGSDILVKSSSSSLKNRKNILKVALTNLEASLALPWESLIVQPQLGKPTDRGETPLTL
WIAQKNTLKKELSFLSQAQIFPDKLSCRAADIFFLAEQSPLKSLPAYLLIYGGSEEVTCI
FVKNHAIAVARSFSNHSTKKSCDDIHATLQYIQETFPQTVLPAIHVAQISPNLQKILEQK
LSLPLVVCQSMTYGVEDEDWEIYGDTIAAAHHGASRRPLTFPYDATSVSPAAQKHWLLRS
SLLIGKYALMATVVVSLGSVLKLKSLSSSASNHFAFACPEEGVLPRSLKAAEKTVKAIGK
KNSASNYPLLPTIPTSEQTLKFLLALGKSSPSIKFSYFSYTMTSYPSKDNPSLPYSALVE
VKGGQGQPEDIPQFLKKISSHPKLQHVSESLEDQRSFKLQFTLSS

CPn_0767　　　863878　864177
CT645 hypothetical protein
NIMLSYLLRTAINVYSFLILAYIFASWVPDCQSARWYQLVSKCVDPFLNFFRRFVPRIGF
IDPSPFVGLLCLGILPFVILRVLRFIILNIFHSPWLLQYL

CPn_0768　　　864144　865163
yohI/nir3-predicted oxidoreductase
YFSFSMAAPIFIKNILLRSSIVYAPLAGFSDYPYRCMSALYQPGLMFCEMVKVEGILYAP
ERTSKLLDYNENMRPIGAQLCGSNPETSGEAAKILEGLGFDLIDLNCGCPTDKITKDGSG
SGLLKTPELIGRILDKIINSVSIPVTVKIRSGWDMEHINVEDTVRIIRDAGASAVFVHGR
TRAQGYHGPSKQEYISRAKAAAGKEFPVFGNGDIFSPEAAQAMLTTGCDGVLVARGTLGA
PWIGKQIQDYLTTGSYEKIPFIKRKAAFLEHMRLVEDYYQSETKFLSETRKLCGHYLISA
AKVRFLRSSLAKATSYQEVYQLVNDYEEADDSSLETFVKC

CPn_0769　　　867763　865121
topA-DNA Topoisomerase I-Fused to SWI Domain
SIQGPHAIRLMKKSLIIVESPAKIKTLQKLLGSEFVFASSIGHIVDLPAKEFGIDVDHDF
EPQYQVLPDKQEVINHIRKLAAKCEKVYLSPDPDREGEAIAWHIANQLPDSPLIQRVSFN
AITKNAVTEALKHPRTIDMALVNAQQARRLLDRIVGYKISPILSRKLQQRSGISAGRVQS
VALKLVVDREKAIDAFVPVEYWNLRVLMQDPKTTKTFWAHLYAVQGKKWEKEIPEGKTEN
DVLLINSEEKARHYAELLEKSSYTITRVEAKAKRRFAPPPFITSTLQQEASRHFRFSASR
TMSIAQTLYEGVDLDSEDSTGLITYMRTDSVRVDPEALTTVREYIQQTFGKEYLPEKANV
YTTKKMTQDAHEAIRPTDINLTPDKLKNKLSDDQFKVYNLIWKRFVASQITPAIYDTLAV
QITTDTEIDLRASGSLLKFKGFLAVYEEKQDDENDQEEDHPLPPLHAQDALIKEEVSQEQ
AFTKPLPRFTEASLVKELEKSGIGRPSTYATIMNKIQSREYTTKENQRLRPTELGKIISQ
FLETNFPPIMDIGFTALMEDELELIADNKKPWKLLLQEFWTTFLPVVITAEKEAVIPRIL
TNIECSKCHKGKLVKIWSKNSYFYGCSEYPECDYRTSEEELAFNKEDYAEDTPWDSPCPL
GGGVMKVRHGRYGTFLGCEKYPECKPISIHKKGEEIEQEEPIPCPAIGCNGKIFKKRSR
YNKIFYSCSEYPECSVIGNSIDAVITKYSGTEKIPYKKKTPTKKKSSAKTTKAAKTPSKK
GKAKSSVKKSSEKKTGPLFLPSPDLAKMIGNEPVSRGEATKKIWDYIKEHQLQAPENKKL
LVPDNNLATIIGPNPIDMFQLSKHLSQHLTKVSNDESSASS

CPn_0770　　　868322　869131
CT442 hypothetical protein
KPPTRNVEKLEFVTSLCSPDDDLITFNKQGLIAGPEEEKVAFLVRSNAMLDAGPETPASF
PEGLREQFQIFPEYVEVLYGNEGLDVWEAGCTWILINIEVTIQLRKHHRKASPWLGMYSRD
EVLAHEAVIIAVRHKFHEPVFEEVLAYQTSRWTWRRFFGPLFRSPGESYLLLFFTILCLGI
LLMVPAGILIMLVLIHYFLMRLCMAQSYLYRAMKKIPYMLGVPPLWVLLRLTDKEIKMFA
FKFIPVLGIVAPKRKLENVRWKQIYQSYFV

IFKCRKGPLVGLGALDMFQKQKLSLKYLPGLHMQQGLQMLQSPLTELSSSYYFQEIIDNP
FFLLGGGLEEHEWINYPFTNLTFSYLNQTFLPQEGLGYTPRLLPQIEEAFSTAEERFIAHQI
VJHGGDFRLPLPNHEDFAQRLELDPLEKIHKVWFTIQHLCGEGIAGPSLQSYWMKLLRNSS
IPLQAVGLVPDCYPLMTTKGEFAPIMKKFGLGLGELRHILKKALGSIPWCPAAACTVKPMVS
TPLPLGIYTLPFYGGGWKIEVGTRGLDGIKLHKETFHFYEHLPKEEQKNLSQQILSAKWLIK

NLRKREQTLLQVMETLLPKG　　　LLGKIPAPYPLGIKDLAEDLGFHETTIFRAIENKAVA
APIGIFPLKHLFPRGIHQDSSHSKENVLGWIRCWIATEGTPLGGTVIGDRITAKGIPGAR
RTVAKYRAQLKILPANPPRKDFYARGSNGRFRDRCB

CPn_0772　　　872400　870464
uvrD-DNA Helicase
KLGLIMTCISELNEAGRKAVTAPLNPVLVLAGAGAGKTRVVTYRILHLINQGIAPREILA
VTFTNKAARELKEPLNQCASTNEFDVPMVCTFHSLGVFILRRSINLLNRENNFTIYDQS
GAPFLLRELAVGMLLAVGYKDLNRWFGDIDKILLWRTILACLALATPTSCEVCKNRKL
TANRLRVPLGWLDSGLFVLHFSGGVSMKVLIHSTILGWVLQPMIACRTARLILHRCLPCHE
MVFAVVGDPCQSIYGWAGANIHNILHFENDYPNAKVLGLEENYRSYGNILNAANALIKNNA
SRLEKELRSVKGPGEKIRLFLGSTDREEADFVAAEIILQLHRVGNIKLRDICIFYRTNSQS
RTFEDALLRRRIPYEIIGGLSFYKRKEIQDILAFLRIFISKSDIVAFDRTVNLPKRGIGS
TTIFALTQYAIAQGLPILKACQQALDTKDVKLSKKQQEGLQEYLALFPQIEHAYNTLSLR
DFIESVVRITGYLEILKEDADTFKDRKSNLEELYHKALESEQQNPKTHLELFLDDLALKG
SDDDLNLTADRVNLMTLHNGKGLEFRVSFLVGLEEQLLPHANSLGGTYENIEEERRLCYV
GITRAQDLLYLTAAQVRSLWGTVRMMKPSRFLKEIPKDYMIQVR

CPn_0773　　　872485　873195
ung-Uracil DNA Glycosylase
FMQNATIDQLPVSWQEQLPLCWREQLKEEWSKPYMQQLLIFLKQEYKEHTVYPEENCVFS
ALRSTPFDQVRVVILGQDPYPGKGQAHGLSFSVPEGQRLPPSLINIFRELKTDLGIENHK
GCLQSWANQGILLLLNTVLTVRAGEPFSHAGKGWELFTDAIVTKLIQERTHIIFVLWGAAA
RKKCELLFNSKHQHAVLSSPHPSPLAAHRGFFGCSHFSKINYLLNKLNKPMINWKLP

CPn_0774　　　873183　873425
CT606.1 hypothetical protein
LEAPHNEGIHSVCFQKTPRLTAKSVVSMEMLLTTQQLPSAEGMPSVANLEADFLRAEALL
AEMREIRGCLEQSLRTLVPSE

CPn_0775　　　874040　873414
yggV family
ERFMKIVIASSHGYKIRETKTFLKRLGDFDIFSLSDFPDYKLPQEQGDSITANALTKGIH
AANHLGCWVIADDTMLRVPALNGLPGPLSANFAGVGAYDKDHRKKLLDLMSSLESLVDRS
AYFECCVVLVSPNQEIFKTYGICEGYISHQEKGSSSGFGYDPIFVKYDYKQTFAELSEDVK
NQVSHRAKALQKLAPHLQSLFEKHLLTRD

CPn_0776　　　874180　875487
CT605 hypothetical protein
FIFVLKNFYDCLLMFFQFLSFTMKKIFYSFVLLSCIFPYVGCAQVFVGLDRIFSEGEYTR
CIQGKKIALISHSAAINSRGQDALSVFYSRKHDCTVEILCTLEHGYYGATPTETVGNOPS
RYPNLRSVSLSYGVKEVPKEVAEHCDVFVYDVQDIGVRSYSFVTVLMQIVKASERYGKQLI
VLDRPNPMGGRIVDGPLPNPTTSGSLAIPYCYGMTPGELALFFKKTYAPNANVVVIPMKG
WNRSHTFDETGLIWMPTSPQMPDPQSPFFYAATGILGALSVASIGVGYTLPFKVLGAHM
DGEKVADELNRMKLPGVLFLPFFYEPFFGKYKMEMCSGVLLVLQDPKIFYPVETQCTIWG
VLKALYPKQVEQTLKSIERIPARRSSICNLFGGDEFLSISHKERYIVWPLRRLCKESRES
FHQLRSSCLLSEYAES

CPn_0777　　　875586　877178
groEL_2-heat shock protein-60
TSEDRVVWVFKSQFEGLSALKRGVHALTKAVTPAFGPRGYNVVIKKGKAPIVLTKNGIRI
AKEIILQDAFESLGVKLAKEALLKVVEQTGDGSTTALVVIDALFTQGLKGIAAGLDPQEI
KAGILLSVEMVYQQLQRQAIELQSPKDVLHVAMVAANHDVTLGTVVATVISQADLKGVFS
SKDSGISKTRGLGKRVKSGYLSPYFVTRPETMDVVWEEALVLILSHSLVSLSEELIRYLE
LISEQNTHPLVIIAEDFDQNVLRTLILNKLRNGLPVCAVKAPGSRELRQVVLEDLAILTG
ATLIGQESENCEIPVSLDVLGRVKQVMITKETFTFLEGGGDAEIIQARKQELCLAIARST
SESECGELEERLAIFIGSIPQVQITADTDTEQREROFQLESALRATKAAMKGGIVPGGGV
AFLRAAHAIEVPANLSSGMTFGFETLLQAVRTPLKVLAQNCGRSSEEVIHTILSHENPRF
GYNGMTDTFEDLVDAGICDPLIVTTSSLKCAVSVSCLLLTSSFFISSRTKT

CPn_0778　　　877400　878092
tsa/ahpC-Thio-specific Antioxidant (TSA) Peroxidase
APVAQSDRVPGYEPGGGORFESSLVRNNKRVEEEVFMTLSLVGKEAPDFVAQAVVNGETCT
VSLKDYLGKYVLFFYPKDFTYVCPTELHAFQDALGEFHTRGAEVIGCSVDDIATHQQWL
ATKKKQGGIEGITYPLLSDEDKVISRSYHVLKPEEELSFRGVFLIDKGGIIRHLVVNDLP
LGRSIEEELRTLDALIFFETNGLVCPANWHEGERAMAPNEEGLQNYFGTID

CPn_0779　　　878502　878095
CT602 hypothetical protein
RFDLIFQHKFTVALFGEAEKGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLLSDYNV
VYFRVREEGYCVDSYFFGLHFLNTQTTLKNIIAIGLPGVGNQHIIEASRSLCQKHNSLLL
FFDHDLYDLLTFNQPF

CPn_0780　　　879241　878591
papQ/amiB-N-Acetylmuramoyl-L-Ala Amidase
HGNKIAVQSLRFMHAKLSFFILLSLLFSGIDCSPLHAAGRSPSLQGVLAEIEDISAKLAS
HEVEIVMLSERLDEQDSKCQKWTAAKPETLAQKIRELESCQKAAKTLAVLTTSVKDLQT
NLQSKLQEIQKDHRALAQDLRLVRRSLLALVDSSSPGAYADFSDPVPENIYIVREGDSLS
KIAKKYKLSVTELKKINKLDSDAIYAGQRLCLQPNKQ

CPn_0781　　　879851　879199
pal-Peptidoglycan-Associated Lipoprotein
QNCYRSRRKTVPLLGCFPSATOKENTMIIHSLWYLCTLLALLALPACSLSPNYGWEDSCN
TCHHTRRKKPSSFCFVPLYTEEDFNPNFTFGEYDSKEEKQYKSSQVAAFRNITFATDSYT
IKGEENLAILTNLVHMKKNPKATLYIEGHTDEPGAASYIILALGARRANAIKEHLRKQGI
SADRLSTISYGKEHFLNSGHNELAWQQNRRTEFKIHAR

CPn_0782　　　881077　879773
rnlB-polysaccharide transporter
GDIIMLRQLCFQVFFFLFAGLVYAEELEYVVRCEHITLPIEVCQTDTKDPSIQKYLSSL
TRLFGKDIALGDKLQPTAAGKESSSPLAISLRLHVPOLGTYLLGGKKTFQTLGGPTIGON
LIVDPGFIIIHAADTHYALTGIPGISAGKIVFALSSLGYLQKLKQGISIIPTTDYGIKNLAP
LFTPYLGLTPKWARAAGNPFYLYVCYKYGVPFIFLGSLEITEGKKVVLPLKGNQLMTPFS
PRKKELLAFVAUTAINDFLFLQFFSLTGSPMGRPPRLLNEIFGTQGNPLFNPEGGGLVFIG
NKLGRFFHFFIMGIGLVAFRLLTKKYPNSGCPAWGPDGPKIAFGCVIKGVRQICIYDIG
GGIDYGLFTGPTNKFSISWAIDGRHLVFGAUNAEEGELYLIGLVTKKTNKIAIGVGEKRF
PGWIAFFQQPIKIGTL

IHMKYLPYIAITAGHKGILLLVFASIGLPKKRLQPKAFQEKLVTIQPKFIVTFPGVVVVP

AKT IRP:VATOPQKQAKCSPPOENVQKALOKPIP... ..TEPPKPSPAPTVAKKTTATEKP
PPSTTKKNTQLSKTQLQTLSEVAQALSLHVDK IEKSETSLKNISWPSTAOLTMHSELKAT
QEDELCELFRTHIALPSKGYVRIKLVLSPNGEIQECSFLSEVSAADKQLLTQRIQALPFQ
KPLEKYKVSKNISFHIKLVSNES

CPn_0784   882359   881892
exbD-Biopolymer Transport Protein
DRADGIFTTTEF/PFGOIPOYKIMKYPFTEEIEEEPLVNLTPLIDIVFVILMAFIVAVPLIK
...

CPn_0785   883039   882296
exbB/tolQ-polysaccharide transporter
DHLYFETLSVNKDFYSHNVHFSHNPIIQAYTEADFFGKSIFFCLLILSVCTWTVLHQKLAI
QKNFLKAGKSLKDFLIKNRHAPLSLDIHPELSPFADLYFTIKRGTLELLDKNRQSAPDRG
PILSSEDIQSLETLLGAIMPKYKALLHKNSFIPATTISLAPFLGLLGTVWGILVAFTHIS
SGSSGNSAIMEGLATALGTTIIGLFVAIPSLIAFNYLKAHSSELISEIEQTAYLLLNSIE
VKYRNTNL

CPn_0786   883137   885293
dsbD/xprA-Thio:disulfide Interchange Protein
NHGVILNKFKTYLQTALIAPFFSFPALSGSFSSIQAEEITQQVNHPGAELLSEGSYIPGL
QTFRLGIKITASKGSHIYWKNPGEIGSPLKISWQLPKGFVVEEEHWPTPKVFEEEGTTFF
GYEDSALIVADVRAPEGYTPGQEVELRAQVEWLACGDSCLPGNVDLKLTLPYEEKEPSLY
PDTHAEFTKTLHAQPRVLENDHSVQVAQGKGNEIILNISKKINATKAWFVSEKADKLFAY
AETSYSGGTGTAWRLKVKNLSGVQKNEKLHGILLLADHTGRPVESLTIHSEVLGQTGSAV
AGLSQYITILIMAFLGGVLLNIMPCVLPLVTLKVYGLIKSAGEHRSSVIANGLWFTLGVV
GCFWGLAGVAFILKVLGHNIGWGFQLQEPMFVATLIIVFFLFALSSLGLFEMGTMFANLG
GKLQSSEMKSSNNKAVGAFFNGILATLVTTPCTGPFLGSVLGLVMSLSFLQQLLIFTAIG
LGHASPYLVFSVFPKMLSVLPKPGGWMSTFKQLTGFMLLVTVTWLVWIFGSETSTTSVVV
LLGGLWLAGLGAWILGRWGTPVSPKKQRVCASLLFFAFLGGAISVSGLASHYFAEPQQTV
SVNEDSLWQPFSLEKLAQLRAOGRPVFVNFTAKWCLTCQMNKPVLVGDAVQKMFETHGIV
TLEADWTRKDPGITEELARLGRASVPSYVYYPGDNSAPVVLPEKITQNLLEDVVSRFVR

CPn_0787   885604   886401
yabD/ycfH-PHP superfamily (urease/pyrimidinase) hydrolase
. TRRQPVDLADAHVHLSDDAFEEDINSVLQRAQDSGVSLVVNVTTTEKELNRSFAYAERFP
KIRFCHVGGTPPQDVDQDIEEDYRNFHAAAHSKKLAAIGEVGLDYCFATEEGIARQKEVL
QRYLALSLECELPLVVHCRGAFNDFFRMLDQYYHNDPRSRPGMLHCFTGTLEEAQELISR
GWFISISGIVTFKNAQDLRDLVVELPLEHLLIETDAPFLAPVPYRGKKNEPAHVLHTINA
VANVKGMFPQELAALAYKNVLRFLHG

CPn_0788   886521   887432
sdhC-Succinate Dehydrogenase
SLVKSLRMSRHEICPEVSHKKGKYYSTFIFRCIHSLAGIAFTFFLCEHLFTNMLASSYFS
QGKGFVAMVNGFHKIPGLKIIEVAGLVLPFLCHAIIGIVYLFQGKSNCYSGDGSRPHLRY
AKNYSYTWQRWTAWILLFGIAFHVVHLRFIRYPVHVDIHGTTYYAVDIQPSRYDVIVRGT
KGFLTLNLPNTEASSIEVSRHDLGGGADAALLSERNSYLLTPSAGTAFLYVVRDALGSLFI
ALLYTILVIAAAFHGFNGLWTFCCRWGVVVSLRMQGVLRIVCYLAMIVVTFHGVSAVWNL
YSVA

CPn_0789   887436   889316
sdhA-Succinate Dehydrogenase
QMDENRKVIVVGGGLAGLSAAMQLANLGIIVELVSLTKVKRSHSVCAQGGINAALNLKPE
EEDSPYVHAYDTIKGGDFLADQPPVLEMCLAAPRIIKMLDNFGCPFNRGPSGNLDVRRFG
GTLYHRTVFCGASTGQQLMYTLDEQVRRREHAGRVIKRENHEFVRLVTDHSGRACGIILM
NLFNNRLEILRGDAVIIATGGPGVIFKMSTNSTFCLQGMANGRLFLQGMAYANFPLQHVP
TAIPGRDKLRLISESVRGEGGRVWVPGDSSKRIVFPDGSERPCGETGAPWYFLEDMYPAY
GNLVSRDVGARAILRVCEAGLGIDGRMEAYLDVTHLPEKTRHKLEVVLDIYKKFTGEDPN
TVPMRIFPAVHYSMGGAWVDWPAADDPDRDSRFRQMTNIPGCFNCGESDFQYHGANRLGA
NSLLSCLFAGLVSGDEASRFIEAFGASQATSSDFDRALQQEKEENARLLSASGKENIFVL
HEEIAKIVRNVTVKRNNRDLQETMDKLKEFRERLKNVSVLDSSPFANKSFHFVRQMGPM
LELALAITKGALLRNEFRGSHYKPEFPERDDEHWLKTTVAVYAPEEPEISYLPVDTRHVA
PTLRDYTKSSTGKIELTNIPDNIRLPI

CPn_0790   889279   890103
sdhB-Succinate Dehydrogenase
NSRIFLIISVYPYRKREMMENLETFILKIYRGVPGKQYWESFELPLHPGENVISALMEIE
KRPVNILGEKVNPVVWEQGCLEEVCGSCSILVNGVPROACTALIQEYIDATQSREIVLAP
LTKFPLIRDLIVDRSIMFDNLERIQGWVAADIEGETFGPQVTQEQQELLYALSOCMTCGC
CTEACPQIDNKSDFIGPAAISQARYFNTYPGDKRSKKRWRALMGKGGIEGCGQAHNCVRV
CPKKLPLTESISAVGREISKFSLRSLFSALFKKKK

CPn_0791   893104   890111
CT590 hypothetical protein
TCLRSSRKIVVEDISDRNMYSCYSKGISHNYLLHPMSRLDIFVFDSLIANQDQNLLEEIF
CSEDTVLFKAYRTTALQSPLAAKNLNIARKVANYILADNGEIDTVKLVEAIHHLSQCTYP
LGPHRHNEAQDREHLLKMLKALKENPKLKESIKTLFVPSYSTIQNLIRHTLALNPQTILS
TIHVRQAALTALFTYLRCQVGSCFATAPAILIHQEYPERFLKDLNDLISSGKLSRIVNQR
EIAVPINLGCCIGELFKPLRILDLYPDPLVKLKSSPGLKKAFSAANLIETLGDSEAQIQQ
LLSHQYLMQKLQNVHETLTANDIKSTLLHYYQLQESTVRAIFFKEGLFSKEQVAFSTOH
PRELSEIQRVYHYLHAYEEAKSAFIHDTQNPLLKAWEYTLATLADASQPTISNHIRLALG
WKSEDPHSLVSLTVHFVEEEVENIRILVQQCEQTYHEARSQLEYIEGRMRNPLNNQDSQI
LTMCHMRFPQELNKALYEWDSAQEKAKKFLHLPEFLLSFYTKQIPLYFRSSYDAFIQEFA
HLYANAPAGFRILFTHGRTHPNTWSPIYSINEFIRFLSEFFTSTESELLGKHKAVINLEKE
TSRLVHNITAMLHTDVFQEALLTRILEAYQLPVPPSILNHLDQLSQTPWVYVSCGTVVDTL
LLDYFECCEPLTLTEKHPENPHELAAFYADALKDLPTGIKSYLEEDSHSLLSSSPTHVFS
IIAGSHLPREAWDNDWYSYTWLRDVWVKQHQDFLQDTILPQLSIYAFIENFCNKYALQHV
VHDFHDFCCDHSLTLPELYDKGSRFLSSLFTKDKTVALIYIRRLLYLMVREVPYVSEQQL
FEVLDNCCYLGISSRITYEKFRSLIEETIPKMTLLCGADLRHIYKGLLMQSYQKIYTEE
UTYLRLTTAMRHINLAYFAPLLFADGMWPSIYFCFILIPGTTEIDLWKFNYAGLQCGQPLD
HIQELFATCRPWTLYANPIDYGMPPPPPGYRSRLPKEFF

CPn_0792   894955   893108
CT589 hypothetical protein
HIHLINIFGIRIMKHTFTKRVLFFFFLVIPIPLLLILMVVCFFFSAAKANLVQVLHTRA
THLSIEFEYKLTIHKLFLDRLANTLALKSYASPSAEPYAQAYNCMMALSNTDFSLCLIDP
FICGVRTHIVGDPFIRYLKQHPEMKKKLSAAVGKAFLLTIIGKPLLHYLILVEDVASWDS
FTTIGLLVFFYPHSFLQKDLFQSLHITKGNICLVNKVGEVLFCAQCSCGSFVFSLDLPNL
KVFQARCHSAIELEKASGILSGENLITVSINKKRYLGLVLNKIPLNVFYTLSLLVPVSDLI
DCALKVFLHICFFYVLAFLLMWWIFSKINTKLNKPLQFLTFCMEAAWRKNIHNVRFEPOPY

GYEFNELGHIFNGTLLLLLLL... ...ACIDYHFGERLIFELILIIILL:IALLIPCFPTFPKV
TFCGOHLRPRQLGCHFNTWT/QDKKGTLGGTIGLAGE LGLHTVLJAP.ILFLAYASSD
VGLQKISKDTADGFCKTTECGEAVVAMEIKYVEKDRIGELLLLSBKRPCMMLDSCESFV
RLPLETHQALQPCDPLTCLTTTEDILKYFSCLFIEECLKDFLHIFUNTENL:CSLTMHNNN
ETEHSADGTLTILSFS

CPn_0793   896838   894919
rpsU-sigma regulatory family protein-PP2C phosphatase (RsbW
...
JAVTTMTIMTP...FFFFMLDDDVLSH... ...ILSH...
NTLTQIVPLNVDVLCLFSDVLDLDASIFETFNVLLLNEMQKVFGIYNEISLIKVFPNGD
KIVVASSIPEHLGENYNHKIDIPKNTPFLAALKQSPKNQEVFSVMQANVFDAKTQELQGI
LYTTFSAESLLKDLLIHKQSYLTVKTAILSKYGVILKASDPALHLHTVYPDMTKEKFCQV
FLNDDPCPIDSELGPLTLSPLDIGENFYSFKIKDTEIWGCIENVPSIDIAVLSYARKEES
FAPLWRRARMYTAYFFCILLGSLIAFIVARRLSLPIRKLATAMIESRKNKNCLYTDDSLG
FEINRLGHIFNAMVENLHKQQHLAKTNFEMKENAQNALHLGEQAQQRLLPNTLPSYPHIE
LAKAYIPAITVGGDFFDVFVVGEGSKARLFLIVADASGKGVNACGYSLFLKNMLRTFLSR
SSSLQQAIQETSRLFYNNTKNSGMFVTLCVYCYHQTSNTMEYYSCGHPPACYLDPDGETS
WLFHPGMALGFLPEVANITSKLFHPKPGSLFVLYSDGITEAHHNNNDMFGEERLQAAIQG
LTGKSAADAVHRLMLSVKTFVGNSHQHDDITLLILKVLES

CPn_0794   897123   898004
No robust homolog present in Genebank/EMBL as of 11/7/98
KSSKHRSFLLKKSGGNQVSLYOKWWNSQLKKSLCYSTVAALIFMIPSQESFADSLIDLNL
GLDPSVECLSGDGAFSVGYFTKAGSTPVEYQPFKYDVSKKTFTILSVETANQSCYAYGIS
YDGTITVGTCSLGAGKYNGAKWSADGTLTPLTGITGGTSHTEARAISKDTQVIEGFSYDA
SGOPKAVQWASGATTVTQLADISGGSRSSYAYAISDDGTIIVGSMESTITRKTTAVKWVN
NVPTYLGTLGGDASTGLYISGDGTVIVGAANTATVTNGNQESHAYMYKDNQMKD

CPn_0795   898008   899195
No robust homolog present in Genebank/EMBL as of 11/7/98
GTLGGANSSATGVSSDGSVIVGAQTADKSVHAFQYYNGEMKDLGTLGGTSSTAKTVSPD
GKVIMGRSQIADGSWHAFMCHTDFSSNNVLFDLDNTYKTLRENGRQLNSIFNLQNMQLQR
ASDHEFTEFGRSNIALGAGLYVNALQNLPSNLAAQYFGIAVKIRPKYPLFCYFLDHNFSSH
VPNNFNVSHNRLWMGAFIGWQDSDALGSSVKVSFGYGKQKATITREQLENTEAGSGESHF
EGVAAQIEGRYGKSLGGHVRVQPFLGLQFVHITRKEYTENAVQFPVHYDPIDYSTGVVYL
GIGSHIALVDSLHVGTRMGMEQNFAAHTDRFSGSIASIGNFVFEKLDVTHTRAFAEMRVN
YELPYLQSLNLILRVNQQPLQGVMGFSSDLRYALGF

CPn_0796   899280   901340
No robust homolog present in Genebank/EMBL as of 11/7/98
SELYSSYLQPCLNMSIVRNSALPLPCLSRSETFKKVRSHMKFMKVLTPWIYRKDLWVTAF
LLTAIPGSFAHTLVDIAGEPRHAAQATGVSGDGKIVIGMKVPDDPFAITVGFQYIDGHLQ
PLEAVRPQCSVYPNGITPDGTVIVGTNYAIGHGSVAVKWVNGKVSFPMLPDTLDSVASA
VSADGRVIGGNRNINLGASVAVKWEDDVITQLPSLPDAHNACVNGISSDGSIIVGTMVDV
SWRNTAVQWIGDQLSVIGTLGGTTSVASAISTDGTVIVGGSENADSQTHAYAYKNGVMSD
IGTLGGFYSLAHAVSSDGSVVSHEHRYHAFQYADGQMVDLGTLGGPESYAQGVSG
DGKVIVGRAQVPSGDWHAFLCPFQAPSPAPVHGGSTVVTSQNPRGMVDINATYSSLKNSQ
QQLQRLLIQHSAKVESVSSGAPSFTSVKGAISKQSPAVQNDVQKQTFLSYRSQVHGNVQN
QQLLTGAFMDWKLASAPKCGFKVALHYGSQDALVERAALPYTEQGLGSSVLSGFGGQVQG
RYDFNLGETVVLQPFMGIQVLHLSREGYSEKNVRFPVSYDSVAYSAATSFMGAHVFASLS
PKMSTAATLGVERDLNSHIDEFKGSVSAMGNFVLENSTVSVLRPFASLAHYYDVRQQQLV
TLSVVMNQQPLTGTLSLVSQSSYNLSF

CPn_0797   901552   902694
No robust homolog present in Genebank/EMBL as of 11/7/98
VLILTWINVLTKLGLNMSKIKVLGHLTLCTLFRGVLCAAALSNIGYASTSOESPYQKSI
EDWKGYTFTDLELLSKEGWSEAHAVSGNGSRIVGASGAGQGSVTAVIWESHLIKHLGTLG
GEASSAEGISKDGEVVVGWSDTREGYTHAFVFDGRDMKDLGTLGATYSVARGVSGDGSII
VGVSATARGEDYGWQVGVKWEKGKIKQLKLLPQGLWSEANAISEDGTVIVGRGEISRNHI
VAVKWNKNAVYSLGTLGGSVASAEAISANGKVIVGWSTTNNGETHAFMHKDETMHDLGTL
GGGFSVATVSADGRAIVGFSAVKTGEIHAFYYAEGEMEDLTTLGGEEARVFDISSEGND
IIGSIKTDAGAERAYLFHIHK

CPn_0798   902810   903856
No robust homolog present in Genebank/EMBL as of 11/7/98
VVFEIIFVVRVPMKKTCCQNYRSIGVVFSVVLFVLTTQTLFAGHFIDIGTSGLYSWARGV
SGDGRVVVGYEGGNAFKYVDGEKFLLEGLVPRSEALVFKASYDGSVIIGISDQDPSCRAV
KWVNGALVDLGIFSEGMQSFAEGVSSDGKTIVGCLYSDDTETNFAVKWDETGMVVLPNLP
EDRHSCAWDASEDGSVIVGDAMGSEEIAKAVYWKDGEQHLLSNIPGAKRSSAHAVSKDGS
FIVGEFISEENEVHAFVYHNGVIKDIGTLGGDYSVATGVSRDGKVIVGHSTRTDGEYRAF
KYVDGRMIDLGTLCGSASFAFGVSDDGKTIVGKFETELGECHAFIYLDD

CPn_0799   905001   903940
No robust homolog present in Genebank/EMBL as of 11/7/98
KREENMAAIKQILRSMLSQSSLWMVLFSLYSLSGYCYVITDKPEDDFHSSSAVKWDHWGK
TTLSRLSNKKASAKAVSGTGATTVGFIKDTWSRTYAVRWNYWGTKELPTSSWVKKSKATG
ISSDGSIIAGIVENELSOSFAVTWNNEMYLLPSTWAVGSKAYGISSDGSVIVGSAKDAW
SRTFAVKWTGHEAQVLPVGWAVKSVANSVSANGSIIVGSVQDASGILYAVKWEGNTITHL
GTLCGYSAIAKAVSNNGKVIVGRSETYYGEVHAFCHKNGYMSDLGTLCGSYSAAKGVSAT
GKVIVGMSTTANGKLHAFKYVGGRMIDLGEYSWKEACAHAVSIDGEIIVGVQSE

CPn_0800   906550   905249
eno-Enolase
RKEIKIMFEAVIADIQAREILDSRGYPTLHVKVTTGTGCVGEARVPSGASTGKKEALEFR
DTDGPRYQGKGVLQAVKNVKEILFPLVKGCSV/EQSLICSLMMDSDGSPNKETLGANAIL
GVCLATANIAAAATLRRPLYRYLCGCFACSLPCFMMNLILFYZMHADNGLEFQEFMIRPIGA
SSIKEAVNMCADVFHTLKKLLHERGLSTGVGDEYGFAPHLASNEEALELLLLAIEKAGFT
PGKDICLALDLAASIFYNVKTGTYDGRHYEEGIAILCHLCDRYFIOCIEDGLAEEDYDGW
ALLTEVLIEKVQIVIRNLFVTNPELILEGISIVGLANIVLIRPACICTLTETVYAICKLAQM
AGYTTIIHGRTTFTTIADLAVAFNACQIKTCGLCPCERVAKYHRLMEIEEELGSEAI
FTDCHVFEVYEDGEE

CPn_0801   908709   906727
atpB-Extragenase Al^ Subunit B
IIFTMTPQLHALFAAAIAQFEAIAPLCALVRHIJVKCQVLJIFDCZPTTFTIAIVVANVHL
PTLVILAUNKTLAAQLVQEFREEFFHRIAVEYFICYZDYYZGHEAVIARCITYIEEILLINDE
IDKLFICIATRCIIERRLKRUPTLIVICIVCFICYICICPENYTCHALVLEVCTPRHILTAQLVR
MHYQAIPIFQRGAFRERSIVIDIFAYESHLALRLEFLIUFLTSIEYCDFUTHILKEIVP
SATLYRGCHYVIPEAIRFQAIRTIQEELEERMAFFDDPFIEKDRLFHHFTHDIFMIKEIG
FTKGIENYSRHFHSAFIYAHTSLLLYFPEDFLLIIDECHHFTLIVJIPAMYRHHLSRKQLL

VEYCFRLI:AFDNRPLTYEEAQKYFRF/IYVGAT. /EVQESSGHI:/GO:IRPTGIPDP
MPEIRPAT:OVDDLLEEIRLPL:QKHEKILVI:ITKKLAEDHAGFLGELEIPAAYLHSGI
ETAERTQILTDLR/GV:DVLIGVNLLREGLDLPEVSLVAILDADKEGFLRSTSSLIQFCG
RAARNINGKVIFYADQKTRSIEETLRETERRROIQLDYNKEHNIVPKPIIKAIFANPILQ
TGKDSESPKEUORPLGKEDLEEQIKKYEALMQRAAKEFRFNEAAAKYRDAMQACKEQLLYL
F

CPn_0802   202761   208702
CT... hypothetical protein
IRKEEVLDVDNHIYEVLADWLSVGIDPTKSIIYLQSAIPEIYELHLLFSMLISINRVMGI
PSLKDMARNASIEEGSLSYGLIGYPILQSADILLAKAQFVPVGKDNEAHVELTRDIARNF
NRLYGQVFPEPEVLQGELTSLVGIDGQGKMSKSANNAIYLSDSDATITEKVRKMYTDPNR
IRATTPGRVEGNPLFIYHDIFNPHKDEVEEFKARYRQGCIKDIEVKARLAEELIHFLKPI
KERRSEFLSKPLALQNVLEDGTHKMREVAKVTMEEVHDKFGFSHKWRSLLK

CPn_0803   910306   909752
CT584 hypothetical protein
FMAAKTKTLELEDNVFLLLEGNLKRIFATPIGYTTFREFQNVVFNCANGQQEIANFFFEH
LINGKLTQELAPQQKQAAHSLIAEFMMPIRVAKDIHERGEFINFITSDMLTQQERCIFLN
RLARVDGQEFLLMTDVQNTCHLIRHLLARLLEAQKNPVGEKNLQEIQEEITSLKNHFDEL
TKALQ

CPn_0804   911074   910310
gp6D-CHLTR Plasmid Paralog
EIFSSMGNLKTLLESRFKKNTPTKMEALARKRMEGDPSPLAVRLSNPTLSSKEKEQLRHL
LQHYNFREQIEEPDLTQLCTLSAEVKQIHHQSVLLHGERITKVRDLLKSYREGAFSSWLL
LTYGNRQTPYNFLVYYELFTLLPEPLKIEMEKMPRQAVYTLASRQGPQEKKEEIIRNYRG
ERKSELLDRIRKEFPLVETDCRKTSPVKQALAMLTKGSQILTKCTSLSSDEQIILEKLIK
KLEKVKSNLFPDTKV

CPn_0805   911846   911067
minD-chromosome partitioning ATPase-CHLTR plasmid protein GP5D
GYASRMKTIAVNSFKGGTAKTSTTLHLGAALAQYHQARVLLIDFDAQANLTSGLGLDPDC
YDSLAVVLQGEKEIQEVIRPIQDTQLDLIPADTWLERIEVSGNLAADRYSHERLKYVLGS
VQDKYDYVIIDTPPSLCWLTESALIAADYALICATPEFYSVKGLERLAGFIOGISARHPL
TILGVALSFWNCRGKNNSAFAELIHKTFPGKLLNTKIRRDITVSEAAIHGKPVFATSPSA
RASEDYFNLTKELLILLRDI

CPn_0806   913816   911867
thrS-Threonyl tRNA Synthetase
NANNESPPNMEAWNKMIQVTCDQKNYEVLEGTTAAELAKQLKNSHQFIGVLINERPRDLS
THLNEGDTLVFLTSEDPEGREIFLHTSAHLLAQAVLRLWPDAIPTIGPVIDHGFYYDFAN
LSISESDFPLIEDTVKQIVDEKLAISRFTYGDKQQALAQFPQNPFKTELIRELPENEEIS
AYSQGEFFDLCRGPHLPSTAHVKAFKVLRTSAAYWRGDPSRESLVRIYGTSFPTSKELRA
HLEQIEEAKKRDHRVLGAKLDLFSQQESSPGMPFFHPRGHIVNDALIRYWKQLHTAAGYK
EILTPQLMNRQLWEVSGHWDNYKANMYTLQIDDEDYAIKPMNCPGCHLYYKTRLHSYKEF
PLRVAEVGHVHRQEASGALSGLMRVRAFHQDDAHVFLTPEQVEEETLNILQLVSTLYGTF
GLEYHLELSTRPEKDTIGDDSLWELATDALNRALVQSGTPFIVRPGEGAFYGPKIDIHVK
DAIQRTWCCGTIQLDMFLPERFELEYTTAQGTKSVPVMLHRALFGSIERFLGILIENFKG
RFPLWLSPEQVRIITVADRHIPRAKELEEAWKRLGLVVTLDDSSESVSKKIRNAQNMQVN
YHITLGDHEINENVLAVRTRDNRVINDVSVERFLNTILEEKNSLSLTALL

CPn_0807   913950   914879
CT580 hypothetical protein
TLQTGLHMSLFLVFLTAFIWSSSFALSKLVMNASAPIFATGARMVIAGAILALAAWFRGG
FVGISKKIFLYIVLLALTGFYLTNIFEFIGLQSLSSSKTCFIYGLSPLMSALFSYIQLKE
KVTLKKVLGLSLGLVSYICYLTFGGGGDDSQPWTWQIGLPELLILGAASLASFGWTLLRQ
IEKQSTLSVTAINAYAMLIAGMLSIMHSAVVEPWRPLPVQDISQFLYATLALVVISNLIC
YNLYAKLLRKYSSTFLSFCNLVMPLYSGFYGWILLGEKGVSLGLVLAVAFHVAGCRLIYH
EEFRQGYIVS

CPn_0808   916398   914956
CT579 hypothetical protein
LKKLPSWALKSLKRMPQSAEPSLAHIKPIIFKGACIAMTSGVSGSSSQDPTLAAQLAQSS
QKAGNAQSGHDTKNVTKQGAQAEVAAGGFEDLIQDASAQSTGKKEATSSTTKSSKGEKSE
KSGKSKSSTSVASASETATAQAVQGPKGLRQNNYDSPSLPTPEAQTINGIVLKKGMGTLA
LLGLVMTLMANAAGESWKASFQSQNQAIRSQVESAPAIGEAIKRQANHQASATEAQAKQS
LISGIVNIVGFTVSVGAGIFSAAKGATSALKSASFAKETGASAAGGAASKALTSASSSYQ
QTMASTAKAATTAASSAGSAATKAAANLTDDMAAAASKMASDGASKASGGLFGEVLNKPN
WSEKVSRGMNVVKTQGARVASFAGNALSSSHQMSQLMHGLTAAVEGLSAGQTGIEVAHHQ
RLAGQAEAQAEVLKQHSSVYGQQAGQAGQLQEQAMQSFNTALQTLQNIADSQTQTTSAIF
N

CPn_0809   917794   916307
CT578 hypothetical protein
DTNMSISSSGPDNQKNIMSQVLTSTPGGVPQQDKLSGNETKQIQQTRQGKNTEMESDAT
IAGASGKDKTSSTTKTETAPQGGVAAGKESSSESQKAGADTGVSGAAATTASNTATKIAMQ
TSIEEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRS
EVIEIGLALAKAICTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMK
AAEQKSKDLECTMDTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAAGAAVGAAAAGGA
ACAAAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSGIKAFIKTLVKAIAKA
ISKGISKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQLSEM
QQNVAQFQKEVGKLQAAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAY
AAISGAIAGAHKTNNF

CPn_0810   918193   917925
CT577 hypothetical protein
GEIMHKKHKKTKKAVQSKAAFVKRVPEESQEAAIQQLELAVSDLYKELFLAQTFAGLTDK
NQIHGIIAALSTTLESLHILEELTQGLFFSAQEDANFAKELSSVVHIGLKNLTT/VNKQMVK
GAE

CPn_0811   918913   918208
lctII-Low C:i Response Protein B
IQNNFII:CICCCDG:FRNANKPJKFA:SACFHKKTRSRLAELLAAUKKAKADLLFUVIIPVPT
EEEIPFAU:RIIPFA:I:RKLDL:XJIICIL:D/LLEEI/TVAYTF/:Q:KYNFA/:/LF:QLLAA
AUFOII/FYML:L:S:V:IIQ:ILYLYNEAAFCFFLAFDAQPDNPIPFYYIADGLLFLQQPEESN
NFLJVTMD:I:I:NFEFKILKERCQIMKQ:IEKQMVGETKKAFTKRPA:K:KYTTTNKK:XGK
FR

CPn_0812   919091   920862

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musL-DNA Mismatch Re...
GILICWLGNLTKAPMSTRRPIQLLDFLTINQIAAGE...EN.IV:/:/KEL:ENSLDAGADEI
EIETLCGGQCAIIIPDNCCGFRAEDIRIXLDRHGSKIREF.IDIECENSCIFIRGERDPSI
ASISKMEIQSSIECDEGVRTVIHCGDIVSCEPCAROLGTTVIVNSLFYNVFVRRGPQRSM
QSDRLGIRKLIENRILSTANIGWSWISECHHEIQIAKQXIFQERVAYVMGDHFMQDALTI
DKEANGVRIVGVLCSPSFHRPTRCGQKIFINDRPIECLF:IGKKVGDAYALLLPLHRYPVF
VLKLYLPSSWCDFNVHPQKIEARILKEELVGDCIKEAIVETLACPPGIICRTHQEIEESD
SVPLFMFRMLETSDVQEEESVEFDQNLFAYSSEDVGLEKQEYTGRGPKSQMDWIYSSDVR
....
....
ALMKETLTCATFSKHQHVFDVSWLKLLWJV:KFEKGFUGAKIRRLILDSDFMEG

CPn_0813   920843   921934
pepP-Aminopeptidase P
TLIILWKDNHMSHDRILRAQRALSEHNLDAILVEKSEDLAYFLHDEAIAGILLIGQQEVMF
FVYRMDKDLYSHIQRVPLTFLTQDVVADLSLYVCKQRYCKIGFDSASTVYHKFAQRQVLP
CLWEPLECFTEKIRSIKSEEEIRRMQEAAALGSAGYDYVLTLLREGITEKEVVRQLRAFW
AEAGAEGPSFPPIIAFGEHSAFPHSIPTDRPLKKGCIVLIDIGVLNGYCSDMTRMTALG
TPHPKLLESYPVVVEAQKRAMALCKEGVLWGDIDAEAVRVLREHHLDTYFIHGIGHGVGR
HIHEYPCSPRGSQVKLESGHTITVEPGVYFPGIGGIRIEDTLCIDKNKNFSLTARPVISE
LVCL

CPn_0814   921996   923357
CT814.1 hypothetical protein
FFLFFKLSYNFIFNLPLTMYQLLSIGYSFVSFIALLWMLCYSPNYVTDLYRISLSAEEESL
GGIRAFPQAESLLGGACALNFPDLEERLPDLRKELLFLGSNDRPDACGGKFSLQLASSKE
CYIAALKERVYLNVTNSSRGPVYSFSPKGVPTELWIECFSVSVDGRVEVKVRLQGLHKEL
ISKPRDCETLFLNPPANKLDCWEIAGFRVDASFPVKQKIRRIGVDKFLLMHGGAEYADKA
TKERVDFVSSDEENYSRYLAVGDVLLWDGNCWQTCGEFQGASSRAPLFEVKRIDDKVMIA
DLWNVGGTQRQTISLVKGVPSPIEINEVIREIEFTGMRSWSKPIVLVGGQRLILSPDDWV
LRTAKGWEKLSRADQIQDYVTGKVTGPLLVFEKLEKDLRGFVLRGHMFNAQRTLVETISL
PLKQGFEPAVASQEVSSNTRSAAAHPGATNRGGS

CPn_0815   923361   925622
gspD/pilQ-Gen. Secretion Protein D
MVFFRNSLLHLVALSGMLCCSSGVALTIAEKMASLEHSGRGADDYEGMASFNANMREYSL
QLSKLYEEARKLRASGTEDEALWKDLIRRIGEVRGYLREIEELWAAEIREKGGNLEDYAL
WNHPETTIYNLVTDYGTEDSIYLIPOEIGAIKIATLSKFVVPKESFEDCLTQILSRLGIG
VRQVNSWIKELYMMRKEGCSVAGVFSSRKDLEALPETAYIGFVLNSNVDAHTNQHVLKKF
INPETTHVDVIAGRVWIFGSAGEVGELLKIYNFVQSESIRQEYRVIPLTKIDRPGEMISIL
NAAFREDLTKDVSEESLGLRVVPLQYQGRSLFLSGTAALVQQALTLIRELEEGIENPTDK
TVFWYNVKHSDPQELAALLSQVHDVFSGENKASVGAAGDCGSQLNASIQIDTTVSSSAKD
GSVKYGNFIADSKTGTLIMVVEKEVLPRIQMLLKKLDVPKKMVRIEVLLFERKLAHEQKS
GLNLLRLGEEVCKKGCSPSVSWAGGTGILEFLFKGSTGSSIVPGYDLAYQFLMAQEDVRI
NASPSVVTHNQTPARIAVVDEMSIAVSSDKDKAQYNRAQYGIMIKMLPVINVGEEDGKSY
ITLETDITFDTTGKNHDDRPDVTRRNITNKVRIADGETVIIGGLRCKQMSDSHDGIPFLG
DIPGIGKLFGMSSTSDLTEMFVFITPKILENPVEQQERKEEALLSSRPGEREEYYQALA
ASEAAARAAHKKLEMFPASGVSLSQVERQEYDGC

CPn_0816   925600   927102
gspE-Gen. Secretion Protein E
RGKNTMAASILSQELLDILPYTFLKKHCLLPIEESSEAITIAHATATSVIAQDEVKLLIK
KPVRFVLKEESEILQRLQQLYSNREGNVSDMLLTMKEEDGTTISEEEDLLETTDTIPVVR
LLNWILKEAIEERASDIHFEPCEDSMRIRYRIDGVLHDRHSPPSHLRSALTTRLKVLAKM
DIAEHRLPQDGRIKIHIGGQEVDMRVSTVPVIYGERVVLRILDKRNVILDIAGLHMPKGT
EILFKDTITAPEGILLVTGPTGSGKTTTLYSVLQELKGPLTNIMTIEDPPEYKLPGIAQI
AVKPKIGLTFARGLRHLLRDPDILMVGEIRDQETAEIAIQAALTGHLVVSTLHTNDAIS
AIPRLLDMGIESYLLSATLVGVVAQRLVRTICPYCKVAYTPENQEKSFLASLGKDTEMPL
YRGQGCVHCFRSGYKGRQGIYEFLRPNTLFRSEVASNRPYHILRETAEQNGFLPILEHGI
ALAVSGETTLAEVLRVTKRCD

CPn_0817   927106   928287
gspF-Gen. Secretion Protein F
GGRMPRYRYTLDPKERRKRGYLEALHIQEAREKLAQENIQVLDIREVALRRMSIKSTEL
IVFTKQLLLLLRSGLPLYESLVSLRDQYHEQKMGLLLTSFMETLRSGGSLSQAMAAHPNI
FDHFYCSGVAAGESVGNLEGCLQNIIVVLEERAQITKKMVGALSYPCVLLVFSFAVMLFF
LLGVIPSLKETFENMEVKGLTKIVFGVSDCLSAYRYLFLGFASALITVGTLHTNDAIS
ILEKLLFALPGTKKFVVKVAVNRFCSVASAILKGGGTLIEGLDLGCDAIPYDRLKTDMRD
IVQAVIGGGSLSQELAQRSWVPKLAIGMIALGEESGDLADVLGYVAHIYNEDTQKTLASI
TSWCQPVILIFLGGLIGVIMLAILIPLTSNIQTL

CPn_0818   928158   928682
predicted OMP [leader (16) peptide]
GYTKNVGFDNVVVSTRDSDFSWWPDRCDHVGNIDPTHKQYPNIIKCVLRGVGMKROKRKQ
SITLIEMMVVITLIGIIGGALAFNMRGSIHKGKVFQSEQNCAKVYDIIMMEYATQGSSLK
EIIAHKETVVEEASWCKEGRKLLKDAWGEDLIVQLNDKGDDLVIFSKRVQSSNKK

CPn_0819   929117   928956
CT568 hypothetical protein
ASLYGYCLFLIWEKFHNNIGKANFHLKIITTDFLTDIYIVTIRDPIAYPLTGIC

CPn_0820   929042   929650
CT567 hypothetical protein
DESLPCRCCCGTFFRSETGSIRTEMPMCNSIAMKKOKRGFVLMELLMSFTLIALLLGTLG
FWYRKIYTVQKQKERIYNFYIEESRAYKQLRTLFGMSLSSSYEEPCGLFSLIFDRGVYRD
PKLAGAVRASLIIHCTKDQRLELRICNIKDQSYFETQRLLGHVTHVVLSFQRNPDPEKLPE
TIALTITREPKAYPFRTLTYQFAVGK

CPn_0821   929657   930668
CT566 hypothetical protein
HTNLRLGNKFMQFFIFTFLGLFCILVGL/AFDAAHARKRCACAQTIERGENFFSIKRSACA
EIEYQEKIRUACAIERIGKDKGKVTPKGIAKVATKKKQRYRLLUVFFSRPINNGRYNLYA
LLGEDPECVGDTA:KVAIFIRLLRKAY/DTY/PIVI/PGSFYAIANALISNKQEILERCAQLG
FYVIETLFLPEQAEIFYKMLXI:NCNQ:ILJUFLIYEEKGLGHKKLNLIFMDFLLLEAVL
HHIVAYRETS:LI:INV:IFVAVKPUFIIAIQFI/XQ/AAALELPYTRTDFKLGLRDKMQLLLSRY
PLLFLJIKKMFDYTIL:OW:DYLFLVDTUFKAIQ:PGR/PGK::IKL

CPn_0822   932699   931299
CT565 hypothetical protein
FFLIIVLGTIKNIGIGKTMADAETFKIEGGKGGCGFDNILYRKVKDLICNFKV:FWKKFI.
ISRKA:EA:IS:TLVLAG:IALF:GWW:V:LFIA:Y77ILSFHVEIRKMIGIRKQ:IY:ITAKGPIF

NA(LC/IL(LLFFVLNIPSFAVSF(VILCVILSFIT:. .JSTCSKDHCDKHQDTSNKPS

CPn_0823   932424   931501
yscT/SpaR-YopT Tranlocation T
FYALQVRFSKT::INGNKELMGISLPELFSNLGSAYLDYIFQHPPAYVWSVFLLILLARLLP
IFAVAPFLGAKLFPSPIKIGISLSWLAIIFPKVLADTOITNYMDNNLFVVLLVKEMIIGI
VICFVLAFPFYAAQSAGSF:TNQQGIQGLEGATSLISIEQTSPHGILYHYFVTIIFWLVG
VHRIVISGLLLQTLFVIPIHSFFPAEMMSLSAPIWITMIKMCQLCLVMTIQLSAPAALAML
:T':LFL:I:IOP MAIGVL:T':L:LNGFAFM HLSF:TLSAWF IIRGIC VFTLAWFHIVFIML
:L:IEECIN

CPn_0824   932677   932378
yscS/EliQ-YopS/EliQ Translocation Protein
IRTRAVLAFFATSFKSVLFEYSYQSLLLILIVISAPPIILASIVGIMVAIFQAATQIQEQT
FAFAVKLVVIFGTLMISGGWLSNMILRFAGQIFQNFYKWK

CPn_0825   933618   932677
yscR-Yop Translocation R
ERIKVFTIMRSIFRFSLCFFTLSVSCCFADASLYENSCPSRCQPTPPPSNSNPLNVVQQP
VAASSVPSYMPPLNADDVLPRDHLSDGSFSDTYPDITTQAIILIFLALSPFLVMLLTSYL
KIIITLVLLRNALGVQQTPPSQVLNGIALILSIYVMFPTGVAMYKDARKEIEANTIPQSL
FTAEGAETVFVALNKSKEPLRSFLIRNTPKAQIQSFYKISQKTFPSEIRAHLTASDFVII
IPAFIMGQIKNAFEIGVLIYLPFFVIDLVTANVLVAMQMMMLSPLSISLPLKLLLIVMVD
GWTLLLQGLMISFK

CPn_0826   934382   933612
yscL-Yop Translocation L
HDNKRSGVFSSEVNQPQRYYAIVKMKFFSLIFKDDDVSPNKKVLSPEAFSAFLDAKELLE
KTKADSEAYVAETEQKCAQIRQEAKDQGFKEGSESWSKQIAFLEEETKNLRIRVREALVP
LAIASVRKIIGKELELHPETIVSIISQALKELTQNKHIIISVNPKDLPLVEKSRPELKNI
VEYADSLILTAKPDVTPGGCIIETEAGIINAQLDVQLDALEKAFSTILKAKNPVDEPSET
SSSTDSSSLSNDQDKKE

CPn_0827   935273   934434
CT560 hypothetical protein
GCLVTANTFGTLDILMKHSKEDDLSRFLPKNLLVESPHPEEIPLKSLSFTMSWLPTIHPS
WITIAMKEFPPEIQGQLLAWLPEPLVQEILPLLPGISIAPHRCAPFGAFYLLDMLSKKIR
PCGITEEIFLPASSANAILYYTGPVKIALINCLGLYSIAKELKHILDKVVIERVKNALSP
TEKLFLTYCQSHPMKHLETTNFLSSWTTDAELRQFVHKQGLEFLGKALTKENASFLWYFL
RRLDVGRAYIVEQTLKTWYDHPYVDYFKSRLEQCMXVLVK

CPn_0828   936292   935267
yscJ-Yop Translocation J
IKRYAWIMVRRSISFCLFFLMTLLCCTSCNSRSLIVHGLPGREANEIVVLLVSKGVAAQK
LPQAAAATAGAATEQMWDIAVPSAQITEALAILNQAGLPRMKGTSLLDLFAKQGLVPSEL
QEKIRYQEGLSEQMASTIRKMDGVVDASVQISFTTENEDNLPLTASVYIKHRGVLDNPNS
IHVSKIKRLIASAVPGLVPENVSVVSDRAAYSDITINGPWGLTEEIDYVSVWGIILAKSS
LTKFRLIFYVLILILFVISCGLLWVTWKTHTLIMTMGGTKGFFNPTPYTKNALEAKKAEG
AAADKEKKEDADSQGESKNAETSDKDSSDKDAPEGSNEIEGA

CPn_0829   936729   937298
No robust homolog present in Genebank/EMBL as of 11/7/98
KYICFVPTLAKSFYINIRDSRFYSWLCFIMKETYYRDFLHENYLKNKKSMFHKIYKTAGE
FFLANAKWPLVPAGYRRVRGKDFVLSPLVDLVILFPWVTKDSRYSPCSMTFTCICRSIVE
CIPVVSTLFGIGRFCAVWCVEGFSGSTFDKIYHTIVAVLGILGLGILTFILRIIFSVLML
PVWFLFKCYS

CPn_0830   937339   937959
No robust homolog present in Genebank/EMBL as of 11/7/98
DSCSFLLPCFEVEAQTFPQVFSKVVVYKYKSSRILLIALLYNITLVLGLIFIHKKYLGQK
GRVILKIYQNEEEFFRATERPSIGAGYLRVRNKNSVLFPFEDLMLVCPSVPKDFPLSAF
KVTTKLIYWSVLESIPVVGAFFFSIGRLFAMWCIEDFPGSIFSRIYHTIVGVLGILGLGI
IMFILRIIFTLLTLPFWLISCLKSSAA

CPn_0831   938249   938434
No robust homolog present in Genebank/EMBL as of 11/7/98
NKRKNNVLIRKSESEGAFFEATQNYPTIQQGYQLVRIREHNLSVRAHFDLSLSLDASVHP
AA

CPn_0832   939750   938827
lipA-Lipoate Synthetase
VMKCRPTLNTDQPRVRKKLPERFPKWLQRPLPQGSAFHATDATIKRSGMPTVCEEALCPN
RAECWSRKTATYLALGDVCTRSCGFCNIGHSKTPPALDPTEPERIALSAKELGLKHVVIT
MVARDDLEDGGAQGLVDIIQKLREELPQATTEVLASDFQGNVSALHTLLDSGITIYNMNV
ETVARLSPLVRHKATYARSMFMLEQAANYLPDLKIKSGIMVGLGEMEGEVKQTLQDLASI
GVRIVTIGQYLRPSRKHLQVKSYVTPETFDYYRRVGEAMGLFVYAGPFVRSSFNADMILA
SVQDKASA

CPn_0833   941171   939747
lpdA-Lipoamide Dehydrogenase
RGVLFEILITVSENMTQEFDCVVIGAGPSGYVAAITAAQSKLRTALIEEDQAGGTCLNRG
CIPSKALIAGANVVSHIKHAEQFGIHVDGYTIDYPAMAKRKNTVVOGIRQGLEGLIRKNH
ITVLKGTGSLVSSTEVKVIGQDTTIIKANHIILATGSEPRPFPGVPFSSRILSSTGILEL
EVLPKKLAIGGGVICCEFASLFHTLGVEITVIEALCHILAVNNKEVSQTVTNKFTKQGI
RILTKASISAIEESQNQVRITVNDQVEEFDYVLVAIGRQFNTASIGLDNAGVIRDDRGVI
PVDETMRTNVPNIYAIGDITGKWLLAHVASHQGVIAAKNISGHHEVMDYSAIPSVIFTHP
EIAMVCLSLQEAEQQNLPAKLTKFPFKAIGKAVALGASDGFAAIVSHEITQQILGAYVIG
PHASSLIGEMTLAIRNELTLCCIYETVHAHPTLSEVWAEGALLATNHPLHFPPKS

CPn_0834   941544   942014
CT55C hypothetical protein
KIIMPFAKETEMQRTCWKLEY:V:MIIVIN:PYCSAFLQDPFVA:X2IFSSCHICFPEGASK
KKAEDLFAVSSEDWEAVUIDQNPTQFTNKQVIPEWTVLQ:DWPLVVLFLTIGLLAFAFLIL
LFSTLXILVLTWFKNRAYFY:IIGAAVAYRGTRKLFL

CPn_0835   945698   942045
mnt1-SWI/SNF family helicase
HNIMVLFALAIFRQDAMQHILLKHRKEIVVGFVED:TTIRIIPEFAPEGYWLCTLKLQDID
HLIFAD:ICFICCLIHLMTAYFAVVDALIQIFLIQFFPIK:FWVAVF:HFFLDSIPLQAQ
IEMVYTLE:HIITLTILI:LLEEVFQDWLIRTIHASEEFT/FTNKTFLK:IALYRFAKKFFFL
NEHZABLT:F:EN:XX:F:CHIF:SLQWCILVFKAE(LCFFTLSDIFHKLELAITSLFNVGHDI

IPLLADKFKDQLLSLLCYQSLEYRLRYDIRLLRDASFSFSAYLVTPTCLDNGSLIYPNYC
YSPTKGLMQVVGMLSRKQABIVKSKEDVEDELNERGHLIQEFGFCTFINERNCHLTIRNT
EQGVLLFHYDVGDPSSTEIRFVTWTYYTNCGFFLEKKNDLPIQDGLIVEPQDIPAFTVKN
DAALRRLPNFFSSPPNLKDLLIEVHRQSRGKCLDLKPILVGLGESRCWLFGVFLYREDIG
FSLIPTPLOGLCFLPRVIPPENVPQFLTQYAQHERILFPNPQTRPPESYELVIQSIHRPH
PASPLHLQLELKTNLGSVPIGIALOGLKSKHTFLFTQAGFLDLKQNLFQFLKQFLSTQKC
VIAENTVIANITDVFKLDALAPLSVTCCTIANPEDLQFFSQLKAACLPPIPONLFSSDHQ
LAC:L'ZVI:VILDAVMMFE/VPHIP:LMT:: :V:VL: IFTILANTAILL:GU:V:LL:AFPSFL:TT
:L:IE:T:T:L:T:D:L:/V:VL:R:V:T':LSL:L:R:V:T':L:IA:FTC:V
VFDEIHMAKNKSSQIHKILCRIDALMKLLTGTPIENNLLEFKLLDIILPNYLPSDALF
KKLFTKRCSSEELEEIIPSQDLLLKLTRPFILRRTKKLVLPELPDKVESIIACSLSPDQE
KLYMATLQREKSHIQKLETPEEPATNFLHIFALLNHLKQICDHPAVFFKDPDQYKNYESG
KWNAFVKLLKESLNAGYKVVVFSQYIHMIRIITLYLEEIGIKYASIQGKSLNRKEEIETF
TTDPNCQVFVGSLLAAGTGINLTAGNVVIMYDRWWNPAKENQALDRVHRIGQKNTVFIYK
LITEDTLEERIHYLIEKKIRLLDKVIASQDSNILHMLNREDLLTILSYKDEHGTSDSEES
PVDAPVEDDTGVLPPEDS

CPn_0836   946960   945722
brnQ-Amino Acid (Branched) Transport
KMKKQNASHKTNDKKSLSIWSIGGSIFAMFFGAGNIVFPLALGYHYNAHPWSAYFGMWLTA
VCVPLLGLVSMLFYSGDYQKFFFSIGRIPGMIFTTAIILLIGPFCGIPRAIAVSHATLIS
LSEHKSAFIPSLPIFSAICCVLIYIFSCKLSRLIQWLGSVFFPIMLVTLLWVIIRSFMIP
THPMVQEFIPNARQAWLAGFIEGFNTMDLLAAFFFCSIVLISLRQLVAEEKHPTEEEIPL
SFQGISKKNKRSLALGFFLAAILLGHTYLGFVLSAARHAGLLVNVSKGHILGRISAIALG
PNSILAGVSVFIACLTTEIALVGIVADFLARVVSFKKLNYASAVICTLIPTYLISILNFE
TISHLLLPLLQLSYPALIVLACGNIAYKLWNFRYSPVLFYLTLSLTIVLKLVN

CPn_0837   947777   947145
nth-Enodnuclease III
LTMKQFILRTLNALFPNPKPSLEGWSSPFQLLIAILLSGNSTDKAVNSVTPQLFAKAPDA
QSILDLPPGKLYQLIAPCGLGERKSAYIYQLSQILVRDFHGEPPNDMALLTQLPGVGRKT
ASVFLGIAYGKPTFPVDTHILRLAQRWKISEKKSPSAAEKDLARFFGHENTPKLHLQLIY
YARQYCPALHHKIDNCPICSYLAKEANSTRT

CPn_0838   949196   947781
thdF-Thiophene/Furan Oxidation Protein
ISLNTYPNSFHLFNLKLGILSESSFNFSIFMLKHDTIAAIATPPGEGSIAVVRLSGPQAI
VIADRIFSGSVASFASHTIHLGQVIFEETLIDQALLLLMRSPRSFTGEDVVVEFQCHQGFF
ACSQILDALIALGARPALPGEFSQRAFLNGKIDLVQAEAIQNLIVAENIDAFRIAQTHFQ
GNFSKKIQEIHTLIIEALAFLEVLADFPEEEQPDLLVPQEKIQNALHIVEDFISSFDEGQ
RLAQGTSLILAGKPNVGKSSLLNALLQKNRAIVTHIPGTTRDILEEQWLLQGKRIRLLDT
AGQRTTGNDIEKEGIERALSAMEEADGILWVIDATQPLEDLPKILFTKPSFLLWNKADLT
PPPFLDTSLPQFAISAKTGEGLTQVKQALIQWMQKQEAGKTSKVFLVSSRHMMILQEVAR
CLKEAQQNLYLQPPEIIALELREALHSIGMLSGKEVTESILGEIFSKFCIGK

CPn_0839   949230   950159
psdD-Phosphatidylserine Decarboxylase
FLFIVSRGLVQKPQYIDRITKKKVIEPIFYEKTMLFLYNSKLGKKLSVFLSTHPIFSRIY
GWLQRCSWTRRQIRPFMVNRYKISEXELTKPVADFTSFNDFFTRKLKPEARPIVGGKEVFI
TPVDGRYLVYPNVSEFDKFIVKSKAFSLPKLLGDHELTKLYAHGSIVFARLAPFDYHRFH
FPCDCLPQKTRCVNGALFSVHPLAVKDNFILFCENKRTVTVLETEQFGNVLYLEVGAMNV
GSIVQTFSPNQTYAKGDEKGFFAFGGSTVILLFLPNAIRFDNDLLKNSRMGFETRCLMGQ
SLGRSQREEI

CPn_0840   950141   951544
CT700 hypothetical protein
ISERRNLKTLKTFFGIAKRDKSQKWRIMWLVILWALAASLAIALVAKGYYRFVYFRRYAV
QVIREVRLSMELKEWALAEQQLLPILKKRSYRRQCLFEYMRILRKMORFEESEKLLAEAK
KLGLRGPYFFLEIAYKAYRFGAFKECAQAFASVPQDLFEEEDAAKYASALVRLGDLDAAC
SLIEPWISPLSHQETFVTMGHIYFTSKRYKDAIDFYNRANALGVCPVEVTYNLAQAYRIT
SSYAKAGKLFRKLLSNPVYKEEALFNIGLCEQKLGRPKASLIYQSSDLWSRGDALLHKY
AAHAAMDQRDYVLAEPCWELALRCSTFAKDYKCGLGYGFSLCRLRKYGDAERVYCNLIQN
FPECLTACKALAWLCGVGYATLLGSEEGLMYAKKAVELDHSCETLELLSACEARCGNFDA
AYEIQSFLSSRDTSLQEKQRRSQILRILRKKLPLNDHHIVEVDALLAA

CPn_0841   951719   954640
secA-Translocase SecA
IKRHHLGFLKRFFGSSQERILKKFOKLVDKVNIYDEMLTPLSDDELRNKTAELKQRYQNG
ESLDSMLPEAYGVVKNVCRRLAGTPVEVSGYHQRWDMVPYDVQILGAIAMHKGFITEMQT
GEGKTLTAVMPLYLNALTGKPVHLVTVNDYLAQRDCEWVGSVLRWLGLTTGVLVSGTLLE
KRKKIYQCDVVYGTASEFGFDYLRDNSIATRLEEQVGRGYYFAIIDEVDSILIDEARTPL
IISGPGEKHNPVYFELKEKVASLVYLQKELCSRIALEARRGLDSFLDVDILPKDKKVLEG
ISEFCRSLWLVSKGMPLNRVLRRVREHPDLRAMIDKWDVYYHAEQNKEESLERLSELYII
VDEHNNDFELTDKGMQQHVEYACGSTEEFVMMDMGHEYALIENDETLSPADKINKKIAIS
EEDTLPKARAHGLROLLRAOLLMERDVDYIVRDDQIVIIDEHTGRPQPGRRFSEGLHQAI
EAKEHVTIRKESQTLATVTLQNFFRLYEKLAGMTGTAITESREFKEIYNLYVLQVPTFKP
CLRIDHHDEFYMTEREKYHAIVNEIATIHGKGNPILVGTESVEVSEKLSRILRQNRIEHT
VLNAKHIHAQEAEIIAGAGKLGAVTVATNMAGRGTDIKLDNEAVIVGGLHVIGTTRHQSRR
IDPQLPGRCARLGDPGAAKFFLSFEDRLMRLFASPKLNTLIRHFRPPEGEAMSDPHFNRL
IETAQKRVEGRNYTIRKHTLEYDDVMNKQROAIWAFRHDVLHAESVFDLAKEILCHVSLM
VASLVMSDROFKGWTLPNLEEWITSSFPIALNIEELROLKDTDSIAEKIAAELIQEFQVR
FDHMVEGLSKAGGEELDASAICRDVVRSVMVMHIDEQWRIHLVDMDLLRSEVGLRTVGQK
DPLLEFKHESFLLFESLIRDIRITIARHLFRLELTVEPNPRVNNVIPTVATSFHNNVNYG
PLELTTTDSEDQD

CPn_0842   955015   954710
CT702 hypothetical protein (frame-shift with 0843)
KYYTPPTIGRIPWCNIALKTI:EPEYDCNQLLKTQSLLTTMVDTLLNAPKDFPHSKNQKH
ILFCIAIOTTLEIAVIQFLIAGNRRKFWIF:YYNDQVWGEWTPFI

CPn_0843   955210   954994
CT702 hypothetical protein (frame-shift with 0841)
HKHKL:IICMRFKVMNYIDUYIFTPTDHUJIFEDILLDNGERAASLDKYQETYIVYVEENTDQG
GLLIFVLC:SLVFKHTLHUFU

CPn_0844   956751   956370
ydzE-GTP-binding protein
PNRIETIMLKIAILGRHVNVCK:LFNPLZFYCILAIVKEXJE/TTRDRLYGELJIAFLVPAQV
IDFYYFIGLIN:EDYFQKIILYNJALITYAPKAIFILLLVIDIPCYITEEDAHIAKLLLFLLKKPL
ILVANIFADRQEELQIHETYKIAIFDIFYFPCTAIDKHIILUTLIJRIKLVANLPEPREEEEE

```
:LEEL:VDGHHESEAALPGHTFPDF:SEVFTEGF:    .FCTIPESPQQAPKTLKIALIGRP
NVGK::IINHLLNEERCIIDHTHGTTRDHIDILYHKDRQYLFIDTAGLRKMKSVKNSIE
WHSSHRTEKAI:HRADICLLVIDATOKLKSYEKRILSLISKRKKPHIILINKWDLLEEVRM
EHYCKDLRATDPYUHQAKMLCISATTKPNLKKIFCAIDELHHVVSNKVPTPIVNKTLASA
LHRNHPQVICGRRLRIYYAIQKTTTPLQFLLFINAKSLLTKHYEYYLIQHTLKSSFNLYGI
PFDLEFKEKPKPIIN
```

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CPn_0845        958151    256850
```
```
...
RPLEDIDIATNASPTIVSTIFPDVISIGVAFGIIVVKQDGRLFEVATFRSDGEYKDGRHP
DRIIFSSMREDALRRDFTVNGHYYDPFEDKVFDFVEGTRDIEKKVIRAIGHPRLRFSEDK
LRILRAIRFSSSLGFTLDPTTERAIIKEAPALVNSVSPERIWQELKKMLKROPYGALSLL
LKLKVLIFIFPELRDIPYSLLRTTIEFARKFNPTHFPEILFLLPLFQGVSEEAATVAFGR
LRISNKELKLIESWYEALPHFQNQSGNRVFWAHFLASPTAPLFLELFSALQKDPSRQQHF
ISRVQELESRLEQFILRIKTSSPVVSAPDLIAKGISPGRLLGDLLREAEILSIENECLDK
EKILLLLQEKGFWK
```

```
CPn_0846        959383    958112
clpX-CLP Protease ATPase
REHMNKKNLTICSFCGRSEKDVEKLIAGPSVYICDYCIKLCSGILDKKPSSTISSAPVSE
TPSQPSDLRVLTPKEIKKHIDEYVICGERAKKTIAVAVYNHYKRIRALLHNKQVSYGKSN
VLLLGPTGSGKTLIAKTLAKILDVPFTIADATTLTEAGYVGEDVENIVLRLLQAADYDVA
RAERGIIYIDEIDKIGRTTANVSITRDVSGEGVQQALLKIVEGTTANVPPKGGRKHPNQE
YIRVNTENILFIVGGAFVNLDKIIAKRLGKTTIGFSDDQADLSQKTRDHLLAKVETEDLI
AFGMIPEFVGRFNCIVNCEELSLDELVAILTEPTNAIVKQYMELFAEENVKLVFKKEALY
AIAKKAKQAKTGARALGMILENLLRDLMFEIPSDPTVEAIHIQEDTIAENKAPIIIRRTP
EAIA
```

```
CPn_0847        960019    959387
clpP-CLP Protease Subunit
KLFDEETQMTLVPYVVEDTGRGERAMDIYSRLLKDRIVMIGQEITEPLANTVIAQLLFLM
SEDPKKDIQIFINSPGGYITAGLAIYDTIRFLGCDVNTYCIGQAASMGALLLSAGTKGKR
HALPHSRMMIHOPSGGIIGTSADIQLQAAEILTLKKHLANILSECTGQPVEKIIEDSERD
FFMGAEEAISYGLIDKVVTSAKETNKDTSST
```

```
CPn_0848        961556    960177
tig/murI-Trigger Factor-peptidyl-prolyl isomerase
VQASSPAFPFKSNKKGCLVPRSLSNEQFSVDLEESPGCIVSALVKVSPEVLNKLNKQALK
KIKKEITLPGFRKGKAPDDVIASRYPTNVRKELGELVTQDAYHALSTVGDRRPLSPKAVR
SNSITQFDLQEGAKVEFSYEAFPAISDLPWENLSLPQEEAASEISDSDIEKGLTNIGMFF
ATKTPVERPSQEGDFISISLHVSKSNDENASSAAIFENKYFKLSEEEMTDAFKEKFLGIS
TGHRVVETITSPEIQSFLRGDTLTFTVNAVIEVSIPEIDDEKARQLQAESLDDLKAKLRI
QLEKQAKDKOLQKRFSEAEDALAMLVDFELPTSLLEERISLITREKLLNARLIQYCSDEE
LEKRKSELIKEAEEDATKALKLLFLTHKIFSDEKLTISREELQYMMDVCSRERFGQQPPK
DISNDTLQELVMSARDRLTYSKAIEHVLRKAELLASTPSA
```

```
CPn_0849        961752    965285
motl/snf-SWF/SNF family helicase
ADYIIHSYSRGEMLNFRKLRRDFSANILQDGKKLFEQGAVIDAKILSMNGETVCISAQVR
GLYDNIYECEIEVDRSESDTVDSNCDCSYNYDCQHIVALLFYLEQYFNEMVVAYARSADL
ETDHEINEEVVKKELKETFVAAATKEEERKDREHQKEILREYVHAANALSANPFFLPLEYL
EKDSAELAVLFVSVNEDTFAPANQPIEFQLVLRLPCRSKPFYISNIRTFLEGVLYQEPIV
LNGRRFFFTMQSFNASDRKLIDLLIRYVRYPNHTTEEKLLKSAYLMPPAGEVLAKMFEH
QLADRGGGSLGEKESFSGLFCGNLEEPLCWSLTPAKMKFNLDFFDMPYKALLMTPVILVD
DDEVQPEQTMLLESDAPGIIHHFVYHRFSPQIKRAHLRSFSRLRDIAIPEALFGSFRENA
LPVFQEYAEIANVHLLNSFVTLPYVDEVRAICDMSYLDGELEAKLHFLYGSLRVPAASLA
LQYQDVRAFISDEGILARNLVEERKMLEEVFSGFIYDERDGAFRVKSERKIVEFMTETIP
ANQHRITFNCPENLSGQFIYDETIFELSFREGSDINYYEADLKVHGLLKGVPLDLLVQ
SAKKRFLELPKAGQQSKGTRRGKVNSGKLPCILVLDLEKIAPVVQIFNEIGFKVLDDLVQ
KCPLWSLTGISLDQFEALPVNFSMSERLIEIQKQIRGEIEFDFQDVPQQIQATLRSYQTE
GVHWLERLRKMHLNGILADDMGKLTLQAIIAVTQSKLEKGSGCSLIVCPTSLVYNWKEE
FRKFNPEFRTLVIDGVPSQRRKQLTALADRDVAITSYNLLQKDVELYKSFRFDYVVLDEA
HHIKNRTTRNAKSVMKIQSDHRLILTGTPIENSLEEKWSLFDFPVGLLSGTKNRLDLVNQFNEDPSLLVF
LISLKAGGTGLNLVGADTVIHYDMWWNPAVENQATDRVHRIGQSRSVSSYKLVTLNTIEE
KILTLQNRKKSLVKKVINSDDEVVSKLTWEEVLELLQI
```

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CPn_0850        965254    266390
mreB-Rod Shape Protein-Sugar Kinase
LGKKYWNCCRYDFMSPHRNLFKLKNFSNRLYNRALGRFDKVFNFFSGNVGIDLGTANTLV
YVRGRGIVLSEPSVVAVDAQTHAVLAVGHKAKAMLGKTPRKIMAVRPMKDGVIADFEIAE
GMLKALIKRVTPSRSVFRPRILIAVPSGITGVEKRAVEDSALHAGAQEVILIEEPMAAAI
GVDLPVHEPAASHIIDICGGTTEIAIISLGGIVESRSLRIAGDEFDECIINYMRRTYNLM
IGPRTAEEIKITIGGSAYPLGDQELEMEVRGRDQVAGLPITKRINSVEIRECLAEPIQQII
ECVRLTLEKCPPELSADLVERGMVLAGGGALIKGLDKALSKNTGLSVITAPHPLLAVCLG
TGKALEHLDQFKKRKGNLV
```

```
CPn_0851        966378    968195
pckA-Phosphoenolpyruvate Carboxykinase
REFGIVMVWSTNIKHEGLKSWIDEVAKLTTPKDIRLCDGSDTEYDELCTLMESTGTMIRL
NPEFHPNCFLVRSSADVARVEQFTFICTSTEAEAGPTNNWRDPQEMRRELHOLFRGCMQ
GRTLYIVPFCMGPLDSPFSIVGVELTDSPVYVCSMKINTMRGDDVLRSLGTSGKFLKCLH
IVGKPLSPGEADVSWPCNPKSMRIVHFQDDSSVMSFGSGYGGNALLGKKCVALRLASYMA
HQGWLAEHMLIIGITNPEGKKKYFSASFPSACGKTNLAMLMPKLPGWKIECIGDDIAWI
RKGRDGPLYAVNIPEYGFFGVAPGTGERTNPHALATCPSNSIFTNVALTADGDVWWEGLTE
UPPEPLTDWLGKPWKPGGSPAAHPNGRFTAPLRQCPSLDPEWNSPQCVPLDAIIFGGRRS
ETIPLVYFALGWEHKVTIGACMSGTTTAAIVGCLJKLPHDPFAMLPFCGYNMAYYFQHWL
GFAEHRGLKLPKIRGVNWFRKNNOGEFLWPGFSENLPVLEWIFQRTDGLEDIAERTPIGY
LPITQKFHILPGINLDLQTVQELFGVDAEGWLAEVENIGEYLKIFGSDCPQJITDELLRIK
GELKKK
```

```
CPn_0852        968274    970613
CT711 hypothetical protein
IKLPI(DYYLHTVTLQPSHYINFTPNVTTALSGCKIDTGAIELGHGALFFQELQDKAQC
LKHALGILVQELGAFALRPAQVQTGIGYLPTEESSRIYIGAGIIDRTMPTFTDDEVKAILQ
NHMPFTGKHVGLLDKVFKGYLDGVTPPGGIDPSNPEGAIILNYITLLNNLKPKFAAGST
PTHADYHALYALGHFVKRIEALKAADAPPGKVHAFVQKIMFIYNNMQVLGYPVTDYLN
VUIAUGGINITAAQFVQQYLKNFYGILKDILUINWTLGFOATHIYPADAEYNARDAGVIQSL
```

```
LNLGGNYRQLTENHLPNTGI   GEIIAQIRSFQNGWNGTIIAGNTLPTTMRLTLDSVI
IYTYQCCATIFGMSYGTSTPAKQNVIDAINQEKSYWQARANGFGVTGDCVFDQFATNIGS
GTSYRGIDLFKNKVNEITPTFLIGQASELRYPYNLMGHGMYCTIGEGAMSHLVFLSGRGS
SGWSTQIATFQTQKNSLDPSLLKYFDTMKANKESFVTFAPLQHVYGSSLMLDKTLPTQQNV
IASLGIQMTYSNKAAKYLHELIKEITTFQSADIYYSLSIYLKQMNLQAVADPIGKAVGVI
NDEKTRAMADITRGNKIKAAIDKMLVEIKADAELSKSGIRELVGTLTNFKSQSDGLIRNL
SCLLGFLSGLTLKAVNDPHATYEAFTAEIFTEPFNNWKRQLATFESFVICGGCNGITPGG
QQQLLQAMESSQGDFSTFIQNQQLALCLESSAHQQEWTLVSAALALLNQMVSKIARRIKS
```

```
CPn_0853        970857    971503
CT712 hypothetical protein
NIMHPKIEKRNSLPLTAVAPVFEESYHPSVATTVDYVDATTLSRHLTVLKDVIKEARNLD
LGKAFLTSMKQGFINTGTELAIIQASLADQSSRESRKKEEKIFHQHLGKAAPQAATATSG
VQPTADPVADKMPLQSAFAYVLLDKYIPAQEEALYALGRELNLSGYAQNLFSPLLDMIKS
FNSAPINYNLGSYISQTSGTANFAYGYEMILSRYNNEVSQCRLDIASTVKAKAALANKSA
SVKANVSLTDAQKKQIEDIIASYTKSLDVIHTQLTDVMTNLASITFVPGLNKYDPSYRIV
GGDLSIIALQNDEKVLVDGKVDITTAVNEGGLLNFFTTVLTDVQNYGDLAQTQOLMLDLE
LKAMQQQWSLVSASLKLLHGMYTTVISGFKN
```

```
CPn_0854        972849    971806
ompB-Outer Membrane Protein B
GPFDMNSKMLKHLRLATLSFSMFFGIVSSPAVYALGAGNPAAPVLPGVNPEQTGWCAFQL
CNSYDLFAALAGSLKFGFYGDYVFSESAHITNVPVITSVTTSGTGTTPTITSTTKNVDFD
LNNSSISSSCVFATIALQETSPAAIPLLDIAFTARVGGLKQYYRLPLNAYRDFTSNPLNA
ESEVTDGLIEVQSDYGIVWGLSLQKVLWKDGVSFVGVSADYRHGSSPINYIIVYNKANPE
IYFDATDGNLSYKEWSASIGISTYLNDYVLPYASVSIGNTSRKAPSDSFTELEKQFTNFK
FKIRKITNFDRVNFCFGTTCCISNNFYYSVEGRWGYQRAINITSGLQF
```

```
CPn_0855        974001    972994
gpdA-Glycerol-3-P Dehydrogenase
GLMKQHIGYLGMGIWGFCLASLLANKGYPVVAWSRNPDLIKQLQEERRHPLAPNVVISPN
LSFTTDMKEAIHNAFMIVEGVTSAGIRPVAEQLKQITDLSVPFVITSKGIEQNTGLLLSE
IHLEVLGDSVTPYLGYLSGPSIAKEVLNGSPCSVVVSAYDSQTLKQIHEAFSLPTFRVYP
NTDIKGAALGGALONVIAIACGIAEGLSFGNNAKAGLVTRGLHEMRKLAAIMDCKPETLN
GLAGLGDLCVTCFSESSRNLRFGHLLAOGLTFEQAKAKIGMVVEGAYTALSAYQVAKHHK
IDMPITTGIYRVLYENLDLKEGIALLLQRNTKEEFL
```

```
CPn_0856        975410    973995
AgX-1 Homolog-UDP-Glucose Pyrophosphorylase
GSRDRNVRLTVMTESVYSPSAMHVNSLADKLKAINQEHILDIWPSLSPKQQQRLFQQLTS
VDIDFFRKQQQLLSSPTAILKDFHPITSFASSGEDPERAHAGTTLLKEKKVACVVLAGGQ
GSRLKCDGPKGLFPVSPIKKKPLFQLVAEKVRAASKLAGQPLPLAFMTSPNTNTRQTRSFF
ESNDYFHLDPNQVDFFCQPLWPLLTLSGDLFLEDMDTLALGPNGNGCIATLLYTSGVWEK
WKNAGIEHVSVIPIDNPLALPFGVCGFHAMSNNEVTIKAALRQTAIEDVGILVKSHDS
GKTSVIEYSEIPQNERFALNEDGKLKYCLANIGLYCLSMDFIRHAAYQOLPLYKVHKHAK
QLGHTSLNEKNAWKFEEFIFDLFCYSDHCQTLVYPROECFAPLKNLEGNHSPDTVRQALS
DRERQLFHKVTGKKLSPNTTFELEADFYYPSTSTSLHWENKAFFEEPFFEAS
```

```
CPn_0857        975808    975392
CT716 hypothetical protein
LLLLROYIKTARGISRLMRDRLGSLSLILKVKIHKYLDTLHNQKRLALTVSRNIQATNKR
IADLHLERYEHFISRDNIKHYDILLEYLKTLQSSLYKQQSESLRFLEIHHQQLQELINRR
KIIEKIKNNKYSKDQEIGT
```

```
CPn_0858        977115    975757
fliI-Flagellum-specific ATP Synthase
RNSETRNQRRTRPSTFCFDSMNHLNKEKLHIHNWQPYRACGLLSKVSGNLIEVDGLSACL
GELCKISSTKDPNLLAEVIGFHNHTTLLMSLSPLHSVALGTEVLPLRRPPSLHLSDHLLG
RVLDAFGNPIDKKEDLPKTHRKPLLSLPPSPMMRQPIDQIFPTGIKAIDAFLTLGKGQRI
GVFSEPGSGKSSLLSAIALGSKSTINVIALIGERGRVREYIEKHSNALKQQRTIIIAAP
AHETAPTKVIAGRAAMTIAEYFREQGHEVLFIMDSLSRWIAALQEVALARGETLSAHQYA
ASVFHHVSEFTERAGNNDKGSITALYAILYYPKMPDIFTDYLKSLLDGHPFLTSQGKALA
SPPIDILSSLSRSAQALALPHHYAAAERLRSLLKVYNEALDIIHLGAYTPGQDEELDKAV
KLLPSIKAFLAQPLSSYCYLDNTLKQLEALADS
```

```
CPn_0859        977597    977055
CT718 hypothetical protein
VFLVTTPQSPGSLSQSHLPHPHDPWDTEPTSLPEDPNDKASQELHSLVHLFRKLSIHLLS
EVEKTVQQLKPDLLELALLICEKFLYKKLENPQELALLLSTALQRHTTLRSLTPIKVFLH
PEDLKTLTDWISTHELPMIKHAEFFPDTSCRRSGFKIETPNGILRQEISEELDHLLSVLT
A
```

```
CPn_0860        978639    977608
fliF-Flagellar M-Ring Protein
RTLVFFQNLAKKLTALGISFLGCLLIGVVSCAILFGRSSNPSLAPTQVKTEKTSGNWLK
LTQMGNPKLIESLTKKECLEKDLTSFHPIASAKVAIALSTEDDVMSPLHLSVILTLRKEE
SLTPSLLFSITDYLCSSLFGLKREHISLSDNLGNLYIPESITVNSLFIHTLENYLGKIFP
KEHFALAYHAKAEKPTLCLTLNENYIAHLTKEESEKIVAHTKHYLYQNYDDSYDIVIETL
PFARLQNKKSFPAKVLIGSMILVISLMIYALASFYLARHAYERVSPEPRKIKRGINISKL
LEIIOKESPEKIALILSYLCPKKAEALLNRLPEDLKHQVLKYKL
```

```
CPn_0861        JT9752    978925
nifU-NifU-related protein
ASYPFTWKFLMTLPLEFHIFWSSLSAKYMKKFLTPHCAGTFSEEDAEAKEAHLVTGKQGH
RLMGNCVTFYWLVDKKNCVILDAKFQYFGHPYLIPLAEAVCNLVCGKSYSEAYKMTLDDI
DKSLRVHAHQPALPEDSISLYHFVIDALDTAVEQCLEIPLEDCSLPLQNSPMNLDFEDAN
PYSQSDWEALTHEQKLYALRATIAEKIGPYIAMDGGEVTVESLENFIVTIAYSGNCSQCP
SSLGSTLNSIGQLLRAYIVPELQVKVDESSLNLGHP
```

```
CPn_0862        980124    979722
ytho-MiFS-related protein
GRGTIFRITGGKTICIHEKFQHRKAPPIFWLHHQVAIPPGERVKEHYAUHGDIFSLPPG
GALKLAEKTEESIRQLWGLKDGHIFRFPPHIFHDVHIIVIAALVENLSMPVGHNHIILLPAH
DQQLLIHGLCRHGCLHTTVTWVTVNHFGPIVEEQLLETLGPRGLLFGLHAAHHHLTHVIQP
LGPLLCLCKDRRLLHLDFGDLLURAFLTPELHIADLIFTFGNIGKKLIQELQGIVLDGT
ERVPGCWFPPHTSAGHAGFGAVAANYTAGEERGGALPLFTFHGNIGKKLIQELQGIVLDGT
GLAFGIEVQNRLPNIVVAAIPDIFAELGAFHLIUGSIYPGLUYERFQPLAQVLQNGTIGPF
UCHGALIFGLTERGKDLESGKLARAMHLAIKHLTPLLGGGG
```

```
CPn_0863        980120    980611
(rpmA (Phosphoglycerate Mutase)
```

FHMALLILLPHGOSVWNEKNLFSGWVDIPLSQQG   FSAGRAIONLPIDCIFTSTLVR
JLMTALLAMTHHHSKKIPYIVHEDPKAKEMSRIYSAEEENNMIPLYGSGALNERMYGELQ
GKNKKQTAEOFGEERVKLWRRSYKTAPPQGESLYDTKQRTLPYFEKNILPQLQNGKNVFV
SAHGNSLRSLIMDLEKLGEEEVLSLELPTCKPVVYQWKNHKIEKHPEFFG

CPn_0864   981658   982374
yibC-predicted pseudouridine synthase
YGVWVTKVRIJIKFLASAGVASRRKCDEIIFSGSVTVNGRVAEGPFVLYDPEDKVQVGGTS
··
··
·IVVSEGKKHEIRLFADAAGFPILELKRIRIGSLVLGGLRYGEYRELTDAELGTYMKLSD

CPn_0865   982412   982942
CT865 hypothetical protein
SPMGYVFYVIAGSIFLGISLGAYCQLYYSVKSVLFSWYLLTVYALEKRHALLALSQLVGE
EDAQSOKEIDFLSQCDKLSWRAFLKNSYEIIPTFKEMEDLLSERVQGFLESIETIAEHDR
AILCIENFWASKNLFDFEIAAYEEAVEKYLKLRQRAPLRLASKLFRFLDVPSIRFSS

CPn_0866   983494   982916
birA-Biotin Synthetase
NMKVIYYEIEEIPSTNTMAKSYMHLWDPYALTVISTKCQTAGTGKFGKSWKSSKGDLLNT
FCFFITDLHIDVSRLFRLGTEAVVALCKDLGITEAKIKWPNDVLVHGEKLCGVLPETLPV
EGLLGVVLGIGLNGNTTKQALKDVGQPATSLQEILGHPIDLETTRELLIHHLLGVLQENL
PDSLATKSNRGNI

CPn_0867   983405   984667
rodA-Rod Shape Protein
CIRIPQMHIGFCHCVRGGNFFYFVINNFHILEIYSLLNSNTIMRYHKYFRYVNSWVFLVV
LTLMLLSVVVISSMDPTAMLVTSSKGLLTNKSIMQLRHFALGWVVFFICAYFDYHLFKRW
AWVLYFMICALVGLFFVPSVQNVHRWYRIPFIHMSVQPSEYGKLVTVIMLSYILESRKA
DITSKTTAFLACLVVALPFFLILKEPDLGTALVLCPVTLTIFYLSNVHSLLVKFCTVVAT
IGIIGSLLIFSGIVSHQKVKPYALKVIKEYQYERLSPSNNHQRASLISIGLGGIRGRGWK
TGEFAGRGWLPYGYTDSVFSALGEEFGLLGLLFTLGLFYCLICFGCRTVAVATDDFGKLL
AAGITVYLAMHVLINISHMCGLLPITGVPLILISYGGSSVISTMASLGVLQSIYSHRFAK
Y

CPn_0868   986733   984670
zntA/cadA-Metal Transport P-type ATPase
NFRNGLGVRDLHHFREYYLIINEIIITGRYVFSRLFFTSFSAEVVNTFFESGMSEDTSPL
LSKQNRKLSHNLPLKSAYLSLGTYLIALLSFWLHAKNLSNLFVVFTFFLAGTPALIKSLD
NICQKVVNIDILMTSAAFGSIFIGGALEGALLLVLFAISEALGOMVSGKAKSTLVSLKQL
APTTGWLVLEDGNLQKVAINKIEVGNILRIKSGEVVPLDGEILHGSSSINLMHLTGEKVP
KSCHPGSIVPAGAHNMEGSFDLRVLRTGSDSTIAHIINLVIQAQNSKPRLQQRLDKYSSV
YALSIFAIACGIALLVPLFTSIPLLGPQSAFYRALAFLIAASPCALIIAIPIAYLSAINA
CAKHGVLLKGGVILDRLVSCNSVVMDKTGTLTTGELTCIGCDYFGSKNETFFPSVLALEQ
SSSHPIAEAIVSYLMEQKVSSLPADRYLTVPGGRVRGYFNEQEAFVGRVETGLGKVPSEY
LEDIEQKIYQAKQHGEICSLAYVGNSFALFYFRDIPRPQAKEIIQDLKDLGYPVSMLTGD
HKVSAENTAEILGISEVFFDLTPEDKLAKIRELATQRQIMMVGDGINDAPALAQATVGIA
MGEAGSATAIEAADIVLLHDSLSSLPWIIQKAKQTKKVVSQNLALALAIILLVSWPASLG
IIPLWLAVILHEGSTVTVGLNALRLLKS

CPn_0869   987479   986658
CT728 hypothetical protein
EGWRFFFPKTSENTSDCRQHQILRKIMTQDPHDHFKSRTPEDHIKHVRDKHRVCKGEPHT
TFKGFFYHLANNALSTGVFIFFIRTLFFLIPTNRALQVKSLISLGVGWTFYHGCLKARKA
WAYMELSHRSMLEEKNEIEENFEQEKIELRILFENOGFKDPLLQEMVEYVCSDSTLLLDT
MIREELYIRKEDLPHPLIQGGSRILGGLCGLAIFLPLVLCISYTLAGVFSALMVLVLSFL
KAKILKNDKISEMVWVLGIFITSASIISSLMKLL

CPn_0870   988881   987448
serS-Seryl tRNA Synthetase-2
TTTHPTQGFGGAVILPFSPISIARRIKKSCCSEKSSIYSHFCTLLLLNNETSMLDIKIIRK
TPEECETRLRKKDPKISLEPVLSLDKEVRQLKTDSETLQAQRRLLSQDIHKAKTQGVDAT
NLIQEVETLAADLEKIEQHLDQKNAQLHELLSHLPNYPADDIPVSEDKAGNQVIKSVGDL
PIFSFPPPKHHLELNQELDILDFQAAAKTTGSGWPAYKNRGVLLEWALLTYMLQKQAAHGF
QLWLPPLLVKKEILFGSGQIPKFDGQYYRVEDGEQYLYLIPTAEVVLNGFRSODILTEKE
LPLYYAACTPCFRREAGAAGAQERGLVRVHQFHKVEMFAFTTPNQDDIAYEKMLSIVEEM
LTELKLPYRLSLLSTGDMSFTASKTIDAEVWLPGQKAFYEVSSISQCTDFQSRRSGTRYK
DSQGKLQFVHTLNGSGLATPRLLVAILENNQQADGSVVIPEVLRPYLGGLEILLPKDQ

CPn_0871   988766   989899
ribD-Riboflavin Deaminase
EYMEDFSEQQLFFMRRAIEIGEKGRITAPPNPWVGCVVVQENRIIGEGFHAYACGPHAEE
LAIQNASMPISGSDVVVSLEPCSHFGSCPPCANLLIKHKVSRVFVALVDPDPHKVAGOGIA
MLRQAGIQVYVGIGESEAQASLQPYLYQRTHNFPWTILKSAASVDGQVADSQGKSQWITC
PEAPHDVGKLRAESOAILVGSRTVLSDDPWLTARQPQGMLYPKQPLRVVLDSRGSVPPTS
KVFDKTSPTLYVTTERCPENYIKVLDSLDVPVLLTESTPSGVDLHKVYEYLAQKKILQVL
VEGGTTLHTSLLKERFVNSLVLYSGPMILGDQKRPLVGVLGNLLESASPLTLKSSQILGN
GLKVVWEISPQVFEPIRN

CPn_0872   989903   991216
ribA/ribB-GTP Cyclohydratase & DHBP Synthase
KEPRIFRVACLASESVNARESHIETREEVGSANFVSLEPAIEDLRAGKFVIVVDEASREDE
GDLIIAGEKITVEKMTFLLQHTTGVVCAALSQERLLSLDLPPMVKDNRCRFKTPFTVSVD
AAHGVTTGVSAADRTKVVQLLADPKSKPEDFISPGHFFPLASSPGGVLKRAGHTESTVDL
MELAGLQPCGVLAELVNEDYSMMRLPQILEFARKHNIAVIPVTSIIAHRMLSDRLVSKIS
GAPLPTIYGDFTIHVYESLLECGMOHLALVKGNVAGKSNVLVRVHSECVTGDTLGSKRCDC
GEQLSGAMSYIAEKGTCVLVYLRCQEGRGIGLGHKVPAYALODNGYCTVDANLAMGFPVD
SREYGIGAQILVDLKLTTIKLITHNPQKYFGLQGFGLSITERVPLPVRISEDNEQYLRTK
QEPMGHWLDLFLCNNRVQ

CPn_0873   991188   991694
ribE-Ribityllumizine Synthase
GHAVTIGYNNFEEYMKTLKGHLSAKNLRIAIVGGCFIQAMADALVSTQETFLKFGGSE
IGLHTIPVIGAFELRCTIKKLESSERKFDAIVACGVLIGGETDIIYNGIVNGVAAGIIGALS
LEFCLPITLIGIVAADSAEIAWQRXGIKGRHUIVSGMTTAIEMATLFTQI

CPn_0874   991164   991749
CT753 hypothetical protein
LIFGLHLKILTKQRDRERAGMLKILKIKVLVFPLALLWYVHGIGYAGNGVGLJTNGQTKVR
VGSE/WIFQKLRUYFELLWLTESYIAPLLFCTFIDMAYGEKLFNKKVPALDIAIRGMHHL

HLLIQGSROSGMGLGOILPGG   MTFKQFGTAHKQLLFFLNGYKGFGNTLRGLETAIVL
RHVGCSAKAVGTFKPYFTOGCPGGYAKALHVLRTFFDELGTGTTARLGFECQGEVLLGLRRI
GNYDGLLNLTEVGPSAQGLGIWRTRRGBAEGDLYLGGILGTGGODKGKGGEFTINGAGPCLSML
QQHATIEEAFGPYFTYRANRLOFGGTGRTGHTLVRGATGHGLGFGEASTLAWSFKNLPSD
EAENLVNSFYTYQGEHIPLTFRGLPSLVAGLSVATHGSTVSPENRLRCLYSTMLSLLVKS
LRSHREMLNKQLLPQGTVLDFSETTLSSGGLDVFAESIAVRIHLNGAVSINL

CPn_0875   993363   994022
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RLGRRSRRLFAPPKGTJKLTLVQGANFRTYAEKIJELGERDLGFVVSSAAEKSJJSLAGS
QGEIKDALYRIREVHPLALIEALAENPALIEGMKKMQGRDWIWNLFLTQLSEVFSQAWSQ
GVISEEDIAAFASTLGLGSGTVASIVQGERWPELVDIVIT

CPn_0876   994123   995517
dagA-D-Alanine/Glycine Permease
SIATGETMLYFIEQLNKLSTSFCVFPMILLLGGFLTWKLRGLQFHGLKLGFNLMLQNKLD
DSSSKANEVSSYEAVAGILAGNFGTGNIAGMAVALACGGPGALVWVWLAALGAIVQYAG
SYLGSKYRKPEGNTGEFIGGPIACLAFGHRKKILAGFFALFTIMTAFCAGNCVQVSCIVP
LCAEGTPGKLLVGILLALVVIPVLAGGNNRILRFSARVIPFIAGFYCISCGIILFQHASA
ILPAIKLICSSAFGIKAGLAGIGGYTLSQVISTGINRAVMATDCGSGMVSILQANTKSKN
PVVDGLVTLVPPVVIVMVVCSITMLVLIVSGAYSSGAQGTLMVMSAFKNSLGSLGSVIVIL
AMALFGYTTILTWFACAEKSLQYMIPGRRANLWLKAIYVLIIPLGGVIDMRMIWALSDTG
FSGMVILNCIALIALLKDVLSTNRDVALLKERECSVADPVRNLDA

CPn_0877   995521   995982
ybcL family
RRRIMQLLSPAFAYGAPIPKKYTCQGAGISPPLTFVDVPGAAQSLALIVEDPDVPKEIRS
DGLWIHWIVYNLSTTITNLAEGAEIFAVQGLNTSGKPVYEGPCPPDKQHRYFFTLFALDV
VLPEEENVTRDQLYEAMEFHIIEQAELMGTYEKS

CPn_0878   996660   995992
SET Domain protein
GCMSTVTTEPCSSIHISLNNDWRDSQPYSLDRASELLHFRFLPSLVFSNWKVEQQIETLC
HKSEKRRLISPLAKWLGKLHKQDLLCPPAPPVSVCWINAHVGYGVFARDEIAPWTYIGEY
TGILRHRQAIWMDENDYCFRYPMPLFTLRYFTIDSGKQGNVTRFINHSEQPNAEAIGVFS
EGLFHVIIRTVAPIYAGQEICYHYGPLYWKHRKKREEFIPEEE

CPn_0879   997463   996645
yycJ-metal dependent hydrolase
YRILWKVSMQGFFPLASGSKGNSAYLGTDSCKILIDLGVSKQVVTRELLSMNIDPEDIQA
IFVTHEHSDHISGIKSFVKAYNTPIVCNLETARALCHLLDSHPEFKIFSTGSSFCFQDLE
VQTFNVPHDAVDPVAFIFHYREEKLGFCTDLGWVTSWITHELYDCDYLLIESNHSPELVR
QSQRPDVKKRVLSKLGHISNQECGOLLQKIITPKLKKLYLAHLSTECNTAELALSTVSE
SIASITSIAPEIALAQGITSPIYFSRLEVACPR

CPn_0880   999864   997444
ftsK-Cell Division Protein FtsK
PMIRERKKSRHPRLPTLPLAAKASLYLFFACFSGLSLWSFHRDQPCTQNWIGLLGWSFSS
FLLYFFGAAAFFIPLYFLWLSFLYFRRTPRPLFFYKAAAFLSLPFCSAILLSHLSPVGTL
PALLDTRLPKFILGNNPPVSYVGGIPFYLFYEGOSFCLKHLIGSVGTALIFGFVMLFSVL
YLCGGIALLKKKTFQDGVKKAFCSFFQTCFKNLKKLINRRNYLPKPSVPFVSKNPFSCTK
SQPSPRRVSETIILDGSISPLPQEEIPGSKKESFFLTPHPCKRFLTKFVEPQENKAKEGK
TIALSSTPTVVRESKGKERAALPKLKSLAVPENDLPQYHLLSKNREARPESLQAELERKA
LILKQTLTSFGIDADLGNICSGPTLAAFEVLPHSGVKVQKIKSLENDIALKLQASSIRII
APIFGKAAVGIEIPTPFPQAVNFRDLLEDYQKTNRKLQIPLLLGKKANGDNLWADLATHP
HLIIAGTTGSGKSVCINTIVHSMIMTTLPSEIKLVIIDPKKVELTGYSQLPHMLSPVITE
SREVVYNALVWLVKEMESRYEILRYLGLRNIQAFNSRTRNKTIEASYDREIRETMPFNVGI
IDELSDLLLSSQDIETPIIRLAQMARAVGIHLILATQRPSREVITGLIKANFPSRISFK
VSNKVNSQIIIDEPGAENLMGNGDMLVLLPSVFGTIRAQGAYICDEDINKVIQDLCSRFP
TQYVIPSFHAFDDSDSDNSGEKDPLFAQAKTLILQTGNASTTFLQRKLKIGYARAASLID
QLEEARIIGPSEGAKPRQILIQNPLEG

CPn_0881   1005646   1006209
No robust homolog present in Genebank/EMBL as of 11/7/98
NKKFAVHMPVPIDNSSRNLQEVPESLEDLEQHAEESPTHQSAESSSSLQLSLASSAISSRV
EQLSSLVLGHENSDFSSLRDVPIFSAIYESSTHTPVPTPLVGVGYINGSOSGYYDTQRES
LHLSQLLGSRRVEVVYNQGNFMEASLLNLCPRRPRRDPSPISLALLELWEAFFLEHPPGS
TFNPIFFW

CPn_0882   1006169   1007404
No robust homolog present in Genebank/EMBL as of 11/7/98
NTPQVALLIQYFFCNGAFYVREALRLTPHAQNIVLVGGICPSLYPEHPRSEYYRVSGDIGS
RFDDRGFVNSGVETLPYSSGSFGIWISFTDPTFNFAIVNTFDPTFNFAIVNEVSRPHTQDTE
TSLIEMRDLSEQQEANNTDSLEQEESLMGIVGHTVGGVSMTVTSSPNIFYRIQTLLGLPE
TLAEAEENPTFPNSTIDSLAEIMMNLVRISDAVSIFWIFPIVOTTYNGVLLAVCIGFFGI
NGICSTFLMLTNPRSRDRWRNLRIMVLCYRSLGSGMNLFDLSNNVRMAARRHVTSCTVA
LYAMVTLFGWTVAIQDALOYGFPSVRDAFYRYCLRHRYCLTQRNEDSLQTTGTRFQVTRT
HLEDQQMVASILNLSVFGLFFGFVGLMTTFCGLEISPSCRWDAANNRTVGIF

CPn_0883   1008904   1007573
dmpP/nqrF-Phenolhydrolase/NADH ubiquinone oxidoreductase
LYELFIKSGIFIVMTWLGGLYFICIASLIFCAIGVILAGVILLSRKLFIKVHPCKLKIND
NEELTKTVESCQTLLVSLLSSGIPIPSPCGGKATCKOCKVRVVKNADEPLETDRSTFSKR
QLEEGWRLSCCCKVQHDMSLEIEERYLHASSWEGTVISNDNVATFIKELVVAVDPNKPIP
FKPGGYLQITVPSYKTNSSDWKQTMAPEYYSDWEHFHLFDQVIDNSOLPADSANKAYSLA
SYPAELPTIKFNIRIATPPFINGKPNGEIPWGVCSSYVFLKKPGDKITVSGPYGESFMKD
DDRPLIFLIGGASSSFGRGHILDLLLHFHSKREIDLWYGARSLKENIYQEEYERILEROFP
NFHYHLVLSEFLFEDIAAGWDKDDPTYTHFLFRAFNLGQLGRLDNPEDYLYYVGGPPLHN
GGILKLGQGLVVERGGIILDDFGG

CPn_0884   1009668   1009009
CT741 hypothetical protein
GGCMLGRIVTCFLFLLGGGLFLFAEEFAAXGKHTFVGOPAVMLAIATLFFYFILWFFEQKRR
KAMEKRKNDLAKGDKVTAMGHIGTVDLFREHFVIIJIIAGGRVEVLKGAIGEILFPNDWKG

CPn_0885   1010680   1009413
yibA-rRNA Methyltransferase
ACILTMGTMQNGIHIBIVGYAAGSFYGGYTGGELKFFEELJIQLFAPLVIGHMIAFEHNGP
GLNGRNKHEFGFFCTYFGIEKGGGIGFTGGTEKAKGIIFAVTNGLLIHQVTHDILKLTRGGWARKH
PELMAYFPFKNKGSLGTLIVKGTGGGGVJHMVILFTGGTFEVRVNFAGIDEWKEILGGGL

NIASIYWEEKVAARGISTYYETKLLYGAPSIQOP   ...SDCNSASFSLRPRSFFQPQITO
AAKIIETAYEFINPEGGETLLGLYCGAGTICIMLSPYVKNVIGVEIIPDAVASAQENIKA
NNKEDCVEYYLEDAKAFCKRNENCKAPDVIIIDPPRCGMQSKYLKYILRIGSPKIVYISC
NPKTQFQECADLISGGYRIKKMQPIDQFPYSTHLENIILLEREIOP

CPn_0886   1011298   1010908
nctA-Histone-Like Developmental Protein
RTLFMALKDTAKKMKDLLCSIGHDLAKAEKGNKAAAORVRTDSIKLEKVAKLYRKESIKA
....

CPn_0887   1011692   1014157
CHLTR possible phosphoprotein
MKKLYHPTLFLRPLIRLSLIFALSLTLISGNFPQQKSFGHCCADMHSALISGKNCEELFA
DFIERVLADRETLTARDMGTVVVLVREYLLKCIRKGDCDYGVKILQKLLALRLPKDARKD
LJILWHRLNPEQAPLRDVVDQLFTIGCHESLQDHLLFELYTVTLHSGYENRKODMLLAKE
OGDYKKAIELAKELVAALEKGSCSPHPEIVQIEKTFLQKTLLALQIKVAQEAOECDALL
TPYCLSEIAYTEAMDALVLRIARGEVSRTNEVDSVLLSHALQHLPFAREKAIPELEVLID
HGAYLESTLLYYAYFSLLELYHQNKDFASLERLLEKGDAVFVPEHPYFPEYGFFLGAYFY
AKGKYESAEKVFLOIIDPAVKLGATFARAYEYLGCIAYVQNHYEKAEEYFLRAYKSWGRE
ESGIGLFLAYAVQKKKTACEDMLYHPKFSFTYRHLLDSLCSLSYPHGENKGSSAIQRVHR
AVPELSEIYSRCIYDMIKYRNVTYTHPIIELAYNQVRNLEKRNLEEICRDAQDPEYDKAL
AFWGALQSGASVPRSLIESSDVDEARITIRCYEALYFHNPDAIAMLPQAFSEECNSWQTA
LRLVWTLVRPKGAPNHAKYWDHLVLRPHGDSLYFFGYDLQEYLIGKEDALKHLSVFAELF
PKSSLLSLVYYLQGYSESSALRKVGWFVKALEEFTEISWSGEHMKTWAYIYYHVKLDLAD
TYISLGNFSQAVHILEEVKEDWQVASHPKLHFLKGEDCYLAMELRWVEGLAYAYFQLHET
AHLSNHLLEHVEKNLISPRSYRDYYGESLQRTLGLCQRFLGV

CPn_0888   1015441   1014119
hemG-protoporphyrinogen Oxidase
AERRFCVKRAIIIGAGISGLAAGWWLHKKFPQAEILVLDKEAYAGGFVRTESPQGFSFDL
GPKGFLTRGDGEYTLXLIHELGLONSLIFSDRAAKNRFVYYRGKAHKISTWTLLRKGLLP
SLIKDFRAPCYTQDSSVODFLKRHSSQNFTSYILDPLITAIRAGHSSILSTHMAFPELAK
REASSGSLLRSYLKNRSPKKSKTDRYLASLSPSMGTLITTIQEKLPATWKFSTSVTHIDC
SPKEACVTTPSETFFADMVIYTGPLQQLPVLLPNYGIENLSKRVLPWNLSSISLGWHHAN
FSLPKGYGMLFADELPLLGIVWNSQIFPQATPGKTVLSLLIEGKWRESEAHAFAIAALSE
YLNINQKPDAFALFSSQDGMPQHAVGFLERKERILPHLPGNLKIVGQNIAGPGLNRCIAS
AYHAICDLHTEETLAQPQSSL

CPn_0889   1016841   1015462
hemN-Coproporphyrinogen III Oxidase
FLMFNVNFKFLEGLHQPAPRYTSYPTALEWEPSDAAPALLAFQRIRENPOPLSLYFHIPF
CQSMCLYCGCSVVLNRREDIVEAYINTLIQEMXLVVETIGFRPQVSRIHFGSGTPSRLSR
ELFTLLFDHIHKLFDLSHAEEIAIEVDPRSLRNDMEKADFFQNVGFNRVSLGVQDTQADV
QEAVRRQSHEESLKAYEKFKELAFQSINIDLIYGLPKQTKESFSKTIQDILAMYPDRLA
LFSFASVFWIKPHQKAMKASDMPSMEEKFATYSQSRHLLTKAGYQAIGMDHFSLPHDPLT
LAFKNKTLIRNFQGYSLPPEEDLLGLGMTSTSFIRGIYLQNAKTLEEYHNTVLRGTFATV
KSKILTEDDRIRKWAIHKLMCTFTINKEEFFNLFGYEFDTYFIESRDRLISMETTGLIHN
SPGSLKVTPLGELFVRVIATAFDHYFLNKVSKKECFSASI

CPn_0890   1017829   1016819
hemE-Uroporphyrinogen Decarboxylase
STLHNWDSMSAFFDLLKSQTASHPPIWLLRQVGRYMPPYOELKGSOSLKTFFHNTEAIVE
ATLLGPSLLHVDAAILFADILSILDGFAVTYDFAPGPRIQFSPEQPFTFTSDPQTIFSYL
LDAIRTLKQKLPVPLIVFAASPFTLACYLIDGGASKDFSKTMSFLYVYPEKFDQLISTII
EGTAIYLKTQMDAGAAAVQLFESSSLRLPSALFTRYVTEPNRRLIAKLKEQAIPVSLFCR
CFEENFYTLQATQADTLHPDYHVDLHRIQKNLMLSLQGNLDPAIFLLPQEKLLHYVEAFL
VPLRTYPNFIFNSGHGILPETPLENVQLVVSYVQRQL

CPn_0891   1021079   1017819
mfd-Transcription-Repair Coupling
NFMAMDFNPVNLDFSISKEFKEETLPLLLENIHPGATAFLAAKMFHDCRASVIMITTPAR
LDDLFENLRTFLDQAPVEFPSSEIDLSPKLVNIDAVGKRDHLLYSLNQHRAPIFCVTTLK
ALLEKTRSPQATSQOHLDLAVGDVLDPEATTELCKSLGYSOVMLTSEKGEFSCRGGIVDI
FPLSSPEPFRIEFWGEKIISIRSYNPSDQLSTGKVSKISISPAYTEEASGGNYSHSLLDY
FSTPPLYLFDNLEILEDDFADISGTLSSLPDRFFSIGTLYDRISTSNQVYFSETPFPNVK
NLKENRVIIEAFHRNMEASRQAIPILYPEQIIQNDENPLLAFLQHLQEYMPPHGKPLKLA
IYSTKTKSLKEARALAETVARGDVEIYEKTGNLTSSFALVNEAFAAISLSEFASTKVLRR
QKQRTHFSVTTEEVFVPIPGETVVHIHNGIGKFLGIEKKPNHLNIETDYLVLEYADKARL
YVPSNQAYLISRYVGTSDKAADLHHLNSSKWKRSRDLTEKSLIVYAEKLLQLEAQRSTTP
AFVYPPHGESVIKFAETFPYEETPDQLKTIDOIYNDHMSPKLMDRLICGDAGFGKTEVIN
RAAVKAVCDCHRQVIVIMVPTTILATQHYETFKERMAGLPIEIAVLSRFSOAKVQKLICEQ
VASGQIDIIIGTHKLINKSLEFKNPGLLIIDEECRFGVKVKDNLKERYPMIDCLTVSATP
IPRTLHMSLSGARDLSVIAHPPLDRLPVSTFVMEHNTETLTAALRHLRGGQANYYIHNR
IESIYTLAETIRNLIPEARIGVAHGQMGAEDLSNIFTKFKNQKTDILVATALIENGIDIP
NANTILIDHADKFGMADLYQMKGRVGRWNKKAYCYFLVPHLDRLSGPAAKRLAALNKOEY
GXGMKIALHDLEIRGACNILGTSQSGHIGTIGFNLYCKLLKKAVSALKKHTSPLLFNDDV
KIEFPYNSRIPDTYIETGSMRIEFYQKIGNAESSEELTAIQEEMRDRFGPLPQEICWLFA
LAEIRLFALCHGISSIKCTANALYVQKCLSKSEQTKKTLPYALSPTPELLVKEVIESIER
GFLINAS

CPn_0892   1023673   1021046
alaS-Alanyl tRNA Synthetase
EFFFMLSNTIRSNFLKFYANRHHTILPSSPVFPHNDPSILFTNAGMNQFKDIFLNKEKVS
YSRATTSQKCIRACGKHNDLDNVGHTSRHLTFFEMLGNFSFGDYFKAEAIAFAWEVSLSV
FNFNPEGYIATVHEKDDEAFALWEAYLPTDIRFLTDKDNFWSMANTGPCGYCSELLFDR
GPSFCNASSPLDDTDGERFLEYWNLVFMEFNRTSECSLLALPNKHVDTGAGLERLVSLIA
GTHTVFEADVLRELIAKTEQLSCKVYHPDDGGAAFRVIADHVRSLSFAIADGLLPGNTER
GYVLRKILRRSVHYGRRLGFRNPFLAEIVPSLADAMGEAYPELKNSLCQIQKYLTLEEES
FFKTLDRIXNLLQQVVLKSSGSSCIGGEDAFKLKDTYCMPIDEISLLAKDYDYSVDMDTF
HKLEQFAKERSKKNVVQSQGTSEIIYNFLHLTSEFIGYDHLSCDTFIEAIISKDHIVSSL
GEKOEIAIVLKVGEPFYAEKIXQVGLSGEIFCSEATFIVTHFTSPKAGLIVHIFRISOGSL
TVEAAVTAQVNRYRRKRIANNITACHLLIKALEITLGDHIRQASYVDOTKIRLDFTHPQ
AISPEDLLSIETLVNFSIRENEFVGIREALYSCYHNSGEIKQFRDKYSDVVVSACHS
HELYYTRIAEATGDIIFFRITKEIGVAMSIRRIEAVTIEKAEAIVIRQQSEVLEEIATLLQ
VHRLSYVSRLTATLDERKQJDKRLIELENSLIQTKLDKLIIMSTIQRGYITCLYHHLAEHE
NHRIZQYAMSTHORIPEKLLGIKTEKMCKYILVSRVGDDLITQYVHAQDLLFAVLTPCG
GKWYIKLQEACEGAPALFATEVLNETLMKWISTQLI

CPn_0893   1024822   1025888
tktB-Transketolase

EFLAFCLGISYSCCFYIEGL   MINKELEIIILGKIAGAIKQICIESIQKASSGHPGL
PLGCAELAAYLYGYVLRQNPROFHWINRDRFYLGASHGSALLYGCLHLACFDVSLEDLGE
FROLHSRTPGHPEYGGETVGYEATRQLKXGLGNAWWMALGMKMLESRFNRFGHZIFECK
YCLACDGCFMEGVSHEVCSPAOGLNLNNDVVIYDYMWVLOGYLNEISVEDTRKRPEAYG
WDVYEIDGYDFTHIHETFSSIKROQERFVLVIAHTIICHGSPKECTNKAHGSPLGVEGTH
ETKQFWHLPEEKFFVPPAVKNFFAHKIQEDRKAQEQWLDEVRVWSKQFPELHEEFVALTS
HKLPKNLESLYGSVEMPDSIAGRAAGNKLIQVLVQHIPYLIGCSACLSSSDGTWIANEKY
IHTYDFSGRNIKYGVREFGMATIMNGLAYSQVFRPFGGTFLVFSDYMRNAIRLAALSKLP
....
....
LDKQVRVVSFFCWELFEAVGYDTKGSIYGGDLGIRVSIEASSALGWYKYIGSEGGLAIAMD
RFGYSGAGDDVSEEGGFTTEGILGRILSQ

CPn_0894   1026823   1025888
amn-AMP Nucleosidase
PRNDKNAKNLRRKHYKGERVSKHTSESRIAQDMLERYSGSSVKQFCPYLLLTNFSYYIQT
FAKLHGVFVFEGSMFSAAHAPHLKTSILDFKLGSPGAALTIDLCSFLPDLKAALMLGMCG
GLRSHYQVGDYFVPVASIRGEGTSDAYFPPEVPALANFVVQKATTEVLEDKKANYHIGIT
HTTNIRFWEFNKKFRKKLYETKAQSAEMECATLFAAGYRRNLPIGALLLISDLPLRKEGI
KTKSSGNFIFNTYTEDHILTGQEVIENLEKVMLKRAASDHKKDQQYRGLPHMEVGEADDT
MASGSETSDSDY

CPn_0895   1026973   1027557
efp-Elongation Factor P
EIDCFMVRVSTSEFRVGLRIEIDGQPYLILQNDFVKPGKGQAFNRIKVKNFLTGRVIERT
YKSGESVETADIVERSMRLLYTDQEGATFMDDETFEQEVVFWEKLENIRQWLLEDTIYTL
VLYNGDVVAVEPPIFMELSIAETAPGVRGDTASGRVLKPAVTNTGAKIMVPIFIDEGELV
KVDTRTGSYESRVSK

CPn_0896   1027574   1027822
CT753 hypothetical protein
EKYFFFTVRNMEAKKIKELSKEAQLLKKLREKSRVLDEKNKRKAWVAKLVAMPESIREIE
KEERVETPQLFQAIAEKILEEGV

CPn_0897   1028794   1027853
(phosphohydrolase)
NFSLDSNTVDQKNKSNPRPMQEKPRHVHRIIHISDVHFHVLPVNPVHCFNKRLKGLLRKV
FGLVHFQATTIGQRFPKVVRSLGADSVCITGDFSLTAMDGEFLLAKHFVETLAKHSSVYL
LPGNHDVYTLKSLAQQTFYTHFPNDQLQQNKVSFHKITDHWWLILLDCSCLNGWFSANGV
VHLAQISAIETFLLSLSPEENVIIANHYPLLSSQNPSHDLINNTHLQNVLKKYPKVRLYL
HGHEHQAAVYNCADTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTHILKNLLDFDAP
LEIANEATWDCQKL

CPn_0898   1030511   1028904
Mitochondrial HSP60 Chaperonin Homolog
TKKRLGSVKILRLELAGVNPAKDKLSNYNADKKLFSGIDKLFQIVKGSYGPKQSLSPTSFF
KERGFYAISQTELSNSYENLGVDFAKAMVNKIHKEHSDGATTGLILLHAILQESYAALEK
GISTHKLIASLKLQGEKLQEALQQQSWPIKDALKVRNIIFSSLHMPTIADHFYNAFSVVG
PEGLISITKERENDKTSMDVFQGFKIPAGYASTYFVSDTASRLTRIAHPLILITDRKISM
IHSLLPLLQEISEQNQHLIIFCEDIDPDVLATLVVNKLQGLLQVTVVTIPQLSTTNQELA
EDIALFTGTHICPCQEASHVLAPEMVTLGSCLSIEISESQTTLIGGLHIPEVLTLKTRQL
AEEIRTTSCLETKKRLIKSTNRLQSSVAILPTDEDNEPLYTLALKIMESALSRGYVPGGG
VALFYASLTLGTPKDDADENSIAISLLQKACCAPLKLLATNADLDGDAVIAKLSSLGTTS
LGISVFSREIEDLIAGGILDSLATTSTILAQALDTAILVLSSKILILENQYEISTL

CPn_0899   1030848   1032215
murF-Muramoyl-DAP Ligase
NHRCCRQNYMRAHLLEDWVSLMLSDVSCPKCDKKITGFAIDSQQVQPGDLFFALPGNATD
GHQFLKHAATAGAVAVVSHDYQGDSFGLELIRVDDTKSALQEAGSNQCNLFQGTLVGIT
GSVGKTTTKEFSKTILSSIYKTHASPKSYNSQLTVPLSLLMAEGDEDVMILEMGVSEPGN
MQDLLRIVQPEIAVITHINDQHAMHFPQGIQEILKEKSYILOKSKLQLLPKDSPYYLDLR
SCSPTAEKFSFSFNDPLADFCYKAISGDSVVIQTPEENYCLPIAFSYKPAYTNLLIAVAL
SWILEVPEEGVIRSLPELKLPPMRFEHSMRNGMQVINDAYNACPEAMIAALDALPLPSDG
GKIILILGHMAELGRYSEEGHALVAEKAASRGDMIFFIGEKWIPVQSVLKSYSCEVSFFS
SAQDVKDILKQVARYGDVILLKGSRALALESLLACF

CPn_0900   1032208   1033281
mraY-Muramoyl-Pentapeptide Transferase
LVFNFLGASMIPLIPMFLKQSLFFSLALTGMTTLVLTVALGVPVMKWLKRKNYRDYIHKE
YCEKLEMLHKDKAEVPTGGGVLLFISLIASLLVWLPWGKFSTWFFIILLTCYAGLGWYDD
RIKIKRKQGHGLKAHKFMVQIAIAAFTLIALPYIYGSTEPLWTLKIPPFMEGMLSLPFWL
GKVFCLGLALVAIIGTSNAVNLTDGLDGLAAGTMSFAALGFIFVALRSSTIPIAQDVAYV
LAALVGACIGFLWYNGFPAQLFMGDTGSLLLGGLLGSCAVMLRAECILVVIGGVFVAEAG
SVILQVLSCRLRKKRLFLCSPLHHHYEYQGLPETKIVMRFWIFSFVCAGLGIAAVLWR

CPn_0901   1033239   1034537
murD-Muramoylalanine-Glutamate Ligase
FCMRRSRYSGCLMEIDMCQRILILGTGITGKSVARFLYQQGHYLIGADNSLESLISVDHL
HDRLLMGASEFPENIDLVIRSPGIKPYHPWVEQAVSLKIPVVTDIOVALKTPEFORYPSF
GITGSNGKTTTTLFLTHLLNTLGIPAIAMGNIGLPILDHMGQPGVRVVEISSFQLATQEE
HIPALSGSVFLNFSRNHLDYHRNLDAYFDAKLRIQKCLRQDKTFWVVWEECSLGNSYQIYS
EEIEEILDKGDALKPIYLHDRDNYCAAYALANEVGWVSPEGFLKAIRTFEKPAHRLEYLG
KKDGVHYINDSKATTVTAVEKALMAVGKDVIVILCGKDKGGDFPALASVLSQTTKHVIAM
GECRQTIADALSEKIPLTLSKDLQEAVSIAQTIAQEGDTVLLSPGCASFDQFQSFKERGA
YFKLLIREMQAVR

CPn_0902   1034507   1035241
nlpD-Muramidase (invasin repeat family)
AVDQRNAISEVNMNRRDMVITAVVVNAILLVALFVTGKRIGVKDYDEGFPNFASSKVTQA
VVGEEKVIEKPVVAEVPCRPIAKETLAAQFIESKPVIVTTPPVPVVSETPEVPTVAVPPQ
PVRETVKEEQAPYATVVVKKCDFLERIAPANIITVAKLMQIHDLTTTOLKIQGVIKVPTS
QDVSNEKTIYRYTANIPRNYYIVGETDCPWTIALRNIIPLDDLLFKMNDLLFYKARRLKPGD
GLRIP

CPn_0903   1036245   1036417
EtaW-Cell Division Protein FtsW
SKQKLEMMKWFVIKLGILKGGILSGLIRVFITIGSAEVLDPGLECTHKALIPGVTYLIGILGV
AGLLYMPWRDFLKIGIVELISAALALFGVFIFGLGIGRGIARKWIATLZITIQIEEVVK
YLVPIVALYFLTPSGLYQKQLKMFLKLTALLFILLLIAIEPGAFGAVLIGACLIVPIM
TSVRIGYWLLGILAVLALVAYPMIGYHRLMVYLHIPELDIKGRGRGFYQAKIAAKSXI
KLIGGNIGASLQKLTYLLFAAGHLVIAAIYAERFGFLGHLVLILLLYMXYTYIYAIAIKAS

43

:LEGAALAMV(TL(ISMOAP@IUGVVSGLLP@K'2.   .FF2OGGSCLIANMCGVTLLLKV
YDEENGK:GU;CRRFRRPHCPGSLUKGSFFS

CPn_0904   1036320   1037396
murG-Peptidoglycan Transferase
RYMMKKIRKVALAVGGSGGHIVPALSVKEAFSREGIDVLLLGKGLKNHPSLQOGISYRE:
GGGLRTVLNPIKIMGRTLSLCCGYLKARKELKIFDPDLVIGFGSYHSLPVLLAGLSHKIP
LFLHEQNLVTCKV2GLPCRYAPGIGVNFGPVTKHFRCPAEEVFLPKRSFSLGSPMMKRCT
...
DVLEGGTMILEKELTEKLLVEKVTFALDSHNREKORNSLAAYSQQRSTKTFHAFICECL

CPn_0905   1037400   1039835
murC&ddlA-Muramate-Ala Ligase & D-Ala-D-Alam Ligase
VHYMKGTPQYHFIGICGIGMSALAHILLDRGYEVSGSDLYESYTIESLKAKGARCFSGHD
SSHVPHDAVVVYSSSIAPDNVEYLTAIQRSSRLLHRAELLSOLMEGYESILVSGSHGKTG
TSSLIRAIFOEAQKDPSYAIGGLAANCLNGYSGSSKIFVAEADESDGSLKHYTPRAVVIT
NIDNEHLNNYAGNLDNLVQVIQDFSRKVTDLNKVFYNGDCPILKGNVQGISYGVSPECOL
HIVSYNQKAWQSHFSFTFLGQEYQDIELNLPGOHNAANAAAACGVALTFGIDINIIRKAL
KKFSGVHRRLERKNISESFLFLEDYAHHPVEVAHTLRSVRDAVGLRRVIAIFQPHRFSRL
EECLQTFPKAFQEADEVILTDVYSAGESPRESIILSDLAEQIRKSSYVHCCYVPHGDIVD
YLRNYIRIHDVCVSLGAGNIYTIGEALKDFNPKKLSIGLVCGGKSCEHDISLLSAQHVSK
YISPEFYDVSYFIINRQGLWRTGKDFPHLIEETGQDSPLSSEIASALAKVDCLFPVLHGP
FGEDGTIQGFFEILGKPYAGPSLSLAATAMDKLLTKRIASAVGVPVVPYQPLNLCFWKRN
PELCIONLIETFSFPMIVKTAHLGSSIGIFLVRDKEELQEKISEAFLYDTDVFVEESRLG
SREIEVSCIGHSSSWYCMAGPNERCGASGFIDYQEKYGFDGIDCAKISFDLQLSQESLDC
VRELAERVYRAMQGKGSARIDFFLDEEGNYWLSEVNPIPGHTAASPFLQAFVHAGWTQEQ
IVDHFIIDALHKFDKQQTIEQAFTKEQDLVKR

CPn_0906   1040514   1039915
CT763 hypothetical protein
KWGSEVLELVNDSQLSREASAFRLDIDFFILNIYPFFRNFKNIELCFFLSISQFNLDFME
EFVAYIVKNLVTNPEAVEIRSIEDEDNESIKLEIRVAAEDIGKIIGRRGNTIHALRTILR
RVCSRLKKKVQIDLVQPENGTDVIADQDYICDNDSSNSTEDTFGESDTCCSGHCHYDEDL
NQEEQEEGNMHHSCECSNHH

CPn_0907   1040816   1040445
*cutA Periplasmic Divalent Cation Tolerance Protein CutA (C-Type Cytochrome Biogenesis Protein)
FAFSKFLIIKSSMTAVLILTSFPSEESARSLARHLITERLASCVHVFPKGTSTYLWEGKL
CESEEHHIQIKSIDIRFSEICLAIQEFSGYEVPEVLLFPIENGDPRYLNWLTILSYPEKP
PLSD

CPn_0908   1041607   1040780
CT764 hypothetical protein
ILAILFMIIIKNNELMIRRFFKTLFPPGPQYSLCYASILIVLSSLVCVPTFCWLFLPELS
LSKFNPSPIRNLFLVSSTLSKVPPTAIAEHLRLSADAPTYLHEFSIKEAESSLHALGIFS
SLVIEKSPDNKGITIFYTLQTPIAYVGNRSNTLCNLEGSCFLGQPYFPSLNLPQIFFSQE
DLKMQKLPKEKHLFTKILLKELAMESPHIIDLSLSDAYPGEIIVTLSSGSLLRLPIKTLD
RALDLYKHMKKSPVIESEKQYVYDLRFPNFLLLKAL

CPn_0909   1041592   1041966
rsbV-Sigma Factor Regulator
IISLIFTRFLLERLLMNLSAKEYGDIIVIYLQGSLDAVSVPSVQEYLEQFIQKKHLKIAL
NFTDVSYISSAGIRLLLSNFKLVQSLGGKMCLCCVKESVTEVMRIAGLDQLILLCQSEQE
CLSKL

CPn_0910   1041970   1043004
miaA-tRNA Pyrophosphate Transferase
FLYMLPFEFEFNTTSSPECDVCLDPQKLFVKLFKRTIVLLSGPTGSGKTDVSLALAPMID
GEIVSVDSHOVYQGMDIGTAKVSLKARQEIPHHLIDIRHVQEPFNVVDFYVAIQACQNI
LSRNKVPILVGGSGFYFHAFLSGPPKGPAADPQIREQLEAIAEEHGVSALYEDLLLKDPE
YAQTITKNDKNKIIRGLEIIQLTGKKVSDHEWDIVPKASREYCCRAWFLSPETEFLKNNI
QMRCEAMLQEGLLEVRGLLNQGIRENPSAFKAIGYREWIEFLDNGEKLEEYEETKRKFV
SNSWHYTKKQKTWFKRYSIFRELPTLGLSSDAIAQKIAKDYLLYS

CPn_0911   1044079   1042985
Fe-S cluster oxidoreductase
SLLLAIFNVNYFMNLCKRISFEEGLELFVSSPIERLQERADAIRKERYPSNEVTYVLDAN
PNYTNICKIDCTFCAFYRKPKSPDAYLLSFDEVRSLLQRYVSSGVKTVLLQGGVHPGLGI
DYLEELVRITVQEFPSIHPHFFSAVEIEHACRVSGISIEQGLQRLWDAGQRTIPGGGAEI
LSERVRKIISPRKMQPGGWINLHKLAHLMGFRTTATHMFGHVNPEDILIHLQTLRDAQD
SCPGFYSFIPWSYKPGNTALRRNVPQQASIETYYRILALGRIFLDNFDHVAASWFGEGKS
LGAKALHYGADDFGGVILDESVHKATGWSIQSSEEEICNIIRSEGFIPVERNTFYQHISC
TVSSL

CPn_0912   1044120   1045760
CT768 hypothetical protein
VVIMDNSDNSFHTLETEQGSFLNDELAVEEVASTESTEISDATLCFAEKKVAFILNKMRE
ALTGSSQGSDLRLFWDLRKQCLPLFNEIEDTAKRADHWRCYIELTKEGRHLKGLQDEEGS
FVVGQIDLAITCLEKDILKFQEGTEDKIFKDREDNFLESQALDKHQAFYKQHHTSLLWLS
SFSSKIIDLRKELINVGMRMRLKSKFFQRLSNLJNQVFPKRKELIEKVSQTFAEDVDAFV
AKYFIGSDKETLKKTVFFLRKEIKNLQHAAKRLFVSSHVFAETRLKLSLSKCWDQLKGMEKE
IRQEQGRLRVVSAENSKEVRQMLEAVSSLLIEGNDLSKVRKDLEGISKKIRALDLTHDDV
ISLKKEMQQLFDQLREKQDAAEHSYQEQLAKDKQVKYEAARSLAERITTFSKTCSEGNIT
SESREEWOTLKELLGKMSFLPPPEKISLDNQLNLALQTIVNFFEEQLLSSPDSREKLVNM
RQVLKQRRERPQELKDKLEQDKKLLGSSGLDFDRAMQYGALVEEDKRALEELDASTLELK
QQIQQLL

CPn_0913   1045709   1045945
No robust homolog present in GenBank/EMBL as of 11/7/98
KKXYFRIEATO:AIAMRRNCIYAFDLDGTLLKGNGWGFYCYGLLAXGLFGYKTLPRCI
YKPFPFKFFPGIFHPSIIR

CPn_0914   1045909   1046199
No robust homolog present in GenBank/EMBL as of 11/7/98
VFFWDLPGFYCSIVTRLLSVPSPCDDLYEVALNFVTLTGDFYAPVLEKLEEAFADTMQ
VILFGGGFVHPIAQQI::GWIAKGYRDGAEGTIYKKCLTGDKKAULLGYIKKINQ
ARGHTFGDHLLDLFLMUGEEKTVVRPGRGKKHAPYYOWNIV

CPn_0915   1046401   1046813

... second column ...

yb+8-to-hp superfam.   homolog
FHLKKSSTLGWILEYPKAGFMDGFCFCLLKVAAKAIDDKKGNNLVVLCVRTISEFTCYFV
FVEGSVNVHVKALAGTTIVEEEKKQKYGFLIVEGITGGNMVVLCYGIR(MVHVRVSEIRGKY
RLEELWKDGFIVTSKLLAS

CPn_0916   1046813   1048084
fabF-Acyl Carrier Protein Synthase
LLNGVRVYMSKKRVVVTGFTVVSCLGNEVUDTFYDNLLAGVSGVRPITSFPCEDYATRFAG
...
DAAYGHLVSGRADH:ICGGTEAAVNRIGLEGFIANRALSERNDAFCQASRPWDRDRDGFV
LGSGAGILVLETLESALRRDAPIFAEMLGSYVTCDAFHITAPRDDGEGITACVLGALNSA
GIPKERVNYVNAHGTSTPLGCDLSEVLAVKKAFGSHVRNLRHNSTKSLIGHCLGAAGGVEA
VVAIQAILTGKLHPTINLDNPIAEIEDFDVVANKAQDWDIDVAMSNSFGFGGHNSTILFS
RYVP

CPn_0917   1048054   1048539
hydrolase/phosphatase homolog
FNDIILEVCTLVMMKTKYEYSFGVIPIKFFGTPDKNTLKACFICHTRGKHWGFPKGHSED
KEGPQEAAERELVEETGLSVVNFFPKVLIEOYSFNNEEQVFVRKEVTYFLAEVRGDIHAD
PHEICDSQWLSLQEGLRLLSFPELRDLTVEADKFINNYLFSS

CPn_0918   1049232   1048579
ppa-Inorganic Pyrophosphatase
ELLMSKKPLYVAHPWHSPTLTCDNYESLCCYIEITPYDSVKFELDKATGLLKVDRPQKFS
NFCPCLYGLLPQTYCGTASGNYSGEQTRREGIQGDKDPLDVCVLTEKNIHHGNILLQARP
IGGLRIIDSGEADDKIIAVLEDDLVFAEIEDISDCPGTVLDMIQHYFLTYKATPNHLIKG
SPAKIETVGIYGKKEAQKVIQLAHEDYLSYIGDTAEVN

CPn_0919   1049375   1050430
ldh-Leucine Dehydrogenase
FMKYSLNFKEIKIDDYERVIEVTCSKVRLHAIIAIHQTAVGPALGGVRASLYSSFEDACT
DALRLARGMTYKAIISNTGTGGGKSVIILPQDAPSLTEDMLRAFGQAVNALEGTYICAED
LGVSINDISIVAEETPYVCGIADVSGDPSIYTAHGGFLCIKETAKYLWGSSSLRGKKIAI
QGIGSVGRRLLQSLFFEGAELYVADVLERAVQDAARLYGATIVPTEEIHALECDIFSPCA
RGNVIRKDNLADLNCKAIVGVANNQLEDSSAGMMLHERGILYGPDYLVNAGGLLNVAAAI
EGRVYAPKEVLLKVEELPIVLSKLYNQSKTTGKDLVALSDSFVEDKLLAYTS

CPn_0920   1051423   1050431
cysQ-Sulfite Synthesis/biphosphate phosphatase
ILEENSMHSELPMYQNIVESVVTEITTQLLNYRSEHRLVPFWESKDGSFITAADYGSOYY
LKQQLAKAFPNIPFIGEETLYPDQDNEKIPEILKFTRLLTSSVSRDDLISTLVPPPSPTS
LFWLVDPIDGTAGFIRHRAFAVAISLIYEYRPILSVMACPAYNQTFKLYSAANGHGLSIV
HSQNLDRRFVYADRKQTKQFCEASLAALNQQHHATRKLSLGLPNTPSPRRVESQYKYALV
AEGAVDFFIRYPFIDSPARAWDHVPGAFLVEEAGGRVTDALGAPLEYRKESLVLNNHAVI
LASGDQETHETTLAALQNQLNVVPTDKLIAL

CPn_0921   1051526   1052293
snGlycerol-3-P Acyltransferase
GELMLIKLWRATYEGMYTFLVGALLKLRYRMQVEGWDTLNINPKQGCLFLANHVAEVDPI
ILEYLFWSRFHVRPMAVEYLFHSRVVQWFLNSVRSIPIFLQVPQKESKRSLERMNVCYEE
ASRALNRGESLLLYPSGRLSRTGKEEIVNQYSAYVLLHRVMECNVVLVRVSGLAGSAFSR
YKQNSTPKLGPAFKEAFRALLRRGIFFMPKRFVKITLCQVDHLFLKQFPTKQDLNTFLAS
WFNQGDDNLPIEVPYA

CPn_0922   1052266   1053927
aas-Acylglycerophosphoethanolamine Acyltransferase
QFAHRSSLRITRKLRRMHDQRNRGHNNHNLRLRPGSTLLEAFLILCSEHEEGIACFDEHL
GSLSYRELRNAIIAVAIKVSKFSEDRVGVMMPASIGAFIAYFGILLAGKTPVMMWSQGL
RELRACTKTVEVRRVLTSQQFIKHLTEVQGFVEYPFDLMYMEDVRKRLSWWEKCRIGLYS
KCSVPWLLRIFGVSQVEDTDAVILFTSGTEKLPKAVPLTHKNLMENQEACLKFFDPNTQ
DVMLAFLPPFHAYGFNSCGLFPLLMGVHVVFASNPLNPKKLVEFIDDKKVTFFGSTPVFF
DYILKTAKKQNSCLESLRLVVIGGDALKDTLYEETKKLQPQIALYQGYGATECSPVISIT
TKESPRKSECVGMPIEGMDVLIISKETHIPVSSGEQGLIVVRGNSVFSGYLGNHEHQSFV
SLGGDQWYLTGDLGHIGPSGDLFLEGRLSRFVKIGGEMVSLEALESILHEHFTENQNEDA
GSLVVCGIPGDKVRLCLFTTLATTIHEVNDILKSAETSSIVKISYVHQVESIPILGIGKP
DYVSLNALAVSLFG

CPn_0923   1053966   1055093
bioF_1-Oxononanoate Synthase_1
VCKESFLTTSDVIDFVTNDFLGFARSPTIYCEVSKRFQIHCQQFPHEKLGIRGSRLMVGP
SSVTDDLESKIASYHGAPNAFIVNSGYMANLGLCHHVSRSTDVLLWDEEVHMSVVHSLSA
ISGQHHTFHHNNLEHLESLLQCYRISSKGRIFIFVSSVVYSFRGTLAPLEQIIALSKKYHA
HLIVDEAHAMGIFGCGDGKGLCHALGYENFYAVLVTYGKALGTMGASLLTSSEVKYDLMQN
SPPLRYSTSLSPHTLISIGTAYDFLASEGEIARKQVFKLKEHFHECFCDSHAPGCVQPIFL
PHTCLEEAISVLETTGIHVGVVAFAKHPFLRVNLHAYNTVDEVNLLAQVMKPYLEKSSHR
VHINHEFHLWRELCCH

CPn_0924   1057301   1055028
priA-Primosomal Protein N'
KRFTAKTKSMGYIESSTFRLYAEVIVGSNINKVLDYGVPENLEHITKGTAVTISLRGGKK
VGVIYQIKTTTOCKKILPILGLSDSEIVLPQDLLDLLFWISOYYFAPLGKTLKLFLPAIS
SNVIQPKQHYRVVLKQSKAKTKEILAKLEVLHPSQGAVLKILLQHASPPGLSSLMETAKV
SQSPIHSLEKLGLDIVDAAQLELQEDLLTFFPPAPKDLHPEQQSAIDKIFSSLKTSQFN
THLLFGITGSGKTEIYLRATSEALKQGKSTILLVPEIALTVQTVSLFKARFGKDVGVLHH
KLSDSDKSRTWRQASEGSLRILIGPRSALFCPMKNLGLIIVDEEHDPAYKQTESPPCYHA
PDVAVMRGKLAHATVVLGSATPCLESYTNALSGKYVLSRLSSRAAAAHPAKISLIMMLE
REKSKTKILFSQPVLKKIAERLEVGEQVLIFFNRRGYHTIVSCTVCKHTLKCPHCDMVLT
FHKYAFALLCHLCNSSPKDLPQCCPKSLCGTMTLQYRGSCTEKIEKILCQIFFQIRTIRID
DTTKFYGSHETLLRKFANKADVLIGTOMIAKGWNFSAVTLAVILHDKGLYIPDFRAS
EQVFQLITQVVIRAIRSHLIXSEILIQCFLPDHPTIHSAMPQDYSAFYCQEITGRELCEYP
PFIRLIPCIFMCKCFKUTWEFAHRVHHILKEULEGTNPLHPVTPCGHFKIKDTFRYQFLI
YSAYVIPVNKKLIIHALMLAKLIIKVKFMIDVDLMTTFF

CPn_0925   1057015   1052226
CT770 hypothetical protein
YHWLFMEHSONFHDTLICOLLDRYGFELYIFTLASLLNVTLMHTAICAICSIIPEKAVEPN
AEFQPITPPPFTHLINEKTKIGIAKKVHILDDLICONAILKEKYPALFLGSLFAPKIFCSI
FYYEFIHEEVLFFNRLAKIIVGLFTTYGFLIHAKTNIFAMPNFFLALAPLAVIRYKIP
TTDYHQGLTQHZGIFLPLYLSFLEYEKIGGLKRNLWAILNRLPFAYTFYGH

115

CPn_0926   1058009   1058557
Thioredoxin Disulfide Isomerase
CHHTQQTYSTRFFKDSDMKFWLQGCAFVTCLLLTLPCCAARRRASGENLQQTRPIAAANL
QWESYAEALEHSKQDHKPICLFFTGSDWCMWCIKMQDQILQSSEFKHFAGVHLHMVEVDF
PQKNHQPEEGRQKNQELKAQYKVTGFPELVFIDAEGKQLARMGFEPGGGAAYVSKVKSAL
KLR

CPn_0927   927   1059818   1058670
FIISIILFLPLALLWVLKKTCQFFILPSSIISQSMSKTAVAIRRMTFLSHIKQLLSLKEI
SAADRVVIQYDDLVVDSLAIKIPHALPHRWILYSQGNSGLMENLFDRGDSSLHQLAKATG
SNLLVFNYPGIMSSKGEAKRENLVKSYQACVRYLRDEETGPKANQIIAFGYSLGTSVQAA
ALDREVTDGSDGTSWIVVKDRGPRSLADVANQICKPIASAIIKLVGWNIDSVKPSERLRC
PEIFIYNSNHDQELISDGLFERENCVATPFLELPEVKTSGTKIPIPERDLLHLNPLSPNV
VDRLAAVISNYLDSENRKSQQPD

CPn_0928   1061035   1059884
*CHLPS 43 kDa protein homolog_3
RRKDFAFTLLNLSNRSDILSGIFSNPHPVSYFSSTHAKQLSDFSKKHPILTKIVTIIVKI
FKLLIGLIIPPLGIYWLCQLVCSLALFPRSSMLYSVLKTCFKKYRLEQEIQODYFVKNLDP
SFKDPAVSESKRITIQQDHLTIDTLAIHFSTARPKRWLLISLGSGDFLEDMIGLXDSLFL
SWKELAKLLGANILIYNYPGVKSSTGKLNLENLATAHNLCAKYLQDKIQGPGANEIITYG
YSLGGVVQSAALQKNPFTNSETSWVAVKDRAPHSLPAAANSFFGPIGKLIAVLARWKMDA
EKNSRELPCPEILVYSADRFRPSEVGDDTALLPEFTLAHAIKRTPFARSKKFIGEVNLLH
SSPLKHPTIQKLAEAILESLSRKN

CPn_0929   1062301   1061186
*CHLPS 43 kDa protein homolog_4
EKFMAPIHGSNAFVEDILHSHPSPQATYFSSTRAQKLHEFKDRHPVLTRIASVIIKIFKV
LIGLIILPLGIYWLCQTLCTNSILPSKNLLKIFKKQPNTKTLKTNYLHALQDYSSKNRVA
SMRRVPILQDNVLIDTLEICLSQAPTNRWMLISLGSDCSLEEIACKEIFDSWQRFAKLIG
ANILVYNYPGVMSSTGSSSLKDLASAHNICTRYLKDKEQGPGAKEIITYGYSLGGLIQAE
ALRDQKIVANDDTTWIAVKDRCPLFISPEGFHSCRRIGKLVARLFGWGTKAVERSQDLPC
LEIFLYPTDSLRRSTVRQNKLLAPELTLAHAIKNSPYVQNKEFIEVRLSSDIDPIDSKTR
VALATPILKKLS

CPn_0930   1062851   1063330
No robust homolog present in Genebank/EMBL as of 11/7/98
NKMSELAPCSTGLQMVPHTQVHHALDTRRVILTIAACLSLIAGIVLVGLGAAAILPSLFG
VIGGMLILFSSIALIYLYKKTREVDQIALEPLPEHISKDQSIIDFVKTRDYASLEKKAT
FAYTHTHYYDGSMVFYREIPRFMLGSYLALRKDMDRQALF

CPn_0931   1064078   1065718
lysS-Lysyl tRNA Synthetase
IDFRVLGWKSDIYTNILEERMTARAEYLDHEDFLYRSHKLQELSELGVVLYPYEFPGVFS
CEDIKKTFASQELGNSEAAMSRSTPRVRFAGRLVLFRAMGKNAFGQILDHNQTIQVMFNR
EFTSVHGLSEDAEITPIKFIEKKLDLGDILGIDGYLFFTHSGELTVLVETVTLLCKSLLS
LPDKHAGLSDKEVRYRKRWLDLISSREVSDTFVKRSYIIKLIRNYMDAHGFLEVETPILQ
NIYGGAEAKPFTTMEALHSEMFLRISLEIALKKILVGGAPRIYELGKVFRNEGIDRTHN
PEFTNIEAYAAYMDYKEVMVFVENLVEHLVRAVNHDNTSLVYSYWKHGPQEVDFKAPWIR
MTMXESIATYAGIDVDVHSDQKLKEILKKKTTFPETAFATASRGMLIAALFDELVSDNLI
APHHITDHPVETTPLCKTLRSGDTAFVERFESFCLGKELCNAYSELNDPIRQRELLEQQH
TKKELLPDSECHPIDEEFLEALCQGMPPAGGFGIGVDRLVMILTNAASIRDVLYFPVMRR
FDAEKTN

CPn_0932   1067160   1065721
cysS-Cysteinyl tRNA Synthetase
VKSDTVMAFSHIEGLYFYNTASQKKELFFPNHTPVRLYTCGPTVYDYAHIGNFRTYVFED
ILKRTLVFFGYSVTHVMNITDVEDKTIAGASKKNIPLQEYTQPYTEAFFEDLDTLNIARA
DFYPHATHYIPQMIQAITKLLEQGIAYIGQDASVYFSLNRFPNYGKLSHLDLSSLRCCSR
ISADEYDKENPSDFVLWKAYNPERDGVIYWESPFGKGRPGWHLECSIMAMELLGDSLDIH
AGGVDNIFPHHENEIAQSEALSGKPFARYWLHSEHLLIDGKKMSKSLGNFLTLRDLLHQE
FTGQEVRYMLLQSHYRTQLNFTEALLACRHALRRLKDFVSRALDPLGEESPLPRTLDS
SSQFIEAFSRALANDLNVSTGFASLFDFVHEINTLIDQGHFSKADSLYILDTLKKVDTVL
GVLPLTTSVCIPETVMQLVAEREEARKTKNWAMADTLRDEILAAGFLVEDSKSGPKVKPL

CPn_0933   1067532   1068578
predicted disulfide bond isomerase
PVILLQNIKRCSLKQLKVLATLLLSLSLPTLEAAENRDSDSIVWHLDYQEALQKSKEAEL
PLLVIFSGSDWNGPCMKIRKEVLESPEFIKRVQGKFVCVEVEYLKHRPQVENIRQQNLAL
KSKFKINELPCMILLSHEEREIYRIGSFGNETGSNLGDSLCHIVESDSLLRRAFPMMTSL
SLSELQRYYRLAEELSHKEFLKHALELGVRSDDYFFLSEKFRLLVEVGKMDSEECQRIKK
RLLNKDPKNEKQTHFTVALIEFQELAKRSRAGVRQDASQVIAPLESYISQFGQQDKDNLW
RVEMMIAQFYLDSDQWHHALQHAEVAFEAAPNEVRSHISRSLEYIRHQS

CPn_0934   1068948   1068526
rnpA-Ribonuclease P Protein Component
YFVHPLTLPKQSRVLRRKQFLYITRSGFCCRGSQATFTTVPSRHPGTCRMGITVSKKFGK
AHERNSFKRVVREVFRHVRHQLPNCQIVVFPKGHKQRPVFSKLLQDFINQIPEGLHRLGK
TKATTGGECTPKSEKCVTAPR

CPn_0935   1069100   1068957
L34-L34 Ribosomal Protein
EDTVKRTYQPSKRKRRNSVGFRTRMATRNGRKLLNPPRHGRHSLVDL

CPn_0936   1069330   1069470
L36-L36 Ribosomal Protein
YLMKVCCSVKADPGKJDKLVRRKGRLYVINKKDPNPYGRQAGPARKK

CPn_0937   1069487   1069798
S14-S14 Ribosomal Protein
VKRMAKKSSVARGAKRRRLVEANFKKRSDLRKIVKCLCSGEEEKENARISLNKMKRDTSP
TPLUJHPSLJTDKHKNYLRKFALSRSCFRQMASMGEIPSVIKASW

CPn_0938   1070355   1069849
*CT798 hypothetical protein (lipoprotein peptide periplasmic)
YFINLSTTLSTMLPTSTILLFYVILKKLSAYIADKKKPFIFIGWFFAAAFFGFIFGLVVLLLL
ISTHHALEEFSQHIGFFDNSOLFDDLLKKSLAVNDEIPSSSLLQEIVLUTEKWFSLNKDRENV
GFISFFEEJAVVLLPGKTYPEKIWVWKKKSMKLWJGRVKLYSGLLQQALKEASK

CPn_0939   1071035
CT790 hypothetical protein
HINRWTIRLSLTLSLSTVLYFFSEEIELIQQGKMEKQMCKLDVKETEFPETVFSRDTETR
VIQVIILHCLAKINGVSLLQGTNLIDALFGRDIERMKGIYVEQDSKNHLVKVRVEVNVDYG
VSIPEKTEEIQGCIVSEISEYTGLHVAAVHVIIKGLTQPKDRIDEEIEEEVSVGDLPSPE
DFLLENSEG

CPn_0940   1073039   1071204
ER IPFFLMKKTASIETIVVSNETEALLLENNLIKQHHPKYNVLLKDDKTFFCLAISLSHSW
PKVEAIRTKAITSSQRQLIFGPYVSAEACHTLLEVISQWFPLRTCSDREFALRKRPCILY
DMKRCLAPCVGYCTPEEYQGTLDKAILFLKGKIEEVVKDLEKVIQKASDNLEFEQAANYY
RTLSLIKQAMAKQQVEKFHFQNIDALGLYRHKQRTILTLLTVRSGKLLGARHFSFFENAQ
EDQDLLSSFILQYYVSQPYIPKEILTPLPLEFPTLSYVLNAESPPRLRSPKTGYGKELLD
LAYRNAKAYAATTLPSSTLPYQDFQNILRMSQYPYRIECYDNAHMQGAHATGVYIVFENN
GFDPKQYRTFSIDSEKTQNDLALLEEVLLRRFHSLTTALPDNIVVDGGNTHYNKTKKIIQ
TLNLTGIQVVTIAKEKSNHSRGLNKEKIFCETFPEGFSLPPTSNLLQFFQILRDEAHRFA
ISKHRKKRGKALFEQEKIPGIGEVKRKRLLQKFKSWKQVMLSSQEELEAIPGLTKKDIAV
LLARQKDFNKSD

CPn_0941   1075504   1073018
mutS-DNA Mismatch Repair
VMTEKKPTPMMEQWHQCKEKAGDSVLLFRMGDFYEAFYDDAVLLSQHLELTLTQRQGIPM
SGIPVSTVDTYVDRLIGKGFKVAVAEQFGEPAKEKESKKIGPMARDIQRFVTPGTLLSST
LLQEKFNNYIVAINRIGSLFGFACLDLSTGSFFIEECENTKELVDEICRLAPSEVLSCNK
FYNKETAIVMQLQQHLKLTLSTYADWAFEHKFASQKLTTHFQVASLDGFGLKGLVPAINA
AGGLLSYIQDKLLPTKHIAIPQTRGKQQKLLIDTASQVNLELLAPLNDPQGKNSLLRIM
DHTSTPMGGRLLRQILISPFYNPKEILVRQDAVEFFLRQVTLRKNIKTYLCQVRDIERLM
TKVTTGLAGPRDIGTLRDSFSAGAQIYEQLASATLPEFFIDKCSLDTKLASLIALLSKSL
NGDLPLRVSDGNIFVDEFHNDLKRLRHNQEHSQEWIWEYQERIRKETGIKKLKICFAQAL
GYYIEVSSEFAPQLPKDFIRRQSRLHAERFTTIELQQFQDDMSNISEKLQTLETQFFKDL
CSHILQLRTEILALSQSLADLDYIISLADLAHAQGYCRPHVDMSDTLCIYRGCHVPAKTL
VDTGKFIPNDTEMRGSQTRMILLTGPNMAGKSTYIRQIALLVIMAQMGSYIPAKSAHIGV
IDKIFTRIGAGDNLSKGMSTFMVEMAETANILHNATDRSLVILDEVGRGTSTYDGLAIAQ
AVVEYLLFTDKKKAKTLFATHYKELTTLEDHCPHVENFHAGVKDKAGQPVFLYEILKGHS
QKSFGIHVARLAGFPLCVVSRAQQILRQLEGPESITRPAQDKMQQLTLF

CPn_0942   1075955   1077754
dnaG/priM-DNA Primase
NCSITKLRTAMYTEESLDNLRHSIDIVDVLSEHIHLKRSGATYKACCPFHTEKTPSFIVN
PAGAHYHCFGCGAHGDAIGFLMQHLGYSFTEAILVLSKKFQVDLVLQPKDSGYTPPQGLK
EELRHINSEAETFFRYCLYHLPEARHALQYLYHRGFSPDTIDRFHLGYGPEQSLFLQAME
ERKISQEQLHTAGFFGNKWFLFARRIIFPVHDALGHTIGFSARKFLENSQQGKYVNTPET
PIFKKSRILFGLNFSRRRIAKEKKKVILVEGQADCLQMIDSGFNCTVAAQGTAFTEEHVKE
LSKLGVLKVFLLFDSDEAGNKAALRVGDLCQTAQMSVFVCKLPQGHDPDSFLMORGSSGL
IALLEQSQDYLTFLISEKMSSYPKFGPREKALLVEEAIRQIKHWGSPILVYEHLKQLASL
MMVPEDMVLSLANPQVTAEPQNIPIKQKVPKIHPHIVMETDILRCMLFCGSNTKILYTAQ
FYFVPEDFKHPECRKLFAFMISYYEKYRKNVPFDEACQVLSDSQILQLLTKRRLNTEALD
TIFVQSLQKMADRRWREQCKPLSLNQNIQDKKLEILEDYVQLRKDRTIITTLLDPESELIP

CPn_0943   1077972   1078238
CT794.1 hypothetical protein
PFMKSFKFLLPFLSVILCCGNLLSSPRSRAISVTESIGMSAVKTLVLSEKAHEFLEGIGY
GVGASSILRDWQTQQWLEIESLLAQNEVM

CPn_0944   1078503   1078997
No robust homolog present in Genebank/EMBL as of 11/7/98
IKIMMHRYFIPLLALLIFSPSLVRAELQPSENRKGGWPTQLSCAEGSQLFCKFEAAYNNA
IEEGKPGILVFFSERPTPEFADLTNGSFSLSTPIAKGFNVVVLCPGLISPLDFFHKMDPV
ILYMGSFLEMFPEVEAVSGPRLCYILIDEQGGAQCQAVLPLETKN

CPn_0945   1079001   1079660
CT795 hypothetical protein
SIFKNKILPSYFGHNFDQLRRHYMRIALSLLSLLMIFPIFGEESRPGSEDGNSNTQEIVG
SQDTQVCLYHSYEQGLQASRIEGKPLVIVVLCNSGDDGQACTIGLSETCEEVLSVLSGSI
FSELANFVVLVPSGVNPLIYPPIEDPILAEIVKFKELFKDESFPTGLSIIVVGVTPEGPG
DIIEVSPVSLTVEEEETLPSEQTTEVESTSELQSEDPAIA

CPn_0946   1082816   1079745
glyQ-Glycyl tRNA Synthetase
GECQKKKCYTLESFVSEHPLTLQSMIATILRFWSEQGCVIHQGYDLEVGAGTFNPATFLR
ALGPEPYKAAYVEPSRRPQDGRYGVHPNRLQNYHQLQVILKPVPENFLSLYTESLRAIGL
DLRDHDIRFIHDDWENPTIGAWGLGWEVWLNGMEITQLTYFQAIGSKPLDTISGEITYGI
ERIAMYLQKKISIYDVLWNDTLTYGOITQASEKAWSEYNFDYANTEMWFKHFEDFAEEAL
RTLKNGLSVPAYDFVIKASHAFNILDARGTISVTERTRYIARIRQLTRLVADSYVEWRAS
LNYPLLSLSSTSEPKETSESVVPMISSTEDLLLEIGSEELPATFVPIGIQQLESLARQVL
TDHNIVYEGLEVLGSPRRLALLVKNVAPEVVQKAFEKKGPHLTSLFSPDCGDVSPQGQOFF
ASQGVDISHYQDLSRHASLAIRTVNGSEYLFLLHPEIRLRTADILMOELPLLIQRMKFPK
YMVWDNSGVEYARPIRWLVALYGEHILPITLGTIIASRNSFGHRQLDPRKISISSPQDYV
ETLRQACVVVSQKERRMIIEQGLRAHSSDTISAIPLPRLIEEATFLSEHPFVSCGQFSEQ
FCALPKELLIAEMVNHQKYFPTHETSSGAISNFFIVVCDNSPNDTIIECNEKALTPRLTD
GEFLFKQDLQTPLTTFIEKLKSVTYFEALGSLYDKVERLKAHQRVFSTFSSLAASEDLDI
AIQYCKADLVSAVVNEFPELQGIMGEYLKHANLPTASAVAVGEHLRHITMGQKLSTIGT
LLSLLDRLDNLLACFILGLKFTSSHDPYALRRQSLEVLTLVGASRLPIDLASLLDRLADH
FPSTIEEKVVWDKSKTIHEILEFIWGRLKTFMGSLEFRKDEIAAVLIDSATKNPIEILDTA
EALQLLKEEHTEKLAVITTTHNRLKKILSGLKLSMTSSPIEVLGDRESNFKQVLDAFPGF
PKETCAHAFLEYFLCLADLSNDIQDFLNTVIIANDDGAIRNLRISLLLTAHDKFSLCHWE
GVAV

CPn_0947   1084433   1084050
pgsA Glycerol 3 P Phosphatydyl transferase
GGRVGLPNYITFGRLFITTGIFMGLYLYLKYGKWFGITTAVVLPTVILALLAISGELTDAIDGRVA
PKFGCYTDLLGKLLDIMADSIYRISTYLCTFYJPIVRILLPLLLVFIFIARDKVLPTLRTVVCAF
MGRVVAARASIKLKAIIASYFLFLZLMIFMGILILLQFKLEIFAISVTVSIIAVYSIAG
GIEYFVMNKNFLSQHAKTRLSSXFHFEKD

CPn_0948   1084481   1084047
pisA Glycerol Synthase
GEGMRIVQVAVEFTPIVKMAAISGAVAGSGKKELAKQNIVFYLLGIYPLGIKFFSGGQVLIFFE
PSFYYEFLGKQJASAISYSVFSSLTLFTITFLIEGJELFSTTGSYGSENNVVKFESAFAAAAAA

YLQEADPAUIVILHDWHVGLLAGLLKNPLNPVHE　　　IHNFGYRGYCSTOLLAASQID
IFHLSHYQLFRDPQTSVLMKGCALYCSDYITTVGLI.JOEIINDYSDYELHDAILARNSVF
JSIINSIDEDVWNPKTDPALAVOYDAJLLGEPDVLFTKKEENRAVLYEKLGISSSDYFPLI
CVISRIVEEKGPEFMKEIILHAMEHSYAFILIGTSQNEVLLNEFRNLQDCLASSPNIRLI
LDFNDPLARLTYAAADMICIPSHREACGLTCLIAMRYGTVPLVRKTCGLADTVIPGVNGF
TFFDTNNFNEFRAMLSNAVTTYRQEPDVWLNLIESCMLRASGLDAMAKHYVNLYQSLLS

CPn_0949　　　1085887　1086483

KKFLSNLESGALSSTVFSLSYEGRIIKALVKDIQYQITTYDVIHLDFEELVEDRPIKLNI
PIRCINAVDCIGVKLGGSLRQVIRAVRVVCKPKDIVPFLELDVRSVGLSQTRKLSDIKIP
AGIETITPLKEVAITVSRR

CPn_0950　　　1086470　1087027
pth-Peptidyl tRNA Hydrolase
PSLEDNMAKLIVAIGNPRHGYANTRHNAGFLLADRLVEELQGPPFKPLSKCHALMTLVES
SSGPLVFIKPTTFVNLSGKAVVLAKKYFNVALSHILVLADDVNRSFGKLRLCFNGGSGGH
NGLKSITASLGSNEYWQLRFGVGRPLEEGVELSNFVLGKFSEEENLQLGSIFVEASTLFT
EWCSKF

CPn_0951　　　1087113　1087457
rs6-S6 Ribosomal Protein
EFLMGKKENQLYEGAYVFSVTLSEEARRKALDKVISGITNYGGEIHKIHDQGRKKLAYTI
RGAREGYYYFIYFSVSPGAITELWKEYHLNEDLLRFMTLRADSVKEVLEFASLPE

CPn_0952　　　1087469　1087723
rs18-S18 Ribosomal Protein
GENMNKPVHNNEHRRKRFNKKCPFVSAGWKTIDYKDVETLKKFITERGKVLPRRITGVSS
RFQGVLSQAIKRARHLGLLPFVGED

CPn_0953　　　1087727　1088248
r19-L9 Ribosomal Protein
FKGRRMKQQLLLLLEDVDGLGRSGDLITARPGYVRNYLIPKKKAVIAGAGTLRLQAKLKEQ
RLIQAAADKADSERIAQALKDIVLEFQVRVDPDNNMYGSVTIADIIAEAAKKNIFLVRKN
FPHAHYAIKNLGKKNIPLKLKEEVTATLLVEVTSDNEYVTVLAQGKQTEENQEG

CPn_0954　　　1088259　1088708
ychB-Predicted Kinase
GRKVCYKDIMQYFSPAKLNLFLKIWGKRFDNFHELTTLYQAIDFGDTLSLKNSMKDSLSS
NVNELLSPSNLIWKSLEIFRRETQIHQPVSWHLNKSIPLQSGLGGGSSNAATALYALNEH
FQTHIPITTLQLWAREIGSDVPFFFLQEQH

CPn_0955　　　1088612　1089175
(frame-shift with 0954)
RAFPNPYSYNNIATLGSRNRKRCSFFFSSGTALGKGRGEHLFSIKKLNHKHKYVLYLDHQ
GIPTEKAYQSLLPQDYSTGNHNACFYGENDLEKSVFRIRTDLKNKKHHMLERMWSPFESHV
LHSGSGATLFVCYLEELEQDSKVSSQIHSLIKQTQGIPVSRLYREPHWYSLKQSTYKNSP
LECFQPQI

CPn_0956　　　1089545　1090909
CT805 hypothetical protein
LVWFSMILPPYSYSLKIGAAVLFFCSILHTFLTPWLYTLCQSYEHKKLVFPECWKRYARL
SELFRILSRVEIVFFLWAVPLFFWFLYTEGYRISMAYFNSRNYGFAVFIMVILILLESRP
IVYFAELVLSSIAKLGKTSPKSWWWTLMIAPPLLSCLLKETGAMIIGATLLMRHFYVFSP
SRRFAYATMGLLFSNISIGGLTSYVSSRALFLIFPALKWEHSFFLSHFAWKAIVAILIST
TIYYFIFRKEFKKFPDIPSDKDPSVEKVPWWIICVNIIFVGSIILSRSTPLFHGALLLFY
LGFQKFTIFYQDPINLSKVCYVGLFYAGLVVFGDLQEWWVLNLMQGLSDFGYHTVSYTLS
IFLDNALVNYLVHNLSVATDCYHYLVVVAGCHAAGGLTLVSNIPNIVGYLILRSAFPSSTI
HMGWLFLGALGPSIISLGVFWLLKNVPEFLYCFFR

CPn_0957　　　1093812　1090963
ide/ptr-Insulinase family/Protease III
KIYTRNCKMFWKLLCPILICTSLSITSCEQQFKVVPNQCPLQVSTPAAADQKIEKIICSN
GLPLLIISDPNLPTSGAALLVKTGNNADPEEYPGMAHFTEHCVFLGNEKYPEVSGFPGFL
SENNGVHNAFTYPNKTVFVFSVEHSAFSDALDQFVHLFINPKFRQEDLDREKYAVHQEFA
AHPLSDGRRAVHRIQQLVAPQGHPCARFGCGNASTLTPVTTEKMAEWFKLHYSPENMCAIA
YTSAPLSKAKKQFSKIFSQIPRSKNYERQEPFLPSGDTSSLKNLYINQAIQPTSNLEIYW
HIYESSHPIPLGCYKALAEVLRNESKNSLVSLLKNEQLITDLDVEFFRSSLNTGEFYISY
ELTEKGDKHYSQVIDSTFQYLRYIQEHGIPNYTLEEISTINALNYCYSSKSPLFDLLCKQ
IVSLGNEDLSTYPYHSLVYPKYSSEDESALLNLVSDPEQARFVLSSKNSEHWEEATOLHD
PIFDMTYYVKALDGVQDYGKVQSLKPIALPKPNLFIPKEVTLPGVHLLKKQEFPFAPALS
YQDDKLTLYHCEDHYYTAPKLSSQIRIRSPQISRSSPOFLVATELYCLAVNDQLLREYYP
ATQAGLSFTSALCGDGIDLRVSGYTTTVPALLNSILTSLPNLEISYETFLVYKKQLLELY
QGALLNCPVRSGLDELASQVMKETYSNTTKLSALEKLSFSEFQAFASNLFNSVHLEVMVL
GNLSEQKKDYLEMLQVFTASRSSHATKPFYYELQSQEISEIHHDYPLTANGMLLLQDK
GGPSICGKVCAEMLFEWLHHITFEELRTOQQLGYMVGARYREFASRPFGFLYIRSDAYSP
EELLAKTSLFLNKVSASPEKFGISQEKFANIRKAYINKILEPEHSLDMMNSALFSLAFER
PFVEFSTPDLKIAIAETLTYEEFLKYCQCFLSNELGTQTSVYIRGTQKTS

CPn_0958　　　1094803　1093793
plsB-Glycerol-3-P Acyltransferase
IYRAIYMOFSRYLRYAFDNOYLPEPLYQKFSVFHQNYIDAATKKAAADOAEVLCLQWVKV
IIEDLYMPFIFPPYHHKKIRAPIDLFRLSIDFFSLVIDDKNSRILNLHRLKEIEEYIARGD
NVVLLANHQTECDPOLMYYALGKTHPELMENMIFVAGDRVTSDPLARPFSMCCDLLCIYS
KRHIATPPELREEKLLHNQKSMQILKTLLNEGGKFIYYAPAGCGRDRKNAEGRLYPSEFSP
EGIEVFPLLAKASNQTTHFYPFALKTYDILPPPPKIENAIGEQRAIFFAPVPFFNFGAELF
FDALCCKEELIHCDKHAQRTLRAEKVFSIVKNLYEEL

AQIYGUTRKVMENEILLNIESKEIRYAILKNCQLFDLTIERKKVRQLKGNIYRGRVTNI
LRNIQIAFINIDEREHEFIHICDILENSKKFEQMFDMDVDALPEEASEAPLLSSEEAPIE
EFLRLCFVLVQVVKEIICKKGARLTSNISIPGRYLVLLPNSPHRGVSRKIEDPHMREQL
FQLIHCDFMIVXHILICRTAUTTAUTEALINEAHDLLLTWKTILEKFYSTEQPCLLYSET
LILKFAYIIFCIDKNYKRLLIDDYATYQKCKHMLKKYSPDASIKIEYYRDSIPMFERFNIE
KEIDKATHRKIWLKXXYLFFDKTEAMITIDVNSCRCTOLEGCVEETLVOINLEAAEEIA
MQLJLPHVXILVIIDFIDMKIRKNORRVLERLKEHMFYDAARCTILCHSEFCLVEMTRQR
NHELLMYLFLPTUIPYCICINALIKTPESVVIEIERDLFKVINIKEHSHLCLVVHPEIASYM
KQHIUGAIHMINLAKQLKAKLQINTCDCSVHLMHYQFFCLITCESIDL

CPn_0960　　　　IF　　S.　1897102
CT909 hypothetical protein
SLSLVSYLSNPGMALVLGMGFGMDCVDNCKLTIPRLMLRIDTERLGVSGGFEAIRERGE
EELLNSPIEVEDCLCBLIGSEQWILSUSLKTCLCLICPUENNFRGAJVAPLOBVISHDE
VGSCVFDCRPLIRQELLLESDCFEECSUQYCPERKNILKFLEDRKKHEGNSPFEYL

CPn_0961　　　1097106　1097207
rl12-L32 Ribosomal Protein
(illegible)

CPn_0962　　　1097301　1098275
plsX-FA/Phospholipid Synthesis Protein
ILSDFMEVQIGIDLMGGDHSPLVVWQVLVDVLKSQSSTIPFAPTLFASEEIRKQIQEEFI
SDLPQEKFPKIISAENFVAMEDSPLAAIRKKSSSMALGLDYLQEDKRLDAFISTGNTGALV
TLARAKIPLFPAVSRPALLVCVPTMRGHAVILDVGANISVKPEEHVGFARMGLAYRQCLG
DSKIPTIGLLNIGSEERKGTEAHRQTFRHLRETFGEAFLGNIESGAVFDGAADIVVTDGF
TGNIFLKTAEGVFEFLQRILGDKLEADIQRRLDYTFYPGSVVCGLSKLVIKCHGKACGSS
LFHGILGSINLAQARLCKRILSNLI

CPn_0963　　　1098374　1103224
pmp_21-Putative Outer Membrane Protein
TPLRFKVAMVAKKTVRSYRSSFSHSVIVAILSAGIAFEAHSLHSSELCLGVFNKQFEEHS
AHVEEAQTSVLKGSDPVNPSQKESEKVLYTQVPLTQGSSGESLDLADANFLEHFQHLFEE
TTVFGIDQKLVNSDLDTRNFSQPTQEPDTSNAVSEKISSDTKENRKDLETEDPSKKSGLK
EVSSDLPKSPETAVAAISEDLEISENISARDFPLQGLAFFYKNTSSQSISEKDSSFQGIIF
SGSGANSGLGFENLKAPKSGAAVYSDRDIVFENLVKGLSFISCESLEDGSAAGVNIVVTH
CGDVTLTDCATGLDLEALRLVKDFSRGGAVFTARNHEVONLAGGILSVVGNKGAIVVEK
NSAEKSNGGAFACGSFVYSNNENTALWKENQALSGGAISSASDIDIOQGNCSAIEFSGNGS
LIALGEHIGLTDFVGGGALAAQGTLTLRNNAVVQCVKNTSKTHGGAILAGTVDLNETISE
VAFKQNTAALTGGALSANDKVIIANNFGEILFEQNEVRNHGGAIYCGCRSNPKLEQKDSG
ENINIIGNSGAITFLKNKASVLEVHTQAEDYAGGGALWGHNVLLDSNSGNIQFIGNIGGS
TFWIGEYVGGGAILSTDRVTISNNSGDVVFKGNKGQCLAQKYVAPQETAPVESDASSTNK
DEKSLNACSHGDHYPPKTVEEEVPPSSLLEEHPVVSSTDIRGGGAILAQHIFITDNTGNLR
FSGNLGGGEESSTVGDLAIVGGALLSTNEVNVCSNQNVVFSDNVTSNGCDSGGAILAKK
VDISANHSVEFVSNGSGKFGGAVCALNESVNITDNGSAVSFSKNRTRLGGAGVAAPQGSV
TICGNQGNIAFKENFVFGSENQRSGGGAIIANSSVNIQDNAGDILFVSNSTGSYGGAIFV
GSLVASEGSNPRTLTITGNSGDILFAKNSTQTAASLSEKDSFGGGAIYTQNLKIVKNAGN
VSFYGNRAPSGAGVQIADGGTVCLEAFGGDILFEGNINFDGSFNAIHLCGNDSKIVELSA
VQDKNIIFQDAITYEENTIRGLPDKDVSPLSAPSLIFNSKPQDDSAQHHEGTIRFSRGVS
KIPQIAAIQEGTLALSQNAELWLAGLKQETGSSIVLSAGSILRIFDSQVDSSAPLPTENK
EETLVSAGVQINMSSPTPNKDKAVDTPVLADIIISITVDLSSFVPEQDGTLPLPPEIIIPK
GTKLHSNAIDLKIIDPTNVGYENHALLSSHKDIPLISLKTAEGMTGTPTADASLSNIKID
VSLPSITPATYGHTGVWSESKMEDGRLVVGWQPTGYKLNPEXQGALVLNNLMSHYTDLRA
LKQEIFAKHTIAQRMELDFSTNVWGSGLGVVEDCQNIGEFDGFKHHLTGYALGLDTQLVE
DFLIGGCFSQFFGKTESQSYKAKNDVKSYHGAAYAGILAGPWLIKGAFVYGNINNDLTTD
YGTLGISTGSWIGKGFIAGTSIDYRYIVNPRRFISAIVSTVVPFVEAEYVRIDLPEISEQ
GKEVRTFQKTRFENVAIPFGFALEHAYSRGSRAEVNSVQLAYVFDVYRKGPVSLITLKDA
AYSWKSYGVDIPCKAWKARLSNNTEWNSYLSTYLAFNYEWREDLIAYDFNGGIRIIF

CPn_0964　　　1104812　1103301
No robust homolog present in Genebank/EMBL as of 11/7/98
QSILESIIKYFYLIHNSKMHMSNPISLFSPAELIAKYNLIPKTSPIYPRRTELIILEENA
CQTRLTNVAQVLHPSSLFSMSKKILNPCGCSGGPLCWVILNILAFIITSVLFIILLPVNL
IVAGLRLFMPLPPPKIVEDLSEPTTEETNEVIQPFIFALQALLFEDNKLRSFKIVEQSVG
KAPLPNPFLNRLVAISPQESQEAMRKIPDLCSQLKKVLKSLGVLTPENKHHALKEIPEGLKN
EHDSNPDKKTFPILIKLLIEALTGKSSLPKTPSTKEKMQAALFIASSCKTCKPTWGEVIT
RSLNRLYSIANEGDNQLLIWVQEFKERELMSIQDGDDAEEYRFAAQQHGERYTEAIEQVL
RNESAAKLQWHIVTMKFFHGKNLGLVTEHLQDTLGALTLRQTTVDTHQGREDADLSAAL
FLNKYLNSGNQLVNSVFKSHQKADPETKALIREFALDILYASLRLPQTSAHTEVFSTLLM
DPETYEPNKACIAYLLYVLKIIEL

CPn_0965　　　1106769　1104925
lpxB-Lipid A Disaccharide Synthase
KGFSFSKVGLAMIPSGLVYLLYPLGFLASLFFGSAFSIQWWLSKKRKEVYAPRSFWILSS
IGATLMIVHGTIQSQFPVTVLHVINLIIYLRNLNITSSRPISFRATLVLAALSVVFVTLP
FLYVNMEWMASPNIFHLPLPPAQLSWHLIGCLGLAIFSGRFLIQWFYIESNNTKDFPLLF
WKIGLLGGLLALVYFIRIGDPINILCYGCGLFPSIANLRLFYKEQRSTPYLDTHCFLSAG
EASGDILGGKLIQSIKSLYPNIRFWGVGGPAMRQEGLQPILNMEEFQVSGFAEVLGSLFR
LYRNYRKILKTILKHKPATLIFIDFPDFHLLLIKKLRKHGYRGKIIHYVCPSIWAWRPKR
KRILEQHLDMLLLILPFEEGLFKNTSLETVYLGHPLVEEISDYKEQASWKEKFLNSDRPI
VAAFPGSRRGDISRNLRIQVQAFLNSSLSQTHOFVVSSSSAKYDEIIEDTLKAEGCQHSQ
IIPMNFRYELMRSCDCALAKCGTIVLETALNQTPTIVMCRLRPFDTFLAKYIFKILLPAY
SLPNIIMNSVIFPEFIGGKKDFHPEEIATALDLLNQHGSKEKQKEDCRKLCKVMTTGQIA
SEEFLKRIFDTLPAV

CPn_0966　　　1108055　1106748
pcnB_2-PolyA Polymerase
LLITIIMVCENNILSGRGLELLKKKSNITLTFTIYSVSNHNIKLKDFSPHALSVIKTLRK
AGYIAYIVGGCIRDLLLNTTPKDFDISTSAKPEEIKAIFKNCILVGKRFRLAHIRFSKQI
IEVSTFRSCGSTDEDVLITKDNLWGTPEEDVLRRDFTINGLFYDPEHEEIIDYTGGVNDLR
NRYLRTIGDPFTRFKODFVRMLRLLKILSRSPFTVETQTQEALIACRQELIKSSQAVFVE
ELIKHLNSGAAKNFFCLLIENHLLEILFPYMDKAFRLNPALEEQTATYLKALDDKILKKE
AEYDRHQLMAIFLFPLVNFMVRYKHQKHPYLSLTSVFDYIKNFLEQFFADSFTSCSKKNF
ILTALILQMQYRLTPLPIFTKKALFFNKKLLHHTRFLEALSLLEIRSIVYPKLDKVYVAWI
RHHQTLKCKKDSHSQK

CPn_0967　　　1108431　1108985
mroA/pgm-Phosphoglucomutase
FTAYKFAFICACRJEKIRRICIDFRRNMQQSVRKLFGTDVJVRGRANFEPMTVETTVLLCGK
AVARVLREGRSIKIIRVVSKDTRLXYMFENALIAGLNCMYIIETIVLGPIPTTCGVAFITR
AYRADACHMISASINDYRDNSILKIFLSLSFKICDVLEQPIETMVSIFADFSPLPCEDHAVGK
NKRVIDAMCRYVEFVKATFIKFICIPTLIGILKIVLLCAIRIACYKVAISVFERLDAEVICYGCE
PTCINNEHLIAALFXPLCAVLIKOAILALIALDIDIDPIIHVDEKIILVIHUMILSICA
GDLKKRCIALPHNKVVATIHFINFYRLKYLEALILIVFTCPIDRIVLIANILAMILSICA
SGHMIFLDYNTDICGIVMALXVILRIMIFCIEMLCDLTAPIVKICPOTLINVAVREKIPLET
IPLIERTICKUVCDAICSICILPYSCFTENICPMVEYHPKHUVIXYLAFALADVIDAFLGI
TCURE

CPn_0968　　　1108989　1111231
plmU-Glucosamine-Fructose-6-P Amidotransferase

●

DRMCGIFGYLCNQDGVSIVLEGLAKLEYRGYDSA \ .VEOEELFIRKTVGRVQELSNLF
QEREIPTAGVICHTRWATHGVPTEINAHPHVDEGRGUAVVHNGIIENFKELRRELTAQGI
GFASDTOSEIIVOLFSLYYQESQDLVFSFCQTLAGLRGSVACALIHKDHPHTILCASOES
PLILGLGKEETFIASDSRAFFKYTRHSQALASGEFAIVSQGKEPEVYNLELKKIHKDVRQ
ITCSEDASDKSGYGYYMLKEIYDQPEVLEGLIQKHMDEEGHILSEFLSDVPIKSFKEITI
VACGGSYHACYLAKYIIESLVSTPVHIEVASEFRYRRPYIGKDTLGILISQSGETADTLA
ALKELRRRNIAYLLGICNVPESAIALCVDHCLFLEACVEIGVATTKAFTSCLLLLVFLGL
KLAMVHGALTHAEOCSFYOGLOSLPDLCQKLLANESLHSWAQPYSYEDKFLFLGRRLMYP
YZMENALELPEIAVTEADATIVSEMKIPEIALLUYTHVIAAPJCDDIYEOPMEINMMEVE
SIEMVIAIAPHEMEDIAAVLAUYEIFVETOBEIAAPLGAITOYNMAYERAIAVEMEIEEI
PRNLAKSVTVE

CPn_0969   1111803 1112999
tyrP_1-Tyrosine Transport_1
VYVMSNKVLGGSLLIAGSAIGAGVLAVPVLTAKGGFFPATFLYIVSWLFSMASGLCLLEV
MTWHKESKNPVNMLSMAESILGHVGKISICLVYLFLFYSLLIAYFCEGGNILCRVFNCQN
LGISWIRHLGPLGFAILMGPIIMAGTKVIDYCNRFFMFGLTVAFGIFCALGFLKIQPSFL
VRSSWLTTINAFPVFFLAFGFQSIIPTLYYYMDKKVGDVKKAILIGTLIPLVLYVLWEVV
VLGAVSLPILSQAKIGGYTAVEALKQAHRSWAFYIAGELFGFFALVSSFVGVALGVMDFL
ADGLKWNKKSHPFSIFFLTFIIPLAWAVCYPEIVLTCLKYAGGFGAAVIIGVFPTLIVWK
GRYGKQHHREKQLVPGGKFALFLMFLLIVINVVSIYHEL

CPn_0970   1113452 1114648
tyrP_2-Tyrosine Transport_2
VYVMSNKVLGGSLLIAGSAIGAGVLAVPVLTAKGGFFPATFLYIVSWLFSMASGLCLLEV
MTWHKESKNPVNMLSMAESILGHVGKISICLVYLFLFYSLLIAYFCEGGNILCRVFNCQN
LGISWIRHLGPLGFAILMGPIIMAGTKVIDYCNRFFMFGLTVAFGIFCALGFLKIQPSFL
VRSSWLTTINAFPVFFLAFGFQSIIPTLYYYMDKKVGDVKKAILIGTLIPLVLYVLWEVV
VLGAVSLPILSQAKIGGYTAVEALKQAHRSWAFYIAGELFGFFALVSSFVGVALGVMDFL
ADGLKWNKKSHPFSIFFLTFIIPLAWAVCYPEIVLTCLKYAGGFGAAVIIGVFPTLIVWK
GRYGKQHHREKQLVPGGKFALFLMFLLIVINVVSIYHEL

CPn_0971   1114693 1115415
yccA-Transport Permease
EGSMGLYDRDYIQDSRVQGTFASRVYGWMTAGLIVTSCVALGLYFSGLYRSLFSFWWVWC
FATLGVSFFINSKIQTLSVSAVGGLFLLYSTLEGMFFGTLLPVYAAQYGGGVIWAAFGSA
ALVFGLAAVYGAFTKSDLTKISKIHTFALIGLLLVTLVFAVVSMFVSMPLIYLLICYLGL
VIFVGLTAADAQAIRRISSTIGDNNTLSYKLSLMFALKMYCNVIMVFWYLLQIFSSSGNR
D

CPn_0972   1116377 1115430
ftsY-Cell Division Protein FtsY
RCINNSLLFPSYLVSFLLLQLTLLLAMFKFFRNKLQSLFKKNISLDLIEDAESLFYEADF
GTELTEELCARLRRTKKADASTIKDLITVLLRESLEGLPSQASQSSQTRPIVSLLLGTNG
SGKTTTAAKLAHYYKERSESVMLVATDTFRAAGMDQARLWANELGCGFVSGQPGGDAAAI
AFDGIQSAIARGYSRVIIDTSGRLHVHGNLMKELSKIVSVCGKALEGAPHEIFMTVDSTL
GNNAIEQVRVFHDVVPLSGLIFTKVDGSAKGGTLFQIAKRLKIPTKFIGYGESLKDLNEF
DLDLFLNKLFPEVEKI

CPn_0973   1116346 1117527
"sucC-Succinyl-CoA Synthetase, Beta"
ECKSKELFMHLHEYQAKDLLASYDVPIPPYWVVSSEEEGELLITKSGLDSAVVKVQVHAG
GRGKHGGVIVAKSSAGILQAVAKLLGMHFTSNQTADGFLPVFEKVLISPLVAIQREYYVAV
IMDRKHRCPVLMLSKAGGMDIEEVAHSSPEQILTLPLTSYGHIYSYQLRQATKFMEWEGE
VMHQGVQLIKKLAKCFYENDVSLLEINPLVLTLEGELLVLDSKITIDDNALYRHPNLEVL
YDPSQENVRDVLAKQIGLSYIALSGNIGCIVNGAGLAMSTLDILKLHGGNAANFLDVGGG
ASQKQIQEAVSLVLSDESVKVLFINIFGGIMDCSVVASGLVAVMETRDQVVPTVIRLEGT
NVELGKEIVQQSGIPCQFVSSMEEGARRAVELSM

CPn_0974   1117523 1118422
"sucD-Succinyl-CoA Synthetase, Alpha"
VCRFRRYMFHSLSKNTPIITOGITGKAGSFHTEQCLAYGTNFVGGVTPGKGGTLWLDLPV
YDSVLEAKQATGCRATMIFVPPPYAAEAILEAEEAGIELIVCITEGIPVRDMLEVARVMD
NSTSQLIGPNCPGIIKPGECKIGIMPGYIHLPGNIGVVSRSGTLTYEAVWQLTQLKIGQS
ICVGIGGDPLNGTSFIDVLQALEEDPYTELILMIGEIGGSAEEEAAAWIQAHCTKPVVAF
IAGVTAPKGKRMGHAGAIISGNSGDAKSKIQVLRESGVTVVESPAHIGKTVDAVLRAKEL

CPn_0975   1119038 1119637
No robust homolog present in Genebank/EMBL as of 11/7/98
GIEEQVALSIAIKILKIILALILFPLVLLAWVIRYQLHANFHCSVVPFPGFSVNQAYKCS
EAKIEEMLDLLDLETLEWSSRCLRQDMTFANRLEEELIQELRVSETEELISLGGKRNLVR
LLLTHFFNPPKRSRVESVGHEVVFPVFDRLKREEEIIGDGPITRSNEELWALLDHGTARG
IHKTLWFSIFFKYLTQIELF

CPn_0976   1120079 1121185
No robust homolog present in Genebank/EMBL as of 11/7/98
ILMLVYCFDPSVPTSPEHRLMAALDRWFFLGGHRARILTLEGNHYRAFQENMSISTVEKI
LKLISYLLIPIVLIALLIRCFLHSRFKCMWKCDSLSDARVPHDVQPFNDFQLFNNQERLN
IWKNRRYVSGIDVYPVDYLRSQPPGFKEIPAICENYVSDGQFSEESKTSYLRAMLT
DIVGYILSLDETYWTNVILKIRAMCITFESFPGKEADPNYSPRVTHHYFDESWKALARHV
LGEGNMVNRLDEALIRTEKPGKEGECITKQFLKDYCKKHLEVMSCPDFIESLVDEKIREF
RCPSILNSAVCDVIDRKCQEHLLKAIINEANRRLFGMKNSSFTMRGNQVLFYTIFSPPKL
PPAASSVYF

CPn_0977   1121329 1122402
No robust homolog present in Genebank/EMBL as of 11/7/98
LYIHQFANILKSSFLMEVYSFSPSVRTSFOHRVMAALDNWFFLGGRRLKVVSLDSCNSGQ
ACEEYVPISTTEKVLKILSYLLIPIVIIALLIRYLLHSNFTAKVSQKFWLKTLQLGIDIK
FLPGGIVNTMDSATLFKAIRLEGKRVDVEYHRLHSSDKVVFYIPAQKLPDDLRLTHWL
PEKETRKTEYVRHMLAHVMGYLTSQKERLQQVVQDSRSGTSLCGAEKVLQYRFIDHPQSQ
OEFQRLLNENITTKCSEDKEVVQSDLFDMAFQCWWPQFISVIQSPTFSEELVHEMSQKLD
LDCIYPEDDEFEQKFLNTLLKAVLHHGFEGISVASMGVIFLICPDSLALOIPFLRNQK

CPn_0978   1122654 1123403
No robust homolog present in Genebank/EMBL as of 11/7/98
KYFFMEVYCFHDAVRTGFQHRVMAALDAWFFLGHRLKVVGLDGCNSGWAYQELVSISTT
FKVLKLLGYLLVPIVIIALLIRCLLHSNFRIDVEKEPWLKIRELGIDIESCKLPGGYVNQ
VSGFIWFEKDKGKHPHIDVDYIHTLHGKDWVVFPIVFQKIPKTGRFGYWFSQKETRKRDYV
HNMIJHVIGYLTHYIEWLQYICKKCIYQGATLGLOPERVLQVLTDNQELQGEVQRLLNEE
GATKGGCDKEVLGHVSDIICQCWWPKFLEVIQGPAFIEELVEEVGGKLNLDFLCLEKAN
TILQELRNCILLPAVVHIIGYIVDIKKVCAGLIIVTEAIQIQGIPFGRG

CPn_0979   1123971 1125443
htrA-DO Serine*Protease*
GIDMITKQLRSWLAVLVGGSLLALPLSCOAVGKKESRVSELPODVCLKEISGFSKVATK
ATPAVVYIESFPKSQAVTHPSPGRRGPYENPFDYFNDEFFNRFFGLPSOREKPQSKEAVR
GTGFLVSPDGYIVTNNHVVEDTGKIHVTLHDGQKYPATVIGLDPKTCLAVIKIKSCNLPY
LSFYNSDHLKVGDWAIAIGNPFGLQATYTVGVISAKGRNQLHIADFEDFICTDAAINPGN
SGGPLLNIDYQVIGVNTAIVSGGGOYICIGFAIPSLMANRIIDQLIRDGQVTRGFLGVTL
...IAULAUAVFFLEGYZ MIAUT VPF...TALPA...M...F ...LA...ING...VY...MFRHAVG
...MEI ITRCLYLGLYPRRYGTFGUTYLL NPFED...ABL...Y...IRL...N...TFAPLLHALE
TKGILIISVEPGSVAASSGIAPGGLILAVNRQKVSSIECLNRTLKDSNNENILLMVSQGD
VIRFIALKPEE

CPn_0980   1126988 1125504
"similarity to Saccharomyces serevisiae hypotnetical 52.9KD
protein"
FVMLNHAKKHAKPYVLIFFSTKDKLSYCDIIFNNCSGKPMNLDSKHFDINSANFLEEFAK
FISFPSISADSDHLQDCENCAHFLVDHVNKIFDVELWETPGHPPIIYASYKSEDPLSPTL
MLYNHYDVQPAQLSDGWKGDPFILREENGNLYARGASDNKGQCFYTLKALQHYYESQGNF
PLNIWLIEGEEESGSLALFTWLEKKKEALRADYLLIVDGGFLSEKHPYVSIGARGIVSM
KISLEEGNKDMHSGVLGGIAYNTNRALSEILSSLHHPDNSIAIEGFYDDLALPSDSDRPD
LPKSDTLRECEENLGFRPQGYEASYSPEESALRPTVEINGISGGYTGPGFKTVIPYRATA
YLSCRLVPNQDPDKAAHQVIHHLKQQVPSSLKFSYEILPGGSRGWRSSANLPIVKVLQEI
YSDLYNEECLRLVMPATIPIGPLLGEAAQTSPIICGTSYLSDDIHAAEEHFSMDQLKKGF
LSICQLLDKLPKIKE

CPn_0981   1127019 1129952
Zinc Metalloprotease (insulinase family)
VTESMKAGDTYRNFIIKSCKDLPEIESKLLEAEHKPTGASIMMIVNNDEENVFNICFRTC
PQTSNGVAHVLEHMVLCGSENYPVRDPFFSMTRRSLNTFINAFTGPDFTCYPAASQIPED
FYNLLSVYIDAVFHPLLTKQSFLQEAMRYEFNSENHLCYTGVVFNEMKGAMMSGEARLSE
ALNAAIFPSVTYGVNSGGEPREIVTLSHEDVRAFHQSQYSINRCLFYFYGNIKPSRHLDF
LEEKLLRQATKLEKQAVSVPLQKRFKEPVRNILTYPVDHQEEDKVLFGSLWLTCSILEQQ
ELLALHVLEIILMGTDASPLKSRLLKSGFCKQTEMSIENDIREIPMTLVCKGCSPAGAQK
LEALIFASLEEIIREGISENIVRGAVHQLELSRKEITGYSLPYGLSLFFRSGLLKQHGGS
AEDGLRIHSLFSELRNSLKNSDYLAKLIRKYFLDNPHFARVILLPFHFARVETLLVNKVAKDNKDEQQL
LLSVSEKLTDENKEKIQQNVRELTESQEQKEDLNGILPNLALDKVPTSGKEFPLIKEGLS
QGEVLHHECFTNDIVFIDVVLDIPPLSGEELPWLRLLVFLMLQLGCGGRSYKEHLEFLLE
HTGGVDVSYDFSPHANKNSFLSPSVSIRGKALSSKSEXLCGIVSDMLTSVDFTDIPRIRE
LLMQHNEALTNSVRNSPMSYAVSMACSGNSITGAMSYLTTGLPYVKKIRELTKNFDQNID
EAVVILQRLYTKCFSGKRQIVISGSAHNYQQLKDNKFYGLLDYLIVIPEPWENPSINLYV
TSRGLHIPARAAFNALAFPIGDIAYDHPDAAALTVAAEILDNVVLHTKIREQGGAYGSGA
AANLSRGSFYCYSYRDPEIATTYKTFLKGVSEIASGNFTKEDIYEGALGVVQGLDMPVAP
GSRASVAFYRLKSGRIPVLRQAFRRSVLEVTKEHICMVMDKYLESTVQETTLISFAGEEM
LRNNVLTLDKDFPIVPAI

CPn_0982   1131215 1129962
yigN family
KKELASVMNLPVSLACLLLSGCVFFLGVFVSSSLYARKKRAFLEXIQKLEHENQLLQTSL
NLSRHQEQLIEDFSNRLALSSHKLIKDMKEEAQNYFGDTSKSFQSILSPIQTTLTTFRQS
LETFETKHAEDRGRLKEQISQLLAVEKKLEHETHVLTDILKHPGSRGRMGEIQLERILEL
AGMLKYCDYDSQTTSAQGAFRADIIIRLPQDRCLIIDAKAPISDSYFSVEEIDKGDLVDK
IKEHIKTLKSKSYWEKFHQSPEYVILFLPGESLFNDAIRLAPELMEIGASSNVILSSPLT
LLALLKTIAYMWKQENLQKQIQEVSLLGKELHRRLQVVFTHFQKIGKNLNQTVQSYNDMT
SSFQYRVLPTLRKFEGLETSSSHQIEEPTPIESLATSFPHTCDIDTNLAVIESLEKQD

CPn_0983   1132045 1131206
pssA-Glycerol-Serine Phosphatidyltransferase
KNPLCYEQKKLWQIDMAGLDLEARGKRRVVTPNAITAFGLCCGLFIIFKSVLRTSSSVEL
FHRLQGLSLLLISAMIADFSDGAIARIMKAESAFGAQFDSLSDAVTFGIAPPLIAIKSLD
GIYVGNFFSSLLLTSIIYSLCGVLRVRYNLFSOKTVDVSKPYCFIGLPIPAAAASIVS
LALFLASDFFPDLPAQLRVGLLSFALLFIGGLMISPWKFPGVKHFRFNVSSFLLVVTIGL
AACLFFSGLVDHFVEVFFLVSWLYTLVGFPIFSIIYRKKS

CPn_0984   1132370 1135510
"nrdA-Ribonucleoside Reductase, Large Chain"
GKVMVEVEEKHYTIVKRNGMFVPFNQDRIFQALEAAFRDTRSLETSSPLPKDLEESIAQI
THKVVKEVLAKISEGQVVTVERIQDLVESQLYISGLQDVARDYIVYRDQRKAERGNSSSI
IAIIRRDGGSAKFNPMKISAALEKAFRATLQINGMTPPATLSEINDLTLRIVEDVLSLHG
EEAINLEEIQDIVEKQLMVAGYYDVAKNYILYREARARARANKDQDGOEEFVPQEETYVV
QKEDGTTYLLRKTDLEXRFSWACKRFPKTTDSQLLADMAFMNLYSGIKEDEVTTACIMAA
RANIEREPDYAFIAAELLTSSLYEETLQCSSQDPNLSEIHKKHFKEYILNGEEYRLNPQL
KDYDLDALSEVLDLSRDQQFSYMGVQNLYDRYFNLHEGRRLETAQIFWMRVSMGLALNEG
EQKNFWAITFVNLLSTFRYTPATPTLFNSGMRHSQLSSCYLSTVKHDLSHIYKVISDNAL
LSKWAGGIGNDWTDVRATGAVIKGTNGKSQGVIPFIKVANDTAIAVNQGGKRKGAMCVYL
ENWHLDYEDFLELRKNTGDERRRTHDINTASWIPDLFFKPLEKKGCMWTLFSPDDVPGLHE
AYGLEFEKLYEEYERKVESGEIRLYKKVEAFCLWRKMLSMLYETGHPWITFKDPSNIRSN
QDHVGVVRCSNLCTEILLNCSESETAVCNLGSINLVEHIPNDKLDEEKLKETISIAIRIL
DNVIDLNFYPTPEAKQANLTHRAVGLGVMGFODVLYELNISYASQEAVEFSDECSEIIAY
YAILASSLLAKERGTYASYSGSKWDRGYLPLDTIELLKETRGEHNVLVDTSSKKDWTPVR
DTIQKYGMRNSQVMAIAPTATISNIIGVTQSIEPMYKHLFVKSNLSGEFTIPNTYLIKKL
KELGLWDAEMLDDLKYFDGSLLEIERIPNHLKKLFLTAFEIEPEWIIECTSRRQKWIDMG
VSLNLYLAEPDGKKLSNMYLTAWKKGLKTTYYLRCQAATSVEKSFIDINKRGIQPRWMKN
KSASTSIVVERKTTPVCSMEEGCESCQ

CPn_0985   1135432 1136571
"nrdB-Ribonucleoside Reductase, Small Chain"
ISVHKYCGRKKNNPRLFNGRRLRILSITEKRAGAKMEADILUGKLKRVEVSKKGLVNCNQV
DVNQLVPIKYKWAWEHYLNGCANMWLPTEVFMARDIELWYGDELGEDERRVILLNLGFFS
TAESLVGNNIVLAIFKIIITNPEAROYLLRUAFEEAVIITHTFLYIGGELGLOLDEGRVFNAYN
FRAGIPAKDDFGWFFLTVDVLDGNFGVQGGGGEGLYIGFIKNLWGYVIMFGIFFYGGFVMILS
FHRQNFHTIGEUYQYILRDRTIHLNFGIDLINFGIKEEJPFAWTTELAREEIVALIEKAVE
LEIEYAKDLGLPRGILGILGDOMFIDYVPHIAIMRLERIGLPPIYIEGRNPFIWMGETMDLNK
FKNPFFETRVTEYGYTAGNLGW

CPn_0986   1136712 1137706
yqhH (probable LHNA Methylase)
FLLFMYYQDLGIPPFIKKERRIYIQILVLYVIVRGIYFEIUHEIGTIGIJEPFUNIITGIACELC
GINGILAVVAQAUKDIQVIMIAVEGGGFGLAGYPKIWGWMINIGFQRLGIVGYTARTFPGYYVP
IQFIQFLVVNFPDFWFKMMHIRKEIPIJJGGFVQEIGIRLLQGGAVFAIATIHKFYLIJEGIFA
IGYHILAPRMETGYYIKMFDFGGREWWFFIHMFFFGYGJEIFYTEFIKKAGI

CPn_0987   1137483   1138115
ytuB-like predicted rRNA methylase
LENGIFAIGFFMFAYRTLLTHNVVQVSHEIFKTTVVPGDTVIDATCGNGNDSLFLARLLQ
GEGRLVVYDIQKEALSNALLLFETHLSEQDERSVIEMKEQSHEHILEKDVKLIHYNLGYLP
KGNKEITTLARTTEISLEYALNIVRPDGLITVVCYPGHPEGEKETHSVESLAQRLHPKEW
CVSGFYVANRCRAPRLFIFQRQGSESSVDKG

KFFINLINLDQGILKMKEAAPMHFPFPVRRSVWLNRYSTFRIGGPANYFKAIHTIEEARE
VIRFLHSINYPFLIIGKGSNCLFDDRGFDGFVLYNAIYGKQFLEDARIKAYSGLSFAALG
KATAYNGYSGLEFAAGIPGSVGGAIFMNAGTNESDISSVVRNVETINSEGELCSYSVEEL
ELSYRSSRFHRQQEFILSATFQLSKKQVSADHSKSILQHRLMTQPYTQPSAGCIFRNPEG
TSAGKLIDAAGLKGLAIGGAQISPLHANFIINTGKATSDEVKQLIAIIQSTLKTQGIDLE
HEIRIIPYQPKIHSPVSEK

CPn_0989   1139552   1139016
CT832 hypothetical protein
LRTSLAVKCVLLTIFWLLVMATLSPEKFSGSPISISKEFPQQKMREIILQMLYALDMAPS
AEDSLVPLLMSQTAVSQKHVLVALNQTKSILEKSQELDLIIGNALKNKSFDSLDLVEKNV
LRLTLFEHFYSPPINKAILIAEAIRLVKKFSYSEACPFIQAILNDIFTDSSLNENSLSI

CPn_0990   1139880   1140440
infC-Initiation Factor 3
SVALNFKINRQIRAPKVRLIGSAGEQLGILAIKDALDLAREAGLDLVEVASNSEPPVCKI
MDYGKYRYGLTKKEKDSKKAQHQVRIKEVKLKPNIDENDFSTKLKQARTFVEKGNKVKIT
CMFRGRELAYPEHGFKVVQKMSQGLEDIGFVEAEPKLAGRSLICVVAPGTVKTKKKQEKS
HAQDENQ

CPn_0991   1140394   1140612
rl35-L35 Ribosomal Protein
KQRKNRKSLHPKMKTNKSVSARFKLTASGQLKRTRPGKRHKLSKKSSQEKRNLSKQPLVD
KGQVGHYKRMMLV

CPn_0992   1140622   1140996
rl20-L20 Ribosomal Protein
GKLVMVRATGSVASRRRRKRILKQAKGFWGDRKGHIRQSRSSVMRAMAFNYMHRKDRKGD
FRSLWIARLNVASRIHSLSYSRLINGLKCANISLNRKMLSEIAIHNPEGFAEIANQAKKA
LEATV

CPn_0993   1140975   1142030
pheS-Phenylalanyl tRNA Synthetase, Alpha*
KSFGSHSLGIRISMEMKEEIEAVKQQFHSELDQVNSSQALADLKVRYLGKKGIFRSFSEK
LKQCTDKAKLGSLVLLQNLESLVLLASEQAEAFSKEKIDSSLPGDSQPSGGR
HILKSILDDVVDIFVHLGFCVREAPNIESEANNFTLLNFTEDHPARQMHDTFYLNATTVL
RTHTSNVQARELKKQQPPIKVVAPGLCFRNEDISARSHVLFHQVEAFYVDHNVTFSDLTA
ILSAFYHSFFQRKTELRFRHSYFPFVEPGIEVDVSCECCGKGCALCKHTGWLEVAGAGMI
HPQVLRNGNVDPEIYSGYAVGHGIERLAMLKYGVSDIRLFSENDLRFLQQFS

CPn_0994   1142371   1144440
CT837 hypothetical protein
LFWFHRGGRMKRSRRNFEQALENLEKLKEISLATSNDSYLANPARFNQRKQTGSSVMEMK
EALKNVENYLLEISCVSKSHADKALKESDFLIAGVQNVFSFLENQEDLYKSLLDEYSEVT
KAYDEVKKNLKEVPTYDLSTDEETEEHKEPECFLNNLVEVKRDRSYELFYMLDEQDKRFY
NDALVQIIYKQNKLHETVNEGDPLTKTLLWNSEEVKNIASSLVIVNDMPLRLFYQRALSH
LDIEAVVKVHNAVMALFFSRYEATMVFKSPKKHNIWYFNDFLLFLREAWKDLNNNVIDSQ
ERKQTKLLASALSLGIFESKLVFEEASRYLYFNIQTKLNANGKKPLSPGQYLTDAYEEL
HRLISKYPNGPLFKAMDRVLEHESRPYDPHILGILPSLEGTLKLHGKSIDIIRSPSPVTQ
SSILYANCNEEFLGFLNAKAHRSEVTLVLNIQNRISRKERARSRVIEEALEQEEHAPYVH
AFSFPEPEELLQNLESIHGDIETFADFFSILQEEFHKPLLASSFFLTKELKEFVGSFLKE
KLTALKDIFFAKKKILFRNDKLLLLHLLSYLIVFKLIERTNPNSIVVVSKDGLDYVSVFI
AGFAFFSREAFWDEHSLKLLLTNVLSPTLVARDRLVFVSHIELLSKFVNCLKKNRQGFSS
LKSFFKDDIEGWEFTGYLHELTEVSHKHNL

CPn_0995   1145515   1144415
CT838 hypothetical protein
RMLIWKRHLLTRFWFALTSLLVLALIFYASIHHSLHTLKGASTAASGASVKLSILYYLAQ
ISLKAEFLMPQLVAVATTSTLFAMQNKREIILLQASGLSLKSLMHPLLLSGAVIMMVLYA
NFQWLHPICEKISITKENMDRGTTDKEQGKIPALYLKDQTVLLYSSIEPKTLTLNNVFWI
KDPKTIYTMEKLAFTTLSLPIGLNVTOFFANDSENLELKEFFDMKEFPEIEFNVFYENPFS
KLFSAGNKNRLSEFFKAIPWNATGLGLSTQVPQRILSLLAQFYYVLISPLACMAAIILSA
YLCLRFSRTPTVTLAYLIPLGTVNIFFVFLKAGIVLASSSVLPTLPVHAFPLIVLFLLTN
YAYAKLQ

CPn_0996   1146592   1145519
CT839 hypothetical protein
AMPILWKVLIFRYLKTAAFCTLSLICISIISSLQEIVAYIAKDVPYDTVLRLMAYQIPYL
LPFILPGSCFVSAFSLFRKLSDNNHMTFLRASGASQSIMFPVLMVSGAICCLNFYTCSE
LASICRYQTCKEIANMAMTSPALLLQTLQKKENNRIFIAVDHCAKSKFDNVIVALKGNNE
ISHVGIIKSIIPDTTKDTVKAKDVVFISKLPDSLTESSSPSSQRFYIETLDELLIPKITS
TLFAGKSYLKTRTDYLPWKQLVKQSLKHSHLPETLRRVAIGFLCITLTYAGMILGIHKPR
FRKSIALYFIFPILDLILLIVGKNTKNLPLAFMLFVFPQLVSWVVFAARAYRESRGYA

CPn_0997   1146699   1147664
mesJ-PP-loop superfamily ATPase
AYKHVLSSDLLRDDKQLDLFFASLDVKKRYLLALSGGSDSLFLFYLLKERGVSFTAVHID
HGWRSTGAQEAKELEELCAREGVPFVLYTLTAEECGDKDLENQARKKRYAFLYESYRQLD
AUGIFLAHHANDQAETVLKRLLEGAHLTNLKAMAERSYVEDVLLLRPLLHIPKLYSSLKEAL
DARGIGYLQDPINEDERYLRARMRKKLFPWLEEVFCFHITFPLLTLGEESAELGEYLEKQ
AQPFFGAATLHQDIQGELPCPDCLIQQAFLCKWVMKKFFHNAGIAVIRHFLQMVYDHLGRG
GCATLPMRNKIVIIKRGVVVID

CPn_0998   1147811   1150584
ftsH ATP-dependent zinc protease
LISLVVKRMKUKKMKPKDPKKNFCTVFFFLLDVVVFEZZAFQNFIAGKKAARVGFSHQIEH
LVNLRLIVIPEDGHKIALNDNLVSFLXRFRDVVQTQFCGLLRYHYLELLDQHIRLDLDLQETS
KSGCTFIIKEVTNGILWFGAIGGSPIPEQGYAISVDGEZZGXVIFEPLVVTGPATFQLINL
HLGGEPYITPLGGIPALRTYGGHDLYELIGKYLGIVLFIFTGHTCKRELKDLYQQVVSLTQ
ETUFTFAAYTLYGQVLGTLNRIGSGLVVGECGGERFGOLPGVRLYREFHNKYHIKLVFARDLH
QAQLFKLIGFLGGTVWYFNNQELGSRSLEKQODPEVFGHWFAGGAKEHWTAFKFNIELGFKA

PDQPRNLVLEKTFKSQEPSP,   LFTFLPIILVLLFVYLVFGRQMRCHGGSAMSFGKS
PARMLLKKCQNKVTFADVAGIELAKEELIEIVDFLKNFNKFTSLGRIPKGVLLIGPPGTG
KTLIAKAVSGEADRRFPSIRGSDFVEMFVCVIGASRTRQHFEQAKRMAECIKFIDRVG
RHRCAGICGGHDEREQTLNGLLVEMDGFGTNEGVILMAATNRPDVLDRALLRPGRFDRRV
VMNLPDIKGRFEILMVHAKRIKLDFTVDLMAVARSTFGASGADLENLLNEAALLAARKDR
TAVTAVDVAEARDKVLVGKERRSLEMDAEERKTTAYHESGHAVVGLCVQHGDPVDKVTII
PRGLSLGATHFLPEKNKLSYWKKELYDQLAVLMGGRAAEEIFLGDISGAAQQDISQATKL
VRSMVCEWCMSPQLGNVTYDERSDGLTGYGGYHEKSYSEETAKTIDTELRMLLDAAYQRA
AEIIHSRAEHELMYLLDLQGTFSAREXQEOMEHFVYTCRGIRDGNVGLFERMEFNKGJCGL
FFFCKKFRPTTLAGIIDYKRTT

CPn_0999   1152859   1150766
pnp-Polyribonucleotide Nucleotidyltransferase
QETFMNFQTISINLTEGKILVFETGKIARQANGAVLVRSGETCVFASACAVDLDQKVDFL
PLRVDYQEKFSSTGKTLCGFIKREGRPSEKEILVSRLIDRSLRPSFPYRLMCDVQVLSYV
WSYDGQVLPDPLAICAASAALAISDIPQSNIVAGVRIGCIDNQWVINPTKTELASSTLDL
VLAGTENALIMIEGHCDFFTEEQVLDAIEFGHKHIVTICKRLQLHQEEVGKSKNLSAVYP
LPAEVLTAVKECAQDKFTELFNIKDKKVHAATAHEIEENILEKLQREDDDLFSSFNIKAA
CKTLKSDTMRALIRDREIRADGRSLTTVRPITIETSYLPRTHGSCLFTRGETQTLAVCTL
GSEAMAQRYEDLNGEGLSKFYLQYFFPPFSVGEVGRIGSPGRREIGHGKLAEKALSHALP
DSATFPYTIRIESNITESNGSSSMASVCGGCLALMDAGVPISSPIAGIAMGLILDDQGAI
ILSDISGLEDHLGDMDFKIAGSGKGITAFQMDIKVEGITPAIMKKALSQAKQGCNDILNI
MNEALSAPKADLSQYAPRIETMQIKPTKIASVIGPGCGKQIRQIIEETGVQIDVNDLGVVS
ISASSASAINKAKEIIEGLVGEVEVGKTYRGRVTSVVAFGAFVEVLPGKEGLCHISECSR
QRIENISDVVKEGDIIDVKLLSINEKGQLKLSHKATLE

CPn_1000   1153193   1152891
rs15-S15 Ribosomal Protein
SAFAAIILRRHPMSLDKGTKEEITTKRFQLHEKDTGSADVQIAILTEHIAELKEHLKRSPK
DQNSRLALLKLVGQRRKLLEYLNSTDTERYKNLITRLNLRK

CPn_1001   1153369   1153869
yfhC-cytosine deaminase
YYLELGGEKLINMEKDIFFMQQAFKEARKAYDQDEVPVGCVTVKDDKIIARAHNSVEKLK
DATAHAEILCIGSAAQDLDNWRLLDTVLYCTLEPCLMCAGAIQLARIPRIVWAAPDVRLG
AGGSWVNIFTEEHPFHTVSCTGGVCSEEAEHLMKKFFVEKRREKSEK

CPn_1002   1153844   1154089
CT845 hypothetical protein
KSAERKVKNKIVTLLDQLYEDQESRLQKLGEEIVPNLTPEDLLQPMDFPQLEGNPAFRFE
EGVLSGIGEVRAAILAALSQEN

CPn_1003   1154862   1154092
CT846 hypothetical protein
TSNKTIHPLLAGPDRQIAGKASMRVIFPDKHNNFPNLSKLLKKLPSVILVTSCIAPFFSY
IINKFFGIPGLLEILALSVKGIQKHHFWQFLTYPLITADSLSLNXDOSFEITORLLLRNV
LDFFLFYKAIQHLIRKLGAFSVLVVISGQALIIGAVLWGFMALIHSSQSFFGPESIICGV
LTVQIFLDPEKRFTIGPTPLSVSIKWGFLFVLGFYCCILIFSGAFLLLLASMLAIVLAIL
FCKKEKIPNFYTTSLRF

CPn_1004   1155418   1154879
CT847 hypothetical protein
HLSIEELMSIQPVSNTTTKADKVIPDSTKVISDSITINKQSAFYFCISVMLRLSESTTEY
GKSILAVLEDNTTVQQQRVKELINLPLLKVPDLQKKDGSDDEYKNQNEIQAYQSSNQQIS
ANRQMIQQELSSAQQRAQANQKSVNSTTIESMQILQATSSMLSTLKELTIKANLTNSPSD

CPn_1005   1155957   1155415
CT848 hypothetical protein
NRRPVRLNMWIIDPLSAKKPLQAAINVPGTPITGGPNTATADDIIAKFSKDSNPLIVTVY
YVYQSVLVAQDNLSIIAQELQANSSAQTYLNNQEALYQYVSIPKNKLNDNSSSYLQNIQS
DNQAIGASRQAIQNQISSLGNAAQVISSNLNTNNNIIQQSLQVGQALIQTFSQIVSLIAN
I

CPn_1006   1156493   1155990
CT849 hypothetical protein
TKVNFFIMSITTLGTLPTVNTINSSRPPLEPLNTPKIGAVLFSIYELLLQAIEIRQQTVL
TQSQQLNDNTNIQQQLNQETNQIKYAIVSAGAKEDEITRVQNQNQNYSAQRSNIQDELVT
TRQNGQIILSHASTNINIIQQQSSQDSSFIKTTNSIGSTVNQLNKPLG

CPn_1007   1156689   1156907
CT849.1 hypothetical protein
LWYKSLAGEEKDVSGNECNDYPEVFKDDVSAYVLVTCGQMSSEGKIQVEMTYEGDPAVIS
YLLTKARDSLDES

CPn_1008   1156904   1158223
CT84850 hypothetical protein
VLNYSFIGMLKPMYVLSKRLYRWVNQLIKLGDLVKNSRSFSVEWVFISALLLIFGCLGCA
SVVKVSLVPFLLLFSFLAFFLILCFRGKGYALLLGVFVTLYVAKYVVGETLYVSFWLSGL
CVSFLLAFGLFLQGVWLAQEEEMVKGKEQLRLSEDLDAQRSAYEDLLLTKSQEKEFLDAR
AQGLDRELTECQELLKAAYCKQEYLTIDLKILADQKNGWLEDYAELHNKYIELVSKNGDV
VFPWVAEPSVGEGSQSERVDVSRWVSALQEKEESLERLRNEILVEKQRCSDYEHRCQELG
GLYSQLQEQFLEKSETLSLVRKKLFAVQEKYLTLKKKEELTKQDISFDDISMIQGLLERI
EILEEEVGHLEELVSRSLSL

CPn_1009   1159085   1158186
map-Methionine Aminopeptidase
YRLLIPYILMKRHDPLWCGSIRKWKQCHYPQPPKMSPEALKQHYASQYNILLKTPEQRAK
IYNACGITARILGELCKASGKGVTTNELDELSQELHKKYDAIAAPFHYGSPPFPKTICTS
IIJEVIGIFLFNDIFLKDJDIHNIDVICIVDTYYGDCCPHVMIGEVPEIKKKICQAALECL
HLGIAILYDGIPIJELGEAIFARADTYGGFSVVDQFVGHYZWIIEFIIENPYVPHYRNRSHIP
IAICMIFTIEFHIHWIKKEZVVDPKNLWEARTCDHGPGAGWEHFIAITETGYEILTLLND

CPn_1010   1159675   1159067
CT852 hypothetical protein
VMLILIJHLGLLFVVLFCSIVSCIVPVVALLKNFGRFFYGZPVILRFGFFAVDALILFVTFGR
GFFQFLFGLGFAKDFLLFTVGIKMMLAPMPEFAFDDFCKTEFIFFPLAFPVTTGPA
VCTALLGYMEHSIIYGRGLIFTAMIAWAFGLFTLLCGGFFDRLFGNFGLLALERLFGTAL
GLJKFVHHMLKGIGIAFNLGFYLG

CPn_1011   1160409   1159982
1154462

CT851 hypothetical protein
FMRLKNYFMIQFFFFLPGTGILLLASDGLTNILAL...LANYJVKQRMLVLLRESFFAFI
AMFALYGLAUGLKVLNTPVCAIEVVGGIAVTLAGVRAVLRLUKEESWIPYKFNMSPSYS
PCIIPIALPLMPGPSG

CPn_1012   1162220   1160421
yraB-ABC transporter permease
AIFRLITGHMKKFKFIFYFVIVFGLLFLWEMTSRHPPTFCFFCPPPGGIAGTTLQSLPLLL
...AWFFLFFLI FFFLATTL FFAGTMLTMLWLAL FLL FLFLJGFTTFMFALALCLVVAL
HIFSGLKIAIGSAGFAAIAGEWVASQSGLGILMLESRRNYEMELAFAGLATLSILTLSLF
QITLLIEKLIFSLFRVKRMSLKHKSVAKKALSVLALIPIMLIPWKGNSKSPPDKKNLTSL
TLLLDWTPNPNHIPLYAGVAKGYFKQHGLDLQLQKNTDSSSAVPHVLFEQVDMALYHALG
IMKTSIKGHPIQIVGRLIDSSLQGFLYRSQDPIYKFEDLNGKVLGFCLNNSRDLNRLLET
LNRNGVVPSEVKNVSSDLISPMLLNKIDFLYGAFYNIEGVKLQTLGHMPVKCFLSDTCDLP
TGPQLIVFTKKGTKASEPEIVEAFQKALQESIIFFSKDHPEDAFKLYAKETKSIPKNLYQE
YLQWEETFPLLAQSQDPLSKDLVDKLLETIIKRYPELASEVAKFSLNDLYNPSLPEEQSV

CPn_1013   1162209   1163624
fumC-Fumarate Hydratase
RENSLNHRGNIDMRQEKDSLGIVEVPEDKLYGAQTHRSRNFFSWGPELMPYEVIRALVWI
KKCAAQANQDLGFLDSKHCDMIVAAADEILEGGFEEHFPLKVWQTGSGTQSNMNVNEVIA
NLAIRHHGGVLGSKDPIHPNDHVNKSQSSNDVFPTAMHIAAVISLKNKLIPALDHMIRVL
DAKVEEFRHDVKIGRTHLMDAVPMTLGOEFSGYSSQLRHCLESIAFSLAHLYELAIGATA
VGTGLNVPEGFVEKIIHYLRKETDEPFIPASNYFSALSCHDALVDAHGSLATLACALTKI
ATDLSFLGSGPRCGLGELFFPENEPGSSIMPGKVNPTQCEALQMVCAQVLGNNQTVIIGG
SRGNFELNVHKPVIIYNFLQSVDLLSEQMRAFSEFFVKGLKVNKARLQDNINNSLMLVTA
LAPVLGYDKCSKAALKAFHESISLKEACLALGYLSEKEFDRLVVPENMVGNH

CPn_1014   1165456   1163732
ychM-Sulfate Transporter
ALASTLGYCIVKVPWAFKNFIPKLYTSIKEGYSFNTFKKDFQAGITVGILAFPFAIAIAI
GVGVSPIQGLLASIIGGLLASAHGGSNVLISGPSSAFISILYCLSAKYGAEALFTVTLLA
GVFLIAFGLTGLGTFIKYMPYPVVTGLTTGLAIIIFSSQIKDFLGLQMGANIPADFLPKW
IAYWDHLWTWDSKSFAVGLFTLLIMIYFRNYKPRYPGVMIAIVTATTLVWLLKIDIPTIG
SRYGTLPTAIPLPKIPOLSITKILQLMPDALTIAVLSGLETLLSAVVADGMTGWRHQSNC
QLVAQGVANIGTSLFSGIPVTGSLSRTAASIKSEATTPIAGIVHSIFICFILLLLAPLTV
KIPLTCLAAVLILIAWNMSEIHHFIHLFTAPKKDIVVLLTVFILTVMTITAAVQVGHML
AAFLFMKQMSDLSDVISTAKYFDKDSDFLSKAEVVPONTEIYEINGPFFFGIADRLKNLLN
DIEXPPKIFILCMTRVPTIDASAMHALEEFFLECCDROGTLLLLAGVKKTPLADLKRYHLD
ELIGVDHIFSNIKSALLFAQALTNLESKTSTRHLV

CPn_1015   1165550   1166893
CT857 hypothetical protein (possible IM protein)
KNNYKNFSFFTSVRVRSKVDHEIILEVTMLKLQLCALFLFGYLAIVFEHIVRVNKSAIAL
AMGGLMWLVCFSHIPMADHMILVEEIADMSQVIFFLFSAMAIVELIDAHKGFSVIVKFCR
IQSRTLLLWALIGLSFFLSAALDNLTSIIIISILKRLVKAREDRLLLGAICVIAVNAGG
AWTPLGDVTTTHLWINNKITSWGIIRALFVPSLVCVLVAGFCGQFFLRKRGSTLIAKDVE
LQSAPPKSLWIIFIGLGSLLMVPVWKACLGLYPPFHGALLGLGLVWLTSPHSPGEDRY
HLRVPHILTKIDISSITFFIGILLAVNALSFANLLTDFSLWMDKIFSRNVVAIVIGLLSS
VLDNVPLVAATHGMYTLPLDDTLWKLIAYAAGTGGSILIIGSAAGVAFMGLEKVDFLWYF
KRISWIALASYFGGLFSYFVLESLNFFI

CPn_1016   1167027   1168898
CT858 hypothetical protein
KREVFNKKGKLGAIVFGLLFTSSVAGFSKDLTKDNAYQDLNVIEHLISLKYAPLPWKELL
FGWDLSQQTQQARLQLVLEEKPTTNYCQKVLSNYVRSLNDYHAGITFYRTESAYIPYVLK
LSEDGHVFVVDVQTSQGDIYLGDEILEVDGHGIREAIESLRFGRGSATDYSAAVRSLTSR
SAAFGDAVPSGIAMLKLRRPSGLIRSTPVRWRYTPEHIGDFSLVAPLIPEHKPQLPTOSC
VLFRSGVNSQSSSSSLFSSYMVPYFWEELRVQNKQRFDSNHHIGSRNGFLPTFGPILWEQ
DKGPRYRSYIFKAKDSQGNPHRIGFLRISSYVWTDLEGLEEDHKDSPWELFGEIIDHLEKE
TDALIIDQTHNPGGSVFYLYSLLSMLTDHPLDTPKHRMIFTQDEVSSALHWQDLLEDVFT
DEQAVAVLGETHEGYCMDHHAVASLQNFSQSVLSSWVSGDINLSKPMPLLGFAQVRPHPK
HQYTKPLFMLIDEDDFSCGDLAPAILKDNGRATLIGKPTAGAGGFVFQVTFPNRSGIKGL
SLTGSLAVRKDGEFIENLGVAPHIDLGFTSRDLQTSRFTDYVEAVKTIVLTSLSENAKKS
EEQTSPQETPEVIRVSYPTTTSAS

CPn_1017   1168997   1169935
lytB-Metalloprotease
VIIMRKLILCNPRGFCSGVVRAIQVVEVALEKHGAPIYVKHEIVHNRHVVNALRAKGAIF
VEELVDVPEGERVIYSAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAAKLYASKGYKI
ILIGHKKHVEVIGIVGEVPEHITVVEKVADVGLIPIHDGAASVPLFSSDTPLFYITQTTLSLDDVQEISS
ALLKRYPSIITLPSSSICYATTNRQKALRSVLSRVNYVYVVGDVNSSNSNRLREVALRRG
VPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQACIRKLSSLIPGLQVENDIFAVE
DVVFQLPKELRCS

CPn_1018   1169895   1170629
No robust homolog present in Genebank/EMBL as of 11/7/98
RMSYFNYQKNSVVLRSLCLLAKFFSRLLYRVFFSFREGIYLFSSLYLKYFFYDLGKY
VYSLRHCPYAKLGRLPGASLLKEGNVYGETPWSVLAKICQAFDITSQDILYDLGCGLGKV
CFWFSHVVRCQVIGIDNOPHFIRFSSNMHRKLSSGFALFDTEEFKNVVLSQASYVYFYGS
SFSRRLLNEIILKLSEMAPGSVVISISFPLDSFSRGKECFFTEKSCSVRFPWGKTIAYKN
IRKGS

CPn_1019   1172146   1170638
CT860 hypothetical protein
IHPPNIHTVSYOCISTPPPEGEFDIFVDGNATEEAV/AAEVQVALPAGEQYAMLRATSEL
CFGILTQGECALTUALPPKEKPLQEEQFLVKNGILMPSTSLPNLKPGGSQQTSLASHRNP
LAQQCTHVRSY:CCTIKEDGAKEKVGOSTKSAETOKHTVTKCDATLIPMSLYCTLHKEVPQ
AL:CTKCXQKDREHRDCRQOEOYEQOEOQCEEYKKKTPWCTVECLCQTSECNQVYESYTPI
IPOPIVFFALCIE:QLCVLAGKRVTHLDVLRICTELMYLMLKCRANDTMTRLEERELMERE
AHEIAA:CYCIRQAKYARWLCIATATLGILCAIAGMVGEIGGDCIIJFVQRIGGPFKDATAK
TFFFKCIGKVFTCLCIGLCTEAACKVHFLSE:AVRAVAEYRKEVFPMHQDEVTRTIEEVKDNW
KOMLRIFLJNIUJTEHLAAIOGLCQ

CPn_1020   1172664   1172150
CT861 hypothetical protein
CFNCTMCCWCQAJVEVLJKQDPYDPADRCQER:VTPIGYC CTVAIQFAQKGLPKFFTQK
FQCICCDDPITHHKTFLIATPRERILRFCCEPPYICFFTCGWGVWLLQIFFLINTCQKNSTEA
CKALMGHLCTHFK:CPEKTCERKALDKNLCCKQFTCACKHFTCFIJUJMJHLKLFCKTVGSLYCQGSL

DSEQQELLCSRREERSETYA   JEKKIETKVGIKDLCKCLFGGDCDSNCFQKKSPFCC
DTSRKNRIAKAAQAVPVIPPPS.GVFTLSYLLTKQCILSDFSSYGCHKDSVESTQRELDA
LHEXRIETIKVSIEKEKREILWGSLSDSICWLABEVSTGIGIVSIUCCQCBFXBACBFAG
LISLVIKCLEXLIKFWDWLEKHLPIKNEELRRKIITIIQWVVYLTPVTLSICTLRVENLGF
SPIIEGAIKGIQPAIESTHAALRCAILFSOAEIYKLKGKLTKIQLDIELKSFDRDDHYER
SQELLDNMESSFEALSRILNYHRELDQVYLHSLRG

CPn_1021   1174270   1173698
CT851 hypothetical protein
T'KCL.W... . . . . : .'.''..
TYCKIFKISSEDLEKVYKEGVHAYLDKDVAKJITVFKWLVFFNPFVSKFWFSLGASLHHS
EQYSQALHAYGVTAVLRDKDPYPHYYAYICYTLTNEHEEAEKALEHAWVRAQHKPLYNEL
KEEILDIRKHK

CPn_1022   1175709   1174216
CT863 hypothetical protein
FSFFFYALKLQIMNMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSS
STDALISLALGQIILATQQELLLQSTNVHOLLFLPPEVVELEZQVVDLLUKLEHAETITS
EPQETQTOSRSEQTLPQQSSSKQSALSPRSLKPEISDSKQQQALQTPKDSAVRKHSEAPS
PETQARASLSQASSSSCRSLPPQESAPERTLLEQQKASSFSPLSQFSAEKQKEALTTSKS
HELYKERDQDRQQREQHDRKHDQEEDAESKKKKKKRGLGVEAVAEEPGENLDIAALIFSD
QMRPPAEETSKKETTFKKKLPSPMSVFSRFIPSKNPLSVGSSIHGPIQTPKVENVFLRFH
KLMARILGQAEAEANELYHRVKQRTDDVDTLTVLISKINNEKKDIDWSENEEHXALLNRA
KEIGVTIDKEKYTWTEEEKRLLKENVQMRKENMEKITQMERTDMQRHLQEISQCHQARSN
VLKLLKELMDTFIYNLRP

CPn_1023   1176008   1176331
No robust homolog present in Genebank/EMBL as of 11/7/98
GLDFLEIFIMKKVVTLSIIFFATYCASELSAVTVVAVPLSEAPGKIQVRPVVGLQFQEEQ
GSVPYSFYYPYDYGYYYPETYGYTKNTGQESRECYTRFEDGTIFYECD

CPn_1024   1177317   1176334
xerD-Integrase/recombinase
IFFFPWFSLCSLKIAPLPILKLHSLASHTMPSTOFHTTILEQFSLFLSVDRGLCQQSIAA
YRQDISSFLTISAISSPODISQNSVYIFAEELYRRKEAETTLARRLIALKVFFLFLKDQQ
LLPYPPIIEHPKIWKRLPSVLTPQEVDALLAVPLQMEKNPRHLAFRDTAILHTLYSTGVR
VSELCDLRLGHVSDDCIRVTGKGSKTRLVPLGSRAREAIDAYLCPFRDQYOKKNPHEDHL
FLSTRGHKLERSCVWRRIHNYAKOVTSKPVSPHSLRHAFATHLLDNKADLRVIQEMLGHA
RIASTEVYTHVAADSLIEKFLAHHPRNL

CPn_1025   1177266   1178879
pgi-Glucose-6-P Isomerase
GAEQFSSYREKTMERKRFIDCDSTKILQELALNPLDLTAPGVLSAERIKKFSLLGGGFTF
SFATERLDDAILAALISLAEERGLHESHLAMQQGQVVNYIEGFPSEMRPALHTARAMVT
DSSFTGEAEDIAVRSRVEAQRLKDFLTKVRSQFTTIVQIGIGGSELGPKALYRALRAYCP
TDKHVHFISNIDPDNGAEVLDTIDCAKALVVVVSKSGTTIETAVNEAFFADYFAKKGLSF
KDHFIAVTCEGSPMDDTGKYLEVFHLWESIGGRFSSTSMVGGVVLGFAYGFEVFLQLLQG
ASAMDQIALQPNARENLPHLSALISTWNRRNFLGYPTEAVIPYSSGLEFFPAHLQQCCHES
NGKSIAQDGRRVGFSTSPVIWGEPGTNGOHLSFPFQCLHQGTDIIPVEFIGFEKSQKGEDIS
FQGTTSSQRLFANHIAQAIALACGSENTNPNKNFDGNRPSSVLVSSQLNPYSLGELLSYY
ENKIVFQGLCWGINSFDQEGVSLGKALANRVLELLEGADASNFPEAASLLTLFNIKFR

CPn_1026   1178961   1179137
ltuA
CSFGFGKICEDRMFFIAVRSRGFLDIHGILAARKGKQVVKSTAGAWIGSRGAVPYSLVS

CPn_1027   1179172   1180755
No robust homolog present in Genebank/EMBL as of 11/7/98
NMFGSVSSPPLSPVIVRERVPSSSGSDLIQPHAVLKISILIFALVTILGIVLVVVLSSALG
ALPSLVLTVSGCIAIAVGLIGLGILVTRLILSTIRKVDAHGYDAAVKEEQYLSRIRELES
ENREIRDRNRAVEDQCAHLSEENKDLRDPEYLHGMTERLIASLEIENQALVAENILLKDW
NASLSRDFRAYKQKFPLGALEPWKEDIACIHEQNLFLKPECIAMVKSLPLETQRLFLYPK
GFQSLVNRFAPRSRFFQTPKYEYNSRNENEDGKVAAVCARLKKEFFSAVLGACSYEELGG
ICERAVALKETLPLPEAVYDTLVQEFPNLLTAESLWKEWCFYSYPVLRPYLSVDYCKRLF
VQLFEELCLKLFTTGSPEDQALVRLFSYYRNHIPAVLASFGLPPPETGGSVFVLLPKQEN
LLWSQIEVLATRYLKDTFVRNSEWTGSFEMMPSYNEMCKEISEGRIRFAEDYETRHSEEF
PPSPLSEEGEGCEEFLPPCSEEEVSVLERPDLDVDSMWVWHPPVPKGPL

CPn_1028   1180995   1181999
mdhC-Malate Dehyrogenase
FFLKGVRHAFKEVVRVAVTGGKGQIAYNFLFALAHGDVFGVDRGVDLRIYDVPGTERALS
GVRMELDDGAYPLLHRLRVTTSLNDAFDGIDAAFLIGAVPRGPMERGDLLKGNGQGIFSL
QGAALNTAAKRDAKIFVVGNPVNTNCWIAMKHAPRLHRKNFHAMLRLDQNRMHSMLAHRA
EVPLEEVSRVVIWGNHSAKOVPDFTQARISGKPAAEVIGDRDWLENILVHSVQNRGSAVI
EARGKSSAASASRALAEAARSIFCPKSDEWFSSGVCSDHNPYGIPEDLIFGFPCRMLPSG
DYEIIPGLPWEPFIRNKIQISLDEIAQEKASVSSL

CPn_1029   1181987   1182844
No robust homolog present in Genebank/EMBL as of 11/7/98
RVFVISTMLWGVSMRQSFDELSQNAFKNIFNKQRFCFIFCSLCCFGVFALFLKLCSRLA
PEISLSTLGLGAFFCAFSVICASAIIVQFLLHKESQGETSKLCCAIKNTWSSLWLSLLVS
MPFFIAMVAVVTVAMLSSFLGSLPWVGKLFHTVLIFIPYLSATALILLFLGSFSCLFFCI
PVLHNQESIDYRKLLECFRGNILRQFIGVVIALVPLALCSWLALDSFYLMTHLVEIADIH
TWSFLAQMFVLIVPIALILTPAVSFFNFSFSFYLAKQEEEKALVK

CPn_1030   1183901   1182843
predicted D-amino acid dehyrogenase
FKVHFMRIAVLGAGYAGLSVTWHLLLHSQQTATIDLFDPIPLGEGASCMSSCLLHAFTCK
KALKPPLADQCINATHALITEACKALNVPIVISCGILRPAIDEDQAQLFTERVEEFPKEV
EWWEKARGCESIPDMVIPPNLGALFIKCVVTLRIGLYICGLADAMHKUTCQFYDELIEDL
ADIEEFYDHIIVTCIANACILPELKDMPVNKVVYQLLEICWPKDLAHLCIFSINAHKYMVA
NFQKNTCIIIAATFEHNOPEETPDPAIAYQEIMPPVLCILFGLKDAQVUICVACMRGSSKC
HLPVICPIREKIWFIAXILCCKLLYGITYDMLAQAVLRICTAYIAKEFLFTI

CPn_1031   1185567   1184098
arcD-Acetinitine:ornithine Antiporter
IKETFMTCRTKCCSKNIJTIAIAFMVVCCIICYIFCSLFQFMAATACACAVILCWILTCFC
MFFIAHTFRILCTIRPDLKFIIFYMYCRFCFCIFCFTCCWGVWLLQIFFILNVCYAVCITHDA
LNYFFPFYFQLINTLPAILLCCLINVFIIFIVLFCIRQACLINVICTIFKIIELIIFCIL
TAFFFKLAVFKTDFWCIIAVTKAQPCLUCCCGLFYTFMLVTLWAFCIICIGIAVVMCYIRAKNP
LCVKJATFLCFLCXLCFIYILFCLLLFFCIGLIGJLAHTIHIPCTAIVLDILVAKWCEVLMNV

ILIIAVLIIWLIWTIIVAEIPFSAAKNGTFPEIF   .EKSPSVSLYITSSVMQLAMLL
VYFIONAWITMLSITGVMVLPAYLASAAFLFKLSKII CYPKKGSIKAPLAMITGILGVVY
ILWLIYAGGLKYLFMALVLLALGIPFYIDAGKKKKNAKTFFAKKEIVGMTFIGLLALTAI
FLFLTGRIKI

CPn_1032   1186153   1185566
CT371 hypothetical protein

LMAYCTPYCTLAFIGCGIGECDDIMPPQPFETFCYDGALLQAKIENFNTVPYTSVLPKEL
ALGFLNFENAEPAKVN

CPn_1033   1187656   1186187
CT372 hypothetical protein

MNKKKDYSGEFLTTDTVDSIAFLPSEENFCYIKTILFFRVKKKHYAFFYGEFMISFRFLL
LSGLCALGISSYAETPKETTGHYHRYKARIQKKHPESIKESAPSETPHHNSLLSPVTNIF
CSHPWKDGISVSNLLTSVEKATNTQISLDFSILPQWFYPHKALGQTQALEIPSWQFYFSP
STTWTLYDSPTAGQGIVDFSYTLIHYWQTNGVDANQAAGTASSMNDYSNRENNLAQLTFS
QTFPGDFLTLAIGQYSLYAIDGTLYDNDQYSGFISYALSQNASATYSLGSTGAYLQFTPN
SEIKVQLGFQDSYNIDGTNFSIYNLTKSKYNFYGYASWTPKPSCGDGQYSVLLYSTRKVP
EQNSQVTGWSLNAAQHIHEKLYLFGRINGATGTALPINRSYVLGLVSENPLNRHSQDLLG
IGFATNKVNAKAISNVNKLRRYESVMEAFATIGFGPYISLTPDFQLYIHPALRPERRTSQ
VYGLRANLSL

CPn_1034   1188589   1187732
Predicted OMP (CT371) (leader (18) peptide)

KTSWQKYKKYLSYSILVQKIARYVMKTWLFFTFLFSCSSFYASCRYAEVRSIHEVAGDIL
YDEENFWLILDLDDTLLQGGEALSHSIWKSKAIQGLQKQGTPEQEAWEAVVPFWIEIQEM
GTVQPIESAIFLLIEKIQKQGKTTFVYTERPKTAKDLTLKQLHMLNVSLEDTAPQPQAPL
PKNLLYTSGILFSGDYHKGPGLDLFLEICTPLPAKIIYIDNQKENVLRIGDLCQKYGIAY
FGITYKAQELHPPIYFDNIAQVQYNYSKKLLSNEAAALLLRHQMHE

CPn_1035   1190081   1188570
aroE-Shikimate 5-Dehyrogenase

VVQLPLMVPIVHLQIWRFSMIYYGVSVMLCATVSGPSFCEAKQQILKSLHLVDIIELRLD
LINELDDQELHTLITTAQNPILTFRQHKEMSTALWIQKLYSLAKLEPKWMDIDVSLPKTA
LQTIRKSHPKIKLILSYHTDKNEDLDAIYNEMLATPAEIYKIVLSPENSSEALNYIKKAR
LLPKPSTVLCMGTHGLPSRVLSPLISNAMNYAAGISAPQVAPGQPKLEELLSYNYSKLSE
KSHIYGLIGDPVDRSISHLSHNFLLSKLSLNATYIKFPVTIGEVVTFFSAIRDLPFSGLS
VTMPLKTAIFDHVDALDASAQLCESINTLVFRNQKILGYNTDGEGVAKLLKQKNISVNNK
HIAIVGAGGAAKAIAATLAMQGANLHIFNRTLSSAAALATCCKGKAYPLGSLENFKTIDI
IINCLPPEVTFPWRFPPIVMDINTKPHPSPYLERAQKHGSLIIHGYEMFIEQALLQFALW
FPDFLTPESCDSFRNYVKNFMAKV

CPn_1036   1191180   1189984
aroB-Dehyroquinate Synthase

GYDKPCSCRSCIIPTMLQTHMSETIITTPHVVKLISNFFQKKLFSSISTAYPLVIITDVS
VQQHLLGPILDHIKMLGYQVIVLTFPPGEPNKTWETFISLQYQLVDQNISPKSSIIGIGG
GTVLDMTGFLAATYCRGLPLYLIPTTITAMVDTSIGGKNGINLRGIKNRLGTFYLPKEVW
MCPQFLSTLPREEWYHGIAEAIKHGFIADAYLWEFLNSHSKMLFSSSQILHEFIKRNCQI
KAAIVAEDPYDRSLRKILNFGHSIAHAIETLAKGTVMHGQAVSVGMHIETRISLAEGVMK
TPQLIDQLERLLKRFNLPSTLKDLQSIVPEHLHNSLYSPENIIYTLGYDKKNLSQHELKM
IMIEHLGRAAPFNGTYCASPNMEILYDILWSECHVMRHC

CPn_1037   1192286   1191123
aroC-Chorismate Synthase

LHFSRGSRRSFLEELLRTSVSRSHYLVKVMKNSFGSLFSFTTWGESHGPSIGVVIDGCPA
GLELHESDFVPAMKRRRPGNPGTSSRKENDIVQILSGVYKGKTTGTPLSLQILNTDVDSS
PYENSERLYRPGHSQYTYEKKFGIVDTNKGGGRSSARETACRVAAGVVAEKFLANQNIFTL
AYLSSLGSLTLPHYLKISPELIHKIHTSPFYSPLPNEKIQEILTSLHDDSDSLGGVISFI
TSPIHDFLGEPLFGKVHALLASALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENI
TLKSNNCGGTLGGITIGVPIEGRIAFKPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCV
AIRAVPVVEAMINLVLADLVLYQRCSKL

CPn_1038   1192750   1192199
aroL-Shikimate Kinase II

WKLELRNVMTIILCGLPTSGKSSLGKALAKFLNLPFYDLDDLIVSNYSSALYSSSAEIYK
AYGDQKFSECEARILETLPPEDALISLGGGTLMYEASYRAIQTRGALVFLSVELPLIYER
LEKRGLPERLKEAMKTKPLSEILTERIDRMKEIADYIFPVDHVDHSSKSSLEQASQDLIT
LLKS

CPn_1039   1194011   1192665
aroA-Phosphoshikimate Vinyltransferase

VCFTMLTYKVSPSSVYGNAFIPSSKSHTLRAILWASVAEGKSIIYNYLDSPDTEAMICAC
KQMGASIKKFPQILEIVGNPLAIFPKYTLIDAGNSGIVLRFMTALACVFSKEITVTGSSQ
LQRRPMAPLLQALRNFGASFHFSSDKSVLPFTMSGPLRSAYSDVEGSDSQFASALAVACS
LAEGPCSFTIEPKERPWFDLSLWWLEKLHLPYSCSDTTYSFPGSSHPQGFSYHVPSSFS
SAAFIAAAALLSKGLQPIRLRNLDILDIOGDKIFFSLHQNLGASIQYDNEEILVFPSSFS
GTSIDMDGCIDALPILTVLCCFADSPSHLVNARSAKDKESDRILAITEELQKMGACIQPT
HDGLLVNPSPLYGAVLDSHDDHRIAMALTIAALYASGDSRIHNTACVRKTFPNFVQTLNI
MEARIEECHDNYSMWSTHKRKVFARESFG

CPn_1040   1194876   1194073
No robust homolog present in Genebank/EMBL as of 11/7/98

RPSGSLFLRTWSPSSSFREHTVCAAPLLYPRRRSPDYLFSPTGCPMSTTTVKHFIHTASR
WFPVLKEIVASNYWHAQWINTLSFLENSGAKKISASEHPTEVKEEVLKHAAEEFRHGHYL
KTQIGRIGETSLPDYTSKNLLGGLLTKYYLHLLDLRTCRVLENEYSLSGQTLKTAAYILV
TYAIELRAGELYPLYHDILKEAQSKITVKSIILEEQGHLQEMERELKDLPHGEELLGYAC
QFEGELGLQFVERLEQMIFDPSSTFTKF

CPn_1041   1196304   1194726
*bioA-Adenosylmethionine-8-Amino-7-Oxononanoate
Amino transferase

LFRRIFIILBIKPTSAIGVFFLVMFLDFSEPSISRKYGGILFNGRGNALTKPQYLRYGGK
WVSROPLALANGRNQAGYMDDSCQGKPNHKDNHKLLCPTMEGGMQKQGSGMQGCIWHPFT
QGALDGTPIRIVIGDSAYLTAEGGTRYLDAIGSWAGNLGIGHGHPYITKKLCEQAQKLEHV
IFANFTHEGALGLVGGIKGAPLLFEGLEREFFFSDNGGTGIIEIAMKGIAVQYYYHGNKAKSHFV
GGNAYGDGPFGAMGIAGTGCIPVPFHDLFLPGSGTGIAAPYWGKEELAIAQAKTVFSESNI
AAFIYEPLIASGVVSMIMYNPEGLKELLKLAKHYGVLAIADEILTVGRGRTGPLFASEFTDI
IYDIICLSGLGYILLALTVTTKEGIIDAFVGQDKHMFALLLFGITFFTVNPLGGSAALASL
GGTLGGHIGGASYLMIERGTGJEFQFAIIGGLWQRCEVIGITVILALDYGAEANGYFSGYRDHLN

CPn_1042   1198628   1196514
*bioD-dethiobiotin synthetase

NRSPFTYFRANFFMQRIIIVGIDTGVGKTIVSAILARALNAEYWKPIQAGNLENSDSNIV
HELSGAYCHPEAYRLHKPLSPHKAAQIDNVSIEESHICAPKTTSNLIIETSGGFLSPCTS
KRLQGDVFSSWSCSWILVSQAYLGSINHTCLTVEAMRSRNLNILGMVVNGYPEDEEHWLT
QEIKLPIIGTLAKEKEITKTIISCYAEQWKEVWTSNHQGIQTVSGTPSLNLH

CPn_1043   1198777   1198672
bioF_2-Oxononanoate Synthase_2

PMLCQQFLIEALARRKSKHTYRSLSLNSHLIDFTSNDYLGFASSPELRKEYITKLHAIES
LGATGSRLLTGHSQLCQRIEEQLAAYHNFESCLIFNTGYTANLGLLYALATDQDRILHDL
YIHASIYDGIRLSKAQSFPFNHNDLNHLEKRLASSHLGRTFVCVESVYSLHGSVAPLQAI
SELCERYSAYLIVDEAHAVGVFGDQGEGLVSALGLQDKVLATVYTFGKALGTHGAAIAGS
SILKDYLINFCRPFIYTTAQPPHALTAIELAYEHNQRAFNQREHLSALIHHFREKAQNLG
LQLMKDNTTTPIQSICVGSGSHRARQAALQIQNSGYDVRPIVSPTVKQREELLRICLHAFN
TKNEIDHLLHTLEQIFLCNVSSL

CPn_1044   1198700   1197699
*bioB-Biotin Synthase

AKHMREETVSWSLEDIREIYHTPVFELIHKANAILRSNFLHSELQTCYLISIKTGGCVED
CAYCAQSSRYHTHVTPEPMMKIVDVVERAKRAVELGATRVCLGAAWRNAKDDRYFDRVLA
HVKSITDLGAEVCCALGMLSEEQAKKLYDAGLYAYHHNLDSSPEFYETIITTRSYEDRLN
TLDVVNKSGISTCCGGIVGMGESEEDRIKLLHVLATRDHIPESVPVNLLWPIDGTPLQDQ
PPISFWEVLRTIATARVVFPRSMVRLAAGRAFLTVEQQTLCFLAGANSIFYGDKLLTVEN
NDIDEDAEMIKLLGLIPRPSFGIERGNPCYANNS

CPn_1045   1199602   1198901
*conserved hypothetical bacterial membrane protein

GTLPMNTSHRKTLVFSYLSSTFTLLLVLSNLVLSSKLIPTTFFNFIIPGGLILYPLTFLI
SDVVNEIFGPKKARVHIFSAFIANLLASSIVQIFMFFPVASPEMQTAWHCLFDLSPLRFL
ASLLAFIVSQQLDIVLYTFFKNRTPNSSLWLRSNGSTWISQIPDTFIVDTCILYFGMGLS
FPQTLNIMFYSYIYKITFCVLTTPLFYLAVNTIRKFLGMPSTKIANTVPLINQP

CPn_1046   1200675   1199590
*Tryptophan Hyroxylase

VHYCERTLDPKYILKIALKLRQSLSLSFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALA
RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKS
YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI
ASVMRTLDKINFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKNQ
RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL
DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL
CQ

CPn_1047   1200537   1201343
dapB-Dihydrodipicolinate Reductase

FGSRNMGSSMHVGVIGCSGRTGKVIVSALEQSSEYTLGPGFSRSSALTLFQVIAHNDVLV
DFSHPLLTKEVVAHLLISPKPLIIGTTGFPGKCKEAHDSLEELTHIVPVVVCPNASLGAY
IHKRLVMLLSQLCNPQFDIRIRETHHRYKKDSLSGTAQDLLDTIQQVKQEDWGEEYEVGQ
RDSSKKTIEVQSSRVGDIPGEHEVAFISSGEQILVRHTVFSRNVFGRGILSILDWLKTLN
PQPGLYSLGDTLELVLRNEHCLLKKTTDH

CPn_1048   1201588   1202604
asd-Aspartate Dehydrogenase

DGERKGMRIAVLGVTGLVGQKFVALLHKWYRDWVIAEVVASNSKYGQSYGDACIWQEPIG
PMPEMVRDLPIRKIEEVQSDIVVSFLPSSAESMEAYCLSQGKVVFSNASTYRMHSSVPII
IPEVNSDHFQLLEEQPYFGKIITSPNCCVSGITLALAPLRKFSLDHVHIVTLQSASGAGY
PGVPSLDLLANTVPHIVGEEEXILRETVKILGSSKQPLPCKLSVTVHRVPVAYGHTLSLH
VTFSKDVDLDEILYSYQEKNKEFPNTYQLYDNPWSPQARKHLSHDDMRVHLGPITYGGDF
RTIKMNVLIHNLVRGAAGTLLASMENYFFDYLKREMCLR

CPn_1049   1202586   1203914
lysC-Aspartokinase III

EGNVSKIVYKFGGTSLATAENICLVCDIICKDKPSFVVVSAIAGVTDLLVDFCSSSLRER
EEVLRKIEGKHEEIVKNLAIPFPVSTWTSRLLPYLQHLEISDLDFARILSLGEDISASLV
RAVCSTRGWDLGFLEARSVILTDDSYRRASPNLDLMKAHWHQLELNQPSYIIQGFIGSNG
LGETVLLGRGGSDYSATLIAELARATEVRIYTDVNGIYTMDPKVISDAQRIPELSFEEMQ
NLASFGAKVLYPPMLFPCMRAGIPIFVTSTFDPEKGGTWVYAVDKSVSYEPRIKALSLSQ
YQSFCSVDYTVLGCGGLEEILGILESHGIDPELMIAQNNVQFVMDDDIISQEAQEHLVD
VLSLSSVTRLHHSVALITMIGDNLSSPKVVSTITEKLRGFQGPVFCFCQSSMALSFVVAS
ELAEGIIEELHNDYVKQKAIVAT

CPn_1050   1203884   1204798
dapA-Dihydrodipicolinate Synthase

LCKTKSYSRHVGRIMHLLTATVTPFFPNGTIDFASLERLLSFQDAVGNGVVLLGSTGEGL
SLTKKEKQALICFACDLQLKVPLFVGTSGTLLEEVLDWIHFCNDLPISGFLMTTPIYTKP
KLCGQILWFEAVLNAAKHPAILYNIPSRAATPLYLDTVKALAHHPOFLGIKDSGGSVEEF
QSYKSIAPHIQLYCGDDVFWSEMAACGAHGLISVLSNAWPEEAREYVLNPQEQDYRSLWM
ETCRWVYTTTNPIGIKAILAYKKAITHAQLRLPLSIEDFDLENVSPAVESMLAWPKLRTS
VFSYS

CPn_1051   1204956   1205270
No robust homolog present in Genebank/EMBL as of 11/7/98

FFMTPKSIQQLHLIKTIDPVRKISPVTTYKSSFFROSLLRFLELFWMFLYCIRSIRFHCV
HIATFICRGLILFLTTLFLSMICILHFITLPWICKEDPRIIRKNK

CPn_1052   1205402   1206169
No robust homolog present in Genebank/EMBL as of 11/7/98

FFIQKMKYNSREKIKSALRICSGYGITVFRNNFSLSCYDKIFYGLSCYVFNKIPNSIGRCR
SFCFFRSKKTEVETKEVKIKDEIRPSLEFGNDFVKVAEGFPFRKAALESLGSGRSIGNLCA
ISNFLDSGMLSRNFSKEIWNNTIFTRSKNTNDAEFSGEPFRYTAGNYLNILRSKLAGSYEL
GVTAGLLGGRLKDVGDGIRTRATGGGILCGVIKSGMVTRPLGGTYYIVNKARPLLFFFRLTSD
VRRDLKKKFRLEFCKD

CPn_1053   1206438   1206701
No robust homolog present in Genebank/EMBL as of 11/7/98

KKGSDLIIFAKIDHHNLYLTFLSGLIVASFILSTISLGINYGEFAGHIEVLVYGKFICIGGEP
SRLATSGNDTYYGIVSLSGIRYEFFCGSGGIDFNIDMHVAPKIGAVLSRTRFEAKEIPG
GGKDYAFFGLTARESLMIGEKLAMTFGVGEVIQKKYGQGTPYYPKTNLKFQYRHLGNNGF
ELGVKGAF

CPn_1054   1207010   1209466
No robust homolog present in Genebank/EMBL as of 11/7/98
SRWIHRFIMQVLLSPQLPPPPQHSVGSISSPSKLRVLAITFLVFGMLLLISCALFLTLGI
FGLSAAISFGLGIGLSALGGVLMISCLLCLLVKREIPTVRPEEIPEGVSLAPSEEPALQA
AQKTLAQLPKELDOLDTDIQEVFACLRKLKDSKYESRSFLNDAKKELRVFDFVVEDTLSE
IFELRQIVAQEGWDLNFLINGGRSLMMTAESESLDLFHVSKRLGYLPSGDVRGEGLKKSA
KEDVAPLHGLHCEIHKVAVAFDRNIYAMAEKAFAKALGALEESVYRSLTQSYRDKFLESE
YVRDWYDQEFQKAGERLEKLHALYPEVSVSIRENKIQETRSNLEKAYEAIEENYRCCVRE
QEDYWKEEEKREAEFRERGNKILSPEELESSLEQFDHGLKNFSEKLMELEGHILKLQKEA
TAEVENKILSDAESRLEIVFEDVKEMPCRIEEIEKTLRMAELPLLPTKKAFEKACSQYNS
CAEHLEKVKPYCKESLAYVTSKERLVSLDEDLRRAYTECQKRFQGDSGLESEVRACREQL
RERIQEFETQCLDLVEKELLCVSSRLRNTECDCVSGVKKEAPPGKKFYAQYYDEIYRVRV
QGRWMTMSERLREGVQACNKMLKAGLSEEDKVLKEEEYWLYREERKNKEKRLVGTKIVAT
QQRVAAFESIEVPEIPEAPEEKPSLLDKARSLFTREDHT

CPn_1055   1209583   1210521
No robust homolog present in EMBL as of 11/7/98
CKYLYHHSYPPPPDHSVGAFFCLSKFRVLAITFLVLGVLFLISGALFLTLGISGLSAAIS
FGLGIGLSALGGVLVVSGLLCLLAKREVPTVRPEEIPEGVSVAPSEEPALQATQRTLAQL
PKELDQLDRYIQEVVSCLGKLKDLRCEDOGLLKDAKEKLQVFDFVWKDMMTEFVELQQIM
DQEGWYLKCLIQEMRDIGSTLFMSQVSLFKLWEWLGYLPSGDVRGERLKKSAREVVDRFH
RRICDTRKVAMTFDRNAYGVAKTAFEKAFGALETCVYKSMTESYREAFCEYKKTKILRDE
EXILRICYLELRR

CPn_1056   1210482   1211228
No robust homolog present in Genebank/EMBL as of 11/7/98
GEDIKDMLSRVEEIEMMLRVIELPLLPIKQALEKAFVQYNSYKAKLTKVEPCFRESPAYI
TSEERLQSLDQTLERAYKEYQKRFQEPSRLESEVSGCREHLRAQVKQFETQGLDLIKEEL
IFVSDVLFRKMVSCLVSTVHVPFMEFYYEYFELHRLRLRAQWMANAEIYSKVRKAFPEML
KETLEKAKAPREEEYWLLCEERKSKEKRLILNKIEAAQQRVKDLEPPPIKETGKQKRKKE
YSFFIRLKS

CPn_1057   1211467   1213596
CT356 hypothetical protein
IIHFYFFNFAMPEPLYTNKLITEKSPYLLLYAHTPVNWYPWGAEAFHIAAIENKPVFLSI
GCKHSRWCQVMLQESYTNPEIAAMLNEYFVNVKVDKEELPYVAKLYGDLAQMLAVSGDHQ
ETVSWPLNVFLTPDLVPFFSVNYLGNEGKLGLPSFPQIIDKLHFMWEDAEEREALVEQAM
KVLEIASFLEGCVRKEILDESSLKRTVAALYQDIDPHYGGVKAFPKRLPGLLLQFFLRYS
LEYQESRGLFFVDRSLSMVALGCVRDHIGGGVYSYTIDDKWLIPAFEKRLIDNALMALNY
LEAWACLGKEEYRGIGKQILSYILSELYSPEVGAFYSSEQAENMGAGGQNFYTWSVEEIS
NALGEDAEIFCDYYGISREGFFNGRNILHIPVHREIEELSEKYHRSIEAIEDIVDRSRDI
LKGIRAQRSHRSKDDLSLTFNNGMMIYTFAYAGRLLGEVEYIEIGKKCGEFVRNSLYKHH
ELYRRWREGEAKYRASLEDYGALILGVLALYESGCGSFWLSRAEELMQEVVLSFRSEDGG
FYSVDGRDSTLLIKDSPLSDGETISGNALICQCLLSLHLITEKKHYLTYAEDILQIAQAC
AHTHKFSSLGLLIASQNYFSRKHVKVLIALGCDQEDRSPVLKCLSGLFLPYLSLIWMTQEN
QEHLETVLPEYEHCLIPKGDCTATTIYVLEVDQCKRFKDLELFRRYLISL

CPn_1058   1213742   1214836
CT355 hypothetical protein
EVMKLYQTLRGIVLVSTGCIFLGMHGGYAAEVPVTSSGYENLLESKEQDPSGLAIHDRIL
FKVDEENVVTALDVIHKLNLLFYNSYPHLIDSFPARSQYYTAMHPVVLESVIDEFLNVAD
AKAKRIATDPTAVNQEIEEMFGRDLSPLYAHFEMSPNDIFNVIDRTLTAQRVMGMMVRSK
VMLKVTPGKIREYYRKLEEEASRKVIWKYRVLTIKANTESLASQIADKVRARLNEAKTWD
KDRLTALVISQGGQLVCSEEFSRENSELSQSHKOELDLIGYPKELCGLPKAHKSGYKLYM
LLDKTSGSIEPLDVMESKIKQHLFALEAESVEKQYKDRLRKRYGYDASHIAKLLSEEAPP
LFSLL

CPn_1059   1214848   1215678
kgsA-Dimethyladenosine Transferase
VTRSSPAQLSRFLSEIQNKPKKSLSQNFLVDQNIVKKIVATSEVIPQDWVLEIGPGFGAL
TEELIAAGAQVIAIEKDPMFAPSLEELPIRLEIIDACKYPLDQLQEYKTLGKGRVVANLP
YHITTPLLTKLFLEAPDFWKTVTVMVQDEVARRIVAQPGGRDYGSLTIFLQFFADIHYAF
KVSASCFYPKPQVQSAVIHMKVKETLPLSDEEIPVFFTLTRTAFQQRRKVLANTLKGLYP
KEQVEQALKELGLLLNVRPEVLSLNDYLALFHKMQAG

CPn_1060   1217694   1215727
dxs/tkt-Transketolase
YKRPLVIHITKVMTSSSCPLLDLILSPADLKKLSISQLPGLAEEIRYRIISVLSQTGGHL
SSNLGIVELTIALHYVFSSPKDKFIFDVGHQTYPHLLTGRNNEGFDHIRNDNGLSGFTN
PTESDHDLFFSGHAGTALSLALGMAQTTPLESRTHVIPILGDAAFSCGLTLEALNNISTD
LSKFVVILNDNMSISKNVGAMSRIFSRWLHHPATNKLTKQVEKWLAKIPRYGDSLAKHS
RRLSQCVKNLFCPTPLFEQFGLAYVGPIDGHNVKKLIPILQSVRNLPFPILVHVCTTKGK
GLDQAQNPAKYHGVRANFNKRESAKHLPAIKPKPSFPDIFGQTLCELGEVSSRLHVVTP
AMSIGSRLEGFKQKFPERFFDVGIAEGHAVTFSAGIAKAGNPVICSIYSTFLHRALDNVF
HDVCMQDLPVIFAIDRAGLAYGDGRSHHGIYDMSFLRAMPQMIICQPRSQVVFQQLLYSS
LHWSSPGAIRYPNIPAPHGDPLTGDPNFLRSPGNAETLSQGEDVLIIALGTLCFTALSIK
HQLLAYGISATVVDPIFIKPFDNDLFSLLLMSHSKVITIEEHSIRGGLASEFNNFVATFN
FKVDILNFAIPDTFLSHGSKEALTKSIGLDESSMTNRILTHFNFRSKKQTVGDVRV

CPn_1061   1217932   1217666
CT330 hypothetical protein
FGSLMVEIHHKDPSLKKLFALQQSLETLNSLSDIVATYEAMFSLIYEGLNKALRKDQLCY
LLSVNSKGELLKSPSGDPIVQTFPIHPHH

CPn_1062   1219835   1219159
xseA-Exodeoxyribonuclease VII
RGFPVHUGPPQAVASLTERIKTLLESNFCOIIVKGELSNVSLQPPGHLYFGIKDSQAFLN
NAEFHIFKKYYDRKPKDGDAVIIHGKLAVYAPRCQYQIVANIALVYAGEGDLLQKFEETKR
RLTAEGYFATEKKKDLPFAPQCIGVITSPTGAVIQDILRVLGRRARMYKILVFPVTVQGN
SAAHEDGKALEVHMAENLADVLIIARGCGSIEDLWAFNEEILVKAIHASTIPIVSAVGHE
TDYTLTDFANUVRAPTPSAAAEIVCKSGEEQVQVFEGYLRHLLSHGROLLTSKKQQLLPW
HRFLDRAEFYTTAQQXLDSIIETAIQKLVGQKIHESKJRYDNIISRWLQXDLVSPHTCRLQS
LKKMLSQALSHKALSLQVRCHQLKKSLTYPRQLQQASQKLSJWRQQLDTLISPRLHYQKE
EYFHKIHTULKIAIINVLEQQLRSHVQKI,ELLGPRLSHSGGELNLQNQKIAYANVKETLATIL
HRRYENGVARYCALKEQHGILNPKNVLKRCYAMLFDFTIENISAHISVDSLQEIIARVRIGLQ
HGEAILTVTNIRIGKLIKG

CPn_1063   1219900   1220712

tpi3-Triosephosphate   erase
FCRESMRIKFRENKERKMTPC....LGNWKMHKTICEAKEVVQTLASILQGEPLSCTIGIA
SPFTSLRAIHEVINTTMAPUMLGAQNVHPELSGAFTQELSLPMIGKEVTYESVTLHGHSERR
HIFGESDAFIASKVKSVAQAGLVPVLGVGESLEVREEGKAHQVINKQLLLGLEGMDNGSE
FLIAYEPVWAIGTGKVAEASDVQDIHMFCREVVAERFSEATAEEISILYGGSVKVDNAQR
FGQCSDVDGLLVGGASLECQSFFEVAKNFNV

CPn_1064   1220716   1220895

CPn_1065   1221140   1220928
No robust homolog present in Genebank/EMBL as of 11/7/98
RHRLGRHRRTSDPCFLFYFSIPEESLPPDSCRLNQMPKHEHLPSILLKKPIIDYLKITSI
YEKAIFNTGLP

CPn_1066   1221132   1221488
No robust homolog present in Genebank/EMBL as of 11/7/98
SMSLNKEIGMTVLFYAFLFIFLFLCVILCGLILVQESKSMGLGSSFGVDSGDSVFGVSTP
DILKKVTSWCAVAFCIGCLLLSFSTNLLGKKLDAKEFLLPAAEESDTQASSESVEADES

CPn_1067   1221675   1222292
def-Polypeptide Deformylase
IQVLVVVRDFFTELCQAHVQTMIRRLEYYGSPILRKKSSPIAEITDEIRNLVSDMCDTMEA
HRGVGLAAPQVGKNVSLFVMCVDRETEDGELIFSESPRVFINPVLSDPSETPIIGKEGCL
SIPGLRGEVFRPQKITVTAMDLNGKIFTEHLEGFTARIIMHETDHLNGVLYIDLMEEPKD
PKKFKASLEKIKRRYNTHLSKEELVS

CPn_1068   1223267   1222365
rnhB-Ribonuclease HII
MSCMPPPFVVTLTTSAQNNLRDQLKEKNFIFSQPQNTVFQARSNTVTCTLYPSGKLVIQG
KGSEEFIEFFLEPEILHTFTHARVEQDLRPRLGVDESGKGDFFGPLCIAAVYASNAEILK
KLYENKVQDSKNLKDTKIASLARIIRSLCVCDVILYPEKYNELYGKFQNLNTLLAWAHA
TVINNLAPKPAGDVFAISDQFAASEYTLLKALQKKETDITLIQKPRAEQDVVVAAASILA
RDAFVQSIQKLEEQYQVQLPKGAGFNVKAAGREIAKQRGKELLAKISKTHFKTFDEICSG
K

CPn_1069   1223507   1223941
yfgA-HTH Transcriptional Regulator
VIMQEHIHKELLHLGEIFRSSRESQSLSLKDVEAATSIRYSCLEAIEQGCLGKLISPVYA
QGFIKKYATYLGLDGDSILQEHPYVMKIFKEFSDHNMEMLLDLESMGGRNSPERAIHSWS
NLWWAGLIIIGGIMVWWLGSLFSIF

CPn_1070   1225523   1224144
No robust homolog present in Genebank/EMBL as of 11/7/98
RRSLMTFPCGNCNCYYRETPPPNPGGEDIPLQEGGOSGSQGGRVITCQPGTCGREMGISL
GSDNVLGMVEQAGSLLNNLLDSARMQRLGHYCYRTGTPWCREHCPGFLQWIWGGCCACKL
ETVDDPENPSAQFLQQLIQQYGPICVGMSFQQLPHCTQKIEQGEPLGDGDKQEVENGCKL
HRELLKAAQPRCMGESLVKLLQNNGLGEDMQQTPPWSLILQAVSEGALSFVTSSDNPPTC
WILQPEQQPCPPPPTDEEQLQGAVGGAPAFQQKKHPAQECRVTCKLNFRTLLQKLSRLEV
LSLESGYKGPLGQAAKOIVDLIKKSLKRLVASDLATFLGPGIGLSLESQVPEVLVLLCLL
SKGYLPLDPLHPEQTVLDPRVQGPWQRILRKVLVTTTAGENIWRQTQGEAPRQAPPPPDP
WDDDEIERDGIVTGGGFGIPCQCLRCWRKLPTEKRPNRWL

CPn_1071   1227336   1225885
No robust homolog present in Genebank/EMBL as of 11/7/98
KGTTMVCPNNSWFRMCGNFNCEWVEVTTTEETTROSASDISEEAGSSGGAAPITTQPTKI
TKVEKRVQFNTAQGDESTIHMIQEAGELVDSILSHRRTQGCTEYCYDSYATGCGQRCGSF
GRLICGTYKACCLDREDNQVAGLVHECEQTHGPIAVALAAKTMGLNLMELVEKNTILSEE
QKNEFRQHCSEAKTQLYGTMQSLSQNFFLEGVNSIRERGLDDSLVQAVLSFIATRSWEKT
IESEEASGTSSASNSTRIPACYILNTSPLTTSRLSCGSRDARRPSSVGAEPQYVAKKYND
NGMARQLGKIQVTNLKTGDFSALGFFGLLIVKMLNSFLLSASQSTSSILKHTQGEICYTC
PNFRDIVVLLMLAIGYCPANTDETSVVDIHMIDDPIMTIFYRLQYSYRTGKTSASFLKKK
PSLVRQESLDCPTPAESVPLMSSLEEEDENEDDDEDGNLAYQORILECSGHLQTLFLGIK
INKE

CPn_1072   1227924   1228835
No robust homolog present in Genebank/EMBL as of 11/7/98
KKDYILHANWCCWKQMLKIQKKRMCVSVVITVGAIVGFFNSADAAPKKKKIPIQILYSFT
KVSSYLKNEDASTIFCVDVDRGLLQHRYLGSPGWQETRRROLFKSLENQSYGNERLGEET
LAIDIFRNKECLESEIPEQMEAILANSSALVLGISSFGITGIPATLHSLLRQNLSFQKRS
IASESFLLKIDSAPSDASVFYKGVLFRGETAIVDALSQLFAQLDLSPKKIIFLGEDPEVV
QAVGSACIGWGMNFLGLVYYPAQESLFSYVHPYSTATELQEAOGLQVISDEVAQLTLNAL
PKMN

CPn_1073   1229011   1229832
Predicted OMP (CT371)
MRRYLFHVLALCLYRAAPLEAVVIKITDAQAVLKFAREXTLVCFNIEDTVVFPKQMVGQS
AWLYNRELDLKTTLSEEQAREQAFLEWMGISFLVDYELVGANLRNVLTGLSLKRSWVLGI
SQRPVHLIKNTLRILRSFNIDFTSCPAICEDGWLSHPTKDTTFDQAMAIEKNILFVGSLK
NCQPMDAALEVLLSGISSPPSQIIYVDQDAERLRSIGAFCKKANIYFICMLYTPAKQRVE
SYNPKLTAIQWSQIRKNLSDEYYESLLSYVKSK

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.   RNA SECTION   .
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tmRNA   1138494   1189074

Ribosomal protein P RNA   607142   607449

16S rRNA   1000564   1002112

23S rRNA   1004419   1005278

5S rRNA   1005593   1005709

. . . .

tRNAs

tRNA #	Begin	End	Type	Codon
1	89657	89728	Thr	CGT
2	90998	91070	Trp	CCA
:	. . . . .	. . . . .	Met	.AT
:	. . . . .	. . . . .	Ser	.AT
5	296075	296147	Val	TAC
6	296151	296224	Asp	GTC
7	409848	409922	Pro	TGG
8	462141	462214	Arg	CCT
9	672236	672318	Leu	CAA
10	677264	677337	Arg	TCG
11	739403	739486	Leu	CAG
12	781610	781680	Gly	TCC
13	784822	784896	Glu	TTC
14	784922	784994	Lys	TTT
15	836119	836191	Ala	GGC
16	843926	843999	Pro	GGG
17	877400	877473	Arg	ACG
18	1085605	1085676	Gln	TTG
19	1142034	1142118	Ser	TGA
20	1175863	1175944	Leu	TAG
21	1230028	1229942	Ser	CGA
22	1137462	1137389	Val	GAC
23	1030603	1030533	Cys	GCA
24	1000022	999949	His	GTG
25	961607	961536	Gly	GCC
26	807413	807341	Arg	TCT
27	786780	786708	Thr	CGT
28	715971	715889	Leu	TAA
29	708441	708354	Ser	GCT
30	680259	680178	Leu	GAG
31	631445	631373	Phe	GAA
32	626987	626901	Ser	GGA
33	293477	293405	Thr	TGT
34	293399	293317	Tyr	GTA
35	269142	269070	Ala	TGC
36	269065	268992	Ile	GAT
37	164389	164318	Asn	GTT
38	87522	87450	Met	CAT

What is Claimed is:

1.   An isolated nucleic acid encoding a *C. pneumoniae* protein as set forth in Table 3.

5

2.   The isolated nucleic acid of Claim 1, wherein said nucleic acid has a nucleotide sequence of an open reading frame in SEQ ID NO:1.

3.   A probe comprising a hybridizing fragment of an isolated nucleic

10   acid according to Claim 2.

5.   An isolated nucleic acid that hybridizes under stringent conditions to the nucleic acid sequence of Claim 2.

15   6.   An expression cassette comprising a transcriptional initiation region functional in an expression host, a nucleic acid having a sequence of the isolated nucleic acid according to Claim 1 under the transcriptional regulation of said transcriptional initiation region, and a transcriptional termination region functional in said expression host.

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7.   A cell comprising an expression cassette according to Claim 6 as part of an extrachromosomal element or integrated into the genome of a host cell as a result of introduction of said expression cassette into said host cell, and the cellular progeny of said host cell.

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8.   A method for producing a *C. pneumoniae* protein, said method comprising:

growing a cell according to Claim 7, whereby said *C. pneumoniae* protein is expressed; and

30   isolating said *C. pneumoniae* protein free of other proteins.

9.   A purified polypeptide composition comprising at least 50 weight
% of the protein present as a *C. pneumoniae* protein comprising an amino acid sequence
of claim 1.

5   10.   A monoclonal antibody binding specifically to the polypeptide of
Claim 9.

Contig463
Length: 273254..

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      1   ATTGTTCCTG TAAGAACACT TCCAAAGCGC ATTTAATCAT TTTTAGTAAA

     51   AAATAAAAAT ATACTTTTAA ATGTTGAGAA AATTTTTAGC TAAACTTTAT

    101   AAAGGGTTGT TGGTGAAACC TTTGGGTTAC TCCTCAGAAC GACTTTGTGA

    151   TTCTATAGTA TTAAAAGGAT CTTGGAGTAT AACAAGTAAA GATCTTTGAG

    201   GATAGCGTAG GGCCGTATTT TGAATAGCGT CCAATAAAGC GCGTTTGCAA

    251   AACGCTTGAG TTTGGTTGTC CCAATAGAAA GTGCCTTCTT TAGGAAGAAT

    301   CTCTTCTGGA GGCACTTCAT AGACCGAAGT AAAGAGAGGA AGAGCAACGA

    351   TTGCTGCATG ACTTTCTATA GCTGCTTTAA GGCAGTTCTC GTACGCTAGT

    401   AAAGCTTGGC GATAATATTC TTGCTGATTT GGTAACTCTT CAGATTTAGG

    451   GCCGCATACG TGGCCTAAAA AGGTCGGAAG AATACTTTTC TTTTCTGCAG

    501   AGCTTAAATT TAGATTAAAC GTTTGATCTA GAGCTTCGTT TGGAAGTTTT

    551   ACTACTCTCA CTTCGGTAGG GGAAAAGGGG TCTTCTCCTT TTGCGGGACC

    601   CCCTTCGCGT TGCTTGCATG TATCCCACAC GCTTTTATCT TTTAGGGTGG

    651   AGTAAAGGAT AGTAGAGAGG TTCGTTGCAG TGTTGTCGAT CAGATTCGTT

    701   GGGCCTACGG GATTAAAGAT GATCCCTGTG GATTGATTTT TTTCGATCAC

    751   TCTAAGTCCA GTTAAGAAAG TAGGCTGAAA TGGTTGAGAC GCATCTGTTT

    801   GTATCGCTAC CTTGAACTTA GGGTTCAGGT GATTATTGTA AAATTGCATC

    851   TCGTTTGAGT AGCAGTCTAC GTTTTTTTCT TGCCACGCTT TTCCCAAAGG

    901   CTTGAAGTTT TGCTCTAGAA CTTTCTGCCA GTTAGAAGAT ACCTTTGAGG

    951   TCATTGGTG GTAGACTAAG AAGGTTACAA CTGAGAAGAG GGCCGTGGTA

   1001   ATGAGAAGAG CCAAAAATAC AGGGTTCCCT AATACTATCG TTAAAGAGAT

   1051   TCCAGCCACC AAAGCTCCTA AGCTAAAGA AGCTAGGATT GCAAGAGTGG

   1101   ATATTTTTGC TATGGTAAAC TGTTTTTTAG GAGCAATTTC TTTATCCCGA

   1151   GGCACATAGG ATAGTACAGA AACTTGAGAG CTCTCAGTAC GTGAGGGTCC

   1201   TGACATAACA TTTTTTTTGT AAAATACTTT CTATAATTTT AACATATTTG

   1251   TGTTTATCGA TCCGAGAAAA TTGGAGAGTG AGAGCGCATG TCTTGCAATT
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1301  TAGAATGATC GGGGACGACA TCTAGAGCTA TGTAGACATT GCGTGCGTAG

1351  TGGGAGCAAA TATAGCGAGA TATAAAGTAT AAGGGAATTG CTGTTAGGAA

1401  GATAAAGGAG CACAAAGGGT GGATACATAG CCCAATAGCT ATGGTGGTAG

1451  CAATCAGAGC TATCCAGACG AGTGCAATCG CAATAGTAAC GAAGAGGGCA

1501  AGCTTGAAAT TATAGCGAGG ACGAGTAGCT GGGGGAAATA GAGAGGGAGC

1551  CGTTCCATCA AAACCGGGAG TAGCTGAAGA AGCCATAAAC TATTAAAAAT

1601  TAAGTTTTTT TCGGAGCATA AAGCATTTTA AAGTAGTGGG GTCTTTTTTG

1651  TCACGGAGAT GTCCTGGACT TCCCAAGCGT TTCTAACAAA GATACCTGCT

1701  TTTGAGAGGA GAACTTTTGA AACTCCTGCA AGGTCATCCT TCCTTGGCAC

1751  CAGTAGGTTT TTTCAGGAAA TCGCGGAAAG ATTTTGGCGA AAGCTCTTAC

1801  AGTTGAAGGG CTTGTGAAGA TAATTTTTTT GTATTAGAT AAAATATTTT

1851  TTTTAAGTTT TCGCGGCTTC ACTGTGTAGT GAGGGTAAGA GAAAAAAGTA

1901  AATCGATTGT AAAGAAATTC TCTGATCACA GGTCTTGCGA GGGAGGAGTG

1951  GGGGTAGAGA ATGCGGGCTG AAGAGGGCAG TGCCTGTAGC AATGGGAAGA

2001  TGCCTTCAGC GATTCTTGA GTTGCTACTA CGTACTTCAC TTGTCCAAGG

2051  AAAGAGAGAA GTCTTTCTTT GGTGGACTCT CCTATACAGA GGTAGGTCTT

2101  TGTTTTTAGA GTGGCCTTAG AAAGAAGAGA AGTCATTCTG GAAAGGAATA

2151  GGTGAGTGGA TGAGGGACTT GTGAGAATCA CATGGGTTGC TTGTGGAAGG

2201  AATTGAAGAG CACGCTTATT TTGTGGAGTG CTTTTTGCAT AGGGGAAGAG

2251  AGTTAGAATA GGCAAATAAT GAGCTTGGTA TTTACGAGCG GTTTTTTGAT

2301  TCAATCCTAA GTAGAGGGTC ATGAGTCTTT TCGGGTAAAA GGAAGGCTGC

2351  CTAAGTTTTT GTACCTTCAA AGGGATATAT TGAAAATAAT TTTTCTTTTT

2401  CCCTTGGTTC TTCTTGATCA TGCGTTGATT GACATTTTTC ACTTTGAAGG

2451  CTAGGCTGGT TTTTTCTGGA CTTAGAGGTT CTCTCTATTA AGGCTTCGTC

2501  TTTAGAAGTC CTTGCTAAAA GTTTTTGAGA AATTTAAGAA ATTCGCAATA

2551  GTGGAAATAT TTACAAAGGT GGTTGCGGTG GTTTCGTTGT TGCATAAGTT

2601  TTTAGAAAAT GCTTCGGGGA AAAAGGGACA AAGTTTAGCT TCGACAGCGT
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2651   ATTTAGCAGC TCTTGACCAT CTCTTAAATG CGTTTCCTTC CATTGGGGAG

2701   AGAATCATTG ATGAGTTGAA GAGCCAGCGT TCCCATTTAA AGATGATTGC

2751   TTCTGAAAAC TATTCTTCAC TTTCAGTGCA GTTGGCTATG GGGAACTTGC

2801   TCACAGATAA GTATTGTGAA GGAAGTCCCT TTAAGCGTTT CTATTCCTGT

2851   TGTGAAAATG TAGATGCTAT TGAGTGGGAG TGTGTAGAGA CAGCGAAAGA

2901   ACTTTTTGCT GCGGATTGCG CTTGTGTTCA GCCTCATTCT GGGGCTGATG

2951   CTAATTTACT GGCAGTAATG GCCATTCTCA CGCACAAAGT CCAAGGCCCA

3001   GCTGTCAGTA AGTTAGGTTA TAAAACTGTA AACGAATTAA CAGAAGAAGA

3051   ATACACTCTA CTTAAGGCTG AAATGTCTTC TTGTGTTTGC TTAGGACCTT

3101   CATTAAATTC TGGAGGCCAT TTGACCCATG GAACGTACG TTTAAATGTG

3151   ATGTCTAAGC TTATGCGTTG CTTCCCCTAT GATGTCAATC CGGATACGGA

3201   GTGTTTTGAT TATGCAGAGA TCTCCCGGTT AGCTAAGGAG TATAAACCTA

3251   AGGTACTGAT CGCAGGATAT TCTTCCTATT CTCGAAGATT AAACTTTGCA

3301   GTTTTAAAAC AGATTGCAGA GGATTGTGGA TCTGTCTTGT GGGTAGATAT

3351   GGCGCATTTT GCAGGCCTAG TTGCTGGGGG AGTGTTTGTT GATGAAGAAA

3401   ATCCTATTCC TTATGCAGAT ATAGTGACAA CAACAACGCA TAAGACATTA

3451   CGCGGTCCTC GCGGGGGATT AGTTTTGGCA ACTCGAGAGT ATGAAAGCAC

3501   TCTCAATAAG GCGTGTCCTT TGATGATGGG AGGTCCTCTA CCTCACGTGA

3551   TAGCTGCTAA AACAGTGGCT TTGAAGGAAG CTCTCTCTGT GGATTTCAAG

3601   AAATACGCTC ATCAGGTTGT AAATAATGCT CGTCGATTAG CAGAGAGATT

3651   TTTAAGTCAT GGGCTACGTC TTTTGACGGG AGGAACAGAC AACCACATGA

3701   TGGTGATTGA TTTAGGTTCT TTGGGCATTT CTGGAAAAAT TGCTGAAGAT

3751   ATCTTGAGTT CCGTAGGAAT TGCTGTGAAT CGGAATTCAT TACCTTCAGA

3801   TGCTATTGGT AAGTGGGACA CTTCAGGTAT ACGTTTAGGA ACCCCTGCAC

3851   TAACGACTTT GGGTATGGGT ATCGATGAAA TGGAAGAAGT TGCAGATATT

3901   ATTGTGAAAG TATTGCGAAA TATTCGTTTA AGTTGCCATG TTGAAGGGAG

3951   TTCTAAGAAA AATAAAGGGG AACTTCCTGA AGCCATAGCG CAGGAAGCTA

4001   GAGATCGTGT TCGCAACTTG TTGCTGCGTT TCCCGCTCTA CCCTGAAATT

4051   GATTTAGAAG CTTTAGTTTA GTTAGGAGAG ACATTATTTT ATGGCAGACG

4101   GGGAAGTTCA TAAATTACGT GATATTATAG AAAAAGAGTT ATTGGAAGCG

4151   CGCAGAGTAT TTTTCTCAGA GCCTGTAACA GAGAAAAGTG CTTCCGATGC

4201   AATTAAAAAG CTTTGGTATT TGGAATTAAA AGATCCTGGA AAGCCTATAG

4251   TTTTTGTGAT CAATAGTCCT GGGGGATCTG TGGACGCAGG TTTTGCTGTT

4301   TGGGATCAAA TTAAAATGTT AACCTCACCC GTCACTACTG TTGTGACAGG

4351   GTTGGCAGCT TCTATGGGCT CGGTATTGAG TTTATGTGCA GCTCCTGGAA

4401   GGAGATTTGC AACTCCTCAT TCTAGAATTA TGATTCATCA ACCTTCAATA

4451   GGTGGACCGA TTACCGGTCA GGCAACCGAT TTAGACATTC ATGCGAGAGA

4501   GATTTTAAAA ACAAAAGCTC GCATTATAGA TGTCTATGTA GAGGCGACAA

4551   ATCAACCTCG AGATATCATA GAAAAGGCTA TCGATAGAGA TATGTGGATG

4601   ACAGCCAACG AAGCTAAGGA TTTTGGTTTA TTGGATGGCA TTTTATTCTC

4651   CTTCAACGAT CTCTAAATAT TTTATCTATT CTGGAGCAGG AAATCGTTTC

4701   CTTCTTGGTG AAACACTTCC TGAGGTTGAA GATGTTCGGT TCTTATGCCA

4751   AGAGACGAGG GTTGATGGTT TTTTATATTT AAAGCCCTCT TCTTGTGCTG

4801   ATGCGCAACT CATTATTTTT AATTCCGATG GATCACGTCC AACGATGTGT

4851   GGTAACGGCT TGCGTTGTGC GATTGCTCAC TTAGCTTCTC AGAAGGGAAA

4901   ATCGGACATC TCTGTATCTA CGGATAGTGG TCTATATTCA GGATATTTTT

4951   ATTCTTGGGA TCGTGTGCTT GTAGATATGA CTCTCGCAGA TTGGAGAGCT

5001   TCTGTTCATC GATTGGAGTC GCGTCCTGAT CCTCTTCCCA AAGAGGTCGT

5051   TTGTATCCAT ACGGGAGTGC CTCATGCTGT CGTAATTCTT CCTGAGATTT

5101   CTACTTTAGA TCTTTCTATC TTAGGTCCTT TTCTTCGCTA TCATCAGACC

5151   TTCTCTCCAG ATGGGGTGAA TGTCAATTTT GTTCAGATAC TGGGACATTG

5201   CCAGTTGCGC GTTCGTACTT ACGAACGTGG AGTCGAAGGG AAACTGCAG

5251   CTTGTGGAAC AGGGGCTCTA GCTTCTGCTC TTGTTGTGTC AAACTCCTAT

5301   GGATGGAAGG AGTCGATCCA AATCCATACT TGGGGTGGAG AGCTTATGAC

4

5351   TGTGAGTCAA AATAGGGGAC GGGTATATCT TCAGGGCTCT GTAACTAGAG

5401   ATTTATAATT AGATGTGATT TTTGATTTTG TCATGCAAGG ATTTTAAAAT

5451   CTTGTTTAGG GATAGATCTT GCTCTCTAAC TGGGATTTTT CTATAATCGT

5501   AATTTATGAT GACGTATCCT GTACCACAAA ACCCACTTCT TTTAAGAATC

5551   CTTCGTCTTA TGGATGCATT CTCTAAGTCT GACGATGAGA GGGACTTTTA

5601   TTTAGATCGT GTTGAAGGGT TTATTCTCTA CATAGATTTA GATAAAGACC

5651   AAGAGGATCT AAATAAGATT TACCAAGAAT TAGAAGAGAA TGCCGAGCGG

5701   TATTGTTTGA TTCCGAAGTT GACGTTTTAT GAAGTAAAAA AAATCATGGA

5751   AACGTTTATC AATGAAAAGA TTTATGATAT CGATACCAAA GAAAAGTTCC

5801   TTGAGATTTT GCAATCCAAG AATGCCCGTG AGCAGTTTTT AGAGTTTATT

5851   TATGATCACG AGGCAGAGTT AGAAAAGTGG CAGCAATTTT ATGTAGAGCG

5901   TTCTCGAATT CGAATTATAG AATGGCTTCG CAATAATAAG TTCCATTTTG

5951   TCTTTGAAGA AGATCTAGAT TTCACAAAGA ATGTTTTGGA ACAGTTGAAA

6001   ATACATTTGT TTGATGCCAA GGTGGGGAAA GAAATCACTC AAGCGCGTCA

6051   GTTGTTGTCG AACAAAGCTA AGATTTACTA TTCCAATGAA GCATTAAACC

6101   CTCGTCCGAA ACGAGGCCGT CCTCCGAAGC AATCTGCTAA GGTAGAAACA

6151   GAAACAACAA TTTCGAGTGA TATTTATACA AAAGTCCCTC AGGCTGCTCG

6201   TCGTTTCCTT TTCTTACCCG AGATTACTTC ACCCTCTTCA ATTACTTTCT

6251   CAGAAAAATT TGATACGGAA GAAGAATTTC TTGCTAACTT GCGCGGTTCG

6301   ACTCGTGTTG AAGACCAGCT GAATCTTACC AATCTTTCAG AGAGGTTTGC

6351   TTCTCTTAAA GAGCTTTCGG CTAAGCTTGG TTACGACTCT CTTTCTACTG

6401   GAGATTTCTT TGGTGATGAT GATGAGAAAG TGGTCACTAA GACGAAGGGG

6451   AGCAAGCGAG GCCGCAAAAA ATCTTCTTAA TCTTCTATTT TGTGAAGTAG

6501   TTTATTTTTA GACGCTGTTC TTATTGCTTC TTTACATGAT CTTATTACAA

6551   ATCTTTCTTA TTTCTATTTA TTGTTTTGTT AAAATTTTAA CAATAGCTAT

6601   TTATTATTAG TCATTTTTTT AATTAAAAAA CTGTTAAAAT TTTTAAAGCT

6651   AATTTAAGAA ACAGTGAATA GTTCATCATG TCATCACTAC TGAGCTGCGG

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6701    AAGAATAGAG  CCGACTCGGG  TTACCTGTAG  CTTAAAGACG  TATCTTGAGG

6751    ATACGAGTCA  GAATCAGTTG  AGCACACGTC  TAGTTCGGGC  AAGTGTCATC

6801    TTTTTATGCG  CATTGTTGAT  CATTTTGGTT  TGTGTGGCCC  TCTCTAGTTT

6851    GATTCCAAGC  ATTATGGCCT  TGGCGACCTC  TTTTACGGTA  ATGGGGTTAA

6901    TTCTTTTTGT  GATGTCACTT  CTTGGTGACG  TTGCAATTAT  AAGTTATCTT

6951    ACTTATAGCA  CTGTTACGAG  TTACCGGCAA  AATAAGAGAG  CTTTTGAGAT

7001    TCACAAGCCC  GCTCGCTCCG  TTTACTACGA  GGGGGTCCGC  CATTGGGATT

7051    TAGGACGATC  ATCTTTAGGC  ACAGGCGAGA  TTCCTATAGT  AAGGACGTTA

7101    TTCTCTCCAT  TTCAGAACCA  TGGTCTTAAC  CATGCCTTAG  CTGCTAAAAT

7151    TTTCCTATTT  ATGGAGCATT  TCAGCCCTGA  GCCACCGAAC  GAGCCTTTGG

7201    TGGATTGGGC  CTGTTTGATT  CGGGATTTTA  GGCCTCACGT  CAGTTCTTTG

7251    TGCTTTGTTA  TTGAAAAACA  AGGGTCATCG  CTGAGGACTA  AGGAAGGCAA

7301    TACGATTTGT  GAGGCTTTCC  GCTCTGATTA  CGACGCCCAT  TTTGCTATGG

7351    TAGATTGCTA  CCGGTTGATC  CACTCTAAGT  TGATTATAGA  GAAAATGGGA

7401    TTGAAGAATA  TCGATATCAT  TCCGAGTGTC  ATGGTTCGTG  AAGATTATCC

7451    TAGCCGTCCT  GGGGAGGGCT  ATCGCGAAGG  CCTATTACGT  ATGTATGGTG

7501    GCAAGGGGGC  TCTGTGACTT  CCCTACTTTA  GTTCCTAATG  AGCGCTTGCC

7551    CATAGGGCCT  TTCTTTGTCC  CGCAGCACAC  TTCCGGTGCG  AAGGGTAAGG

7601    AGTTTGCTAA  AAGGAATTTT  TCTATAATTT  CGGGATTGGA  TGACATATTA

7651    AAATTATGTA  TTCTTCAAAG  GCGTCCTTTT  GCTTTGCAGT  GGGATAACCT

7701    CTCTGTGAAA  AGTGATTATG  AGGAGGCTGG  GCCCGCTATT  GGGATACGTT

7751    CTCTTGAGCC  ACAAGTTTCT  CAAATTTCTC  CAGCCCACGG  CCGGCTATGT

7801    AGTACTTTGG  TCCAGTGGGC  CCCTATCCTT  GGTTCTGAGG  AGCAGCTAGT

7851    TTGGTTAGAA  GAAACAATGA  AGCGCCTAAA  GTTCCTAAA   AGTTTAGGTA

7901    GTAAGGACGC  TGTTATTGTG  GATTCGGAAA  TGGTTCCTGT  GAACGCCAAT

7951    CCTACTCAAG  AGATACCTGC  AGCTTCCGAG  ACTGTAGAGT  CTTCACCTGT

8001    AGCTCCAGGG  AATACAACAG  ATACCATGCC  TGCAGCTTCG  GGAACTACAG
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6

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8201 TGTTTACAGA TGAAGAAAAA AGTCTGATTT TAGAAGCTAC TCGTGCGCGT

8251 CGTATGGAGT TGGACTTGTA TAATGGCTAT TTAGCTGATT ATGAACTTTC

8301 TAAGGATGAA ATACAGAAAC ACGTTCCTGA TTTACCTGAG AATTGGCGTA

8351 CGAATTGGCG TTGGTCGGAG AGGCTCTATA AATTTTTCTT TAAAACAAAG

8401 AAAGAAGGAT TAGAAGAAAT TTTCTTAAAC AAAGAGTTAG GGAATATGAT

8451 TCTTGCCCGA GGGCTGGCGG CAACTCAGTC ACAAGCACGT ATTAAAGTAT

8501 TCAATTCTTT AGTGGCATGG CTCTTGCAAA GCTTTAACGT AGGGAGGAGC

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8601 ATTCGAGTCT AAGCCTAAAA ATAACATCTT AACGGAATTT TTGGTGGCCT

8651 CTGATGAGGA GATTCTCTTT AAGGGGCTAC GGGTCCTAGA GCCTGGAATC

8701 GAAGGTTGGT ATGACCATCC TGATCAAGCT GGAGAGATTC GGTCGGTACT

8751 CGAGGGTCTG GTGCAGGCTG ACGTATTTC TGGATATTGG GAGAATCAGC

8801 CGTTTGGGAG ATTTGTCCTT AGAGGAGTTG GTGAAAGACG TACCGAGCTT

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8901 TGAGTCTTCG GATGAAGAGG GTGCTTTTAT TATCGATAAC GAACCTAGCA

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9051 AGTTTAGCGT GGGGTAGAGC ACTCCACGAA TCTTAGGGAG CTCCTTGCGA

9101 CCAAGCTTGG AGATCCTCCA TGTTTATTG TTTCTCTAGT AGCCAAATCG

9151 TAGCCGCTCC TAGGAACAAT TTTTTCTTTT TCGCAATATA AAATCCTGAT

9201 TTAGAGAATA GGTCTTCAAG ATCGTGGTCC TTTGGAAGTT GCTGGATACT

9251 TTTGCTGAGA TAGCTATAGG CGTCGGGATC TTTAGAAACA GACTTTCCAA

9301 TCCAGGGGAC GACAGCACGC AAATAGAGCT TATGGGCACT ATAGGTAGGG

9351 TGTGTTTTTT TTGGAGGTGT GAGCTCTAGA ATGCCCAGTT TTCCAGAAGG

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 9401  .CATAAGCACT CGGGAGATTT CTTGTAGGGC TTTATGTGGA TCCGAGAGGT

 9451   TCCTGAGGCC ATAGGCCATC GCTGCTAGGG GATAAGAATG ATTCTCCAAG

 9501   GGCAGTTGAT TAATATCGCT ATGAATAAAA GAGCAAGAGC CCTGGGGAAG

 9551   GTGTTGTTTT GCAATGTCGA GCATTGCTGA GGAAAAGTCG ACGAGAGTTA

 9601   CTGATGCTTG AGGGTGTGCG GCAATATAAC GCTTCGCGAC TTTTCCTGTT

 9651   CCTGCGCAGA GATCCAGGAG AGAGTATCCC GACCCTAGGA TCTGGATCAA

 9701   AGAGCGATTC CAGAAATGGT GCATTCCTAA AGAGAGTATT GTATTTGTGC

 9751   GATCATACTT ACTCGCTATG GAATCGAAGA TCTTTTTACA GTCGGGCTTG

 9801   TTGGTAGAGG GTTCCATAAT ATTCCCGGAA TTTTTCAAAG CTTTCGTAGT

 9851   GTTCTTCTCC TAGACGGTAC TGGCATAGGG CATAGTATTC TTGAAGAAGA

 9901   GAAGGGGGCA GACCTGTATG TTGATGAGCT TCTTTAAGGA CTTCTTCGGG

 9951   TGAAGATTCG AACTGTTGGA GGGCTTCTTC CATCGCAAGG TTGGGTAGGG

10001   GATGTTCTTT CCAAGAGGTG CTGTGTAGAA GAAGAGCAAA TACAAAAGGT

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10101   AGGAAGTACA GGATGTTGTA GCGCTGCATC TCCGATTAGG AGGAGGCCAT

10151   CATAATTTTC AGGGGTTTGT CTGAGTACTT TTGTAGTTAT GAATCTTAGG

10201   ATATGAGGAG TTGGGATGCG CCAGAGATGA CGACAAAGCA CTTTTAAGAG

10251   TCCTATAGAG GAGCGACTTT CTAAAGTTGC GGCAATCCGA GGTTGCGGTG

10301   AGTTAAAGAA AGTGGGAGCT GCATAGAGGT TTACACTGAG GATACGTTGG

10351   TTTGCTGCAA TTCCAAAGCC GGGGACATAC CCCAAGTTAT GAGAGATAGC

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10451   TGAGGAGGTC TGCAGGGGGA GCAAGAACAC AGCGAATATC GTTTCTTTTT

10501   ATGAGTTGTA GGGACAGCGG AAAGGAATTA ATATAACTTA CGCAGCCTAA

10551   GCTTATACAT GGCTGGAGTT GGTTAGACAT GGCGTTCTCC CTTGTTGTGT

10601   GATGAGGGCC GCCATTCCCT CAGCGTCCAT TTTAATAGGT TCTTTAGATG

10651   AGGCCATCTG GAAAACCTTT TCCCCCATAT GTGTTGAAGA AAGGTCATTA

10701   GCACCACAGG AAAGGAGGTC TAGAGCTGCC TCAATACCTA GGTAATTCCA
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8

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10801    TTAAAGATTT TAGAGGGATG GCATGACCCT GGCCTGATTT TCTTAATCTT

10851    TTTCCTAGGA CATTATTTTC TTGGGCGAAT TTTAGAAGTA TGAAGTTTTT

10901    AAAGCCCTGA GTTTCGTCTT GTAAGTCGCG GACTTTTACC ATGTGGGTGA

10951    CGAGGTCTTC AGGTCCTTCT TTATGATAGC AGAGCATGGT TATATTGCTA

11001    TGGATTCCCA GTTGATGAGC CATCTTATGG ATGTTGAGAA AATCAGAAGA

11051    AGAAAGGCGT TTGGGAGCTA AGAAATTACG TATTTTGTCG ACGAGGATTT

11101    CAGCTCCTCC TCCGGGGATG GAATCAAGAC CCGCATCTTT TAATGTGAGA

11151    AGAACATCGC GAATAGAAAG GTTATCAAGA TCTGAGAGAT AGGCATATTC

11201    AATGGCAGTA AGAGCTTTGA TATGGATCTG AGGATCGTAC TCTTTGATTT

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11301    CCCACGATAT GTACTTCTGT AATTGGAGTT TTTATATTTT GGATTTGCTG

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11701    GTAGCACAGT GCTCTGTTTT GTCACATGTT TTTTTTGGC AGCAATCTGG

11751    TTTTTGACAC CCTTTAGAGA GGGGCCTGCC AAGCAAATGG GAACCTACAA

11801    GTAGAATACC CATCCCTAGA CCTAACAATA CTGTGGCACA GCAGATTACG

11851    AGAAAAGTG TCATCATAAG AAATCCTTAG ATAGGATAGT TTCTTAATTT

11901    AAATCCACCC AGATTGGGGA ACTCCAGGCC ATAGCATTGT CTGCCTGAGT

11951    GACCCTGAGA TAGTAGAATA CAAAAGGTGC TTTACCGTTT GGATCTTTTA

12001    GGGTCACTGA ACTTAGGGGT ACCATATCAT CGTATTCATA GTCCAGGTTA

12051    TTGCTATCGG GGAAGAAGGT ATGGAGAACT TCGCCATTGC GGATGATTTC
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12101   TACAGTCTTG AGTAGGGCAG TGCCTGCCAC ATGACCAGAG ATGTGACGGT

12151   TGACGTTGAG TCCAGGTTTC GACCCTGTGG AGAGTTCGGA GCCCATAGGG

12201   GCTGAAGTGA TGTTGAAGCT TAAGACGATC CTAGGTCCTG TTGTAGCGTA

12251   GCAATGACGT GCGAATAAAG CTTCAACAAG AGACTCTCGG GTATATTTAT

12301   TACAAATGAT AGCCGTCAAC CCTGGGGAAT ATTGCACTTG CGGAGAGTCA

12351   AAGTAGTCTT TATAAATTCC TCGATCGTCG AGACCCCCAG CAACAAATCC

12401   GAAGCGGAGA TTCTTCTTTA ATCCTTCAAT TACTGTACCT CGAGGATCTT

12451   CGCTATCTTT ACCTTGGATA GGGAAGGGGT TGTTTAGAGC GGCTGTGGTT

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12551   GTAGAAATTC TCAAAGTCAA AACCATGTTC TTTAGAAGCT GTGAACGAAG

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12751   ATCCGGATAG TGTGATGAAG CGATCTTCTT CATTAAAGTC GGAGACAGTT

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12851   TGATGAAGAA GCATAGAAAT TCAGAGCGCG GTCATCTCGG AAATAACGCA

12901   TACAAGTTTC AATATTTTCT TCAGAGTCGA CGCGTTCGGA TTCGCCGTGG

12951   AGGAGACCCC ACATAAGATT CGGGGCGGAG TCAGCGAAAC ATTTGATAGG

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13201   CGTCTTCAAA TCGCACGGTG ATATCGAAGC GTTTGTTTTT AACGACATAG

13251   GAGGGAGTAA AGATCTCTAT TTTTTTTAGG ACGTTCCGC GGATATCCAT

13301   AGAGAAGACA TCGGGTTCAT CATAGTTTCC TTCTCCTGTA GGATCGATGT

13351   AGAGGTAAAA GGGTTTGCGA CGTTGTGCGA AAAGTTGGGC TCCGTTCCCA

13401   GCATCATCGA CTTGAGGATG GTTTGGAGAG GCTCCCATGA CAATAGTGAG
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13451   GGTTTCTCCT ACTTGAAGTT CGTAGGGGAG AGTAAACTCG AATTGTGGAA

13501   CGGGATTGTC TTTTACAGGA ATGGCGGTTG CTTCGATGAT TTCGCCTTCT

13551   GGCATTTCTG CGTAGATTAC GTTTCTAGTT TGGGAGAGAT CTGTCGCGGG

13601   GGCTTCCCAA TCTGTGGGTT TCCCACTTCC TGCTAAGTCA AATTTACATT

13651   TGGTTCCAGC TGGTAGTGGT GTGGCAAGGG AATAAAGAAA TTTCCAAGTA

13701   GAAATTTGCC CTGCTCGAGC TATCGAAGGG TTAACGTAAC AAACAGATCG

13751   TCGCATAGTA AGAGGGAGGC TTTATATGAC TTAAAAGCGC CATCATATAC

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13851   TTCATCCACA GTATTGAATA TTTTAAAGTA AGAAAGGAAT CCTGTAACAT

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13951   GAATGTTGTC CTACTTGATG GTAGCTTTGC AGTAGGACTC GGATACCTGC

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14601   TTTTCTTGTA CGTCGTGCTC GTCTGCGATC TCTCCTATAA TTTCTTCGAT

14651   AATATCTTCC ATGGTAGCGA TGCCTTCTGT GAATCCGTAT TCATTGACTA

14701   TGATGGCTAG ATGGCGATGT TTTTGTCGGA ACTCTTGGAG AAGAGAGGAG

14751   GCTTTTTTTA TTTCTGGGGC ATAGAATGGG GGTTTGCTAC TGAGGATATG
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14801    GGTTGGCTGA GGTCGTGGCT GCTTGTATAG AGCAGTAAGA GATCTTTAAC

14851    AAGAAGGATT CCTGTGATGT TGTCTAAGTT TTTTTTATAA ACGGGAACGC

14901    GACTGTAGCC TTCTTCGCTT ACGAGAACCA GAGCTTCTTG TAGTGTAGTT

14951    TCTTCGGGAA GTGCGAAAAT ATCTACTTTT GGGATCATGA CTTCACGGAC

15001    AATGAGGTTA TCAAAAGCGG AGAGGGCTTC GGAGAGCTGG CTTTGAAATG

15051    ATGTTGAAGA TCGTACTTGT TGGTTAGGGC GGCGTCTGTA AAAGAGCAGT

15101    TGCAGTGGGA AGAGACCGAG TTGGAATACC GAAGCTAGAA AACGGAGGTG

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16001    AAACTTATTT TAAAATAGGG GTCTTAGGTA AACCTGTGAC TTTTTTCGCT

16051    GTACTATCAT TCCAACGGCC CAACTTACGC AAGACTTCTA CTCGCTCAAA

16101    ACGCTTCAAA ACATTTCTTT TGGTAACCCC TTTGACAGAT TTACCATAAC
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16201   AAAAATGCTA TCACTGGTGC TCAATGCATT CGTATGCAAT TTATATACAA

16251   TTCTTGGAGC TGGCGCTGGA TGCACAATGG CATACTTAGG TTTACGTTTT

16301   TTAGGACTTT TCGCTCTGCG CCGAGCTTGT TTACTCATTC GTGTCATAAA

16351   TAACTCGATA TTGAATTTTT TAATTTCTCC AGACAACGGA AATTGAGGAT

16401   ACGGAGTACT TTATAAGAAA AAGGATAGTA AAGAAGAGT TTTTTTTCAA

16451   GAAGATGACG TCTTTTAGCT GCCTTGATCT TGGTGTAGCT CGTCAGGGAG

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17101   GAGAATAACA AGTCCTGTAA TAAAGTATTT TTTCATGATT CTCCTGCAAG

17151   ATATGAGGAA ATGGGCATTT GTTTCTTTAC TATACAGCTT AAGATTATTT

17201   AAGATAAAAC TTTTCCCGAA TCTTCTGGGG ATAGGAGAAA TCTCCATGGG

17251   ACATCACGAT ACTCTTGAGC ATAATCGATG CCGATCCGGG CAGTTGCTGT

17301   TAGAGTCCCA GAGATTTTTT CTTTGCTGAT ATAGAGAGCT GGGGTATTTA

17351   GGCGTTGCCT ATTGTTTTCC AAAGAGATTC CTAGAGCTTG GCACACTTTT

17401   CCGGGTCCAT TGGTGAGAAG GTGTGGGGGT TTATCTCTCC ATTGGCGGCG

17451   TTGGATCATA AGTTCTTTGC CTTGATCAGG AAGGATGGCC CGGATCAGGA
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17551   ATGCCATAGC AACGGTAGAG GTAAGCAGAG CCTCCTTTCA GGTACATCGC

17601   TCTGTTCCTC TGAGTTTTTC TGTAGTTGTA GGCGTGGCAT GCTTTGTCAT

17651   CAGGGCCACG ATACGCTTCG GTTTCTACAA TGTAACCTGA AGTTATCAGA

17701   CCCTCATGTG TTGTGATGAG TTTATGTCCT AAAAGCTGTT GCGCTAGTGT

17751   AATTACATCT TCCGATAGAA AAAAATGTTC TTGTAGCACG TTACGAGGCT

17801   CTTTTTTTCG TTCCTTTTTT CTTAGAAGGC GTTTTCTTTA TTTTCTTAGG

17851   TTTATCTTCT GTGGTTGTCG CTATAGACCA GACGATTTTT TGCGTAAGGA

17901   GATTCACGGA ATCAATAGTG ACTTTATAG AAGCTCCAGG TTTCATTTTA

17951   TCTGGGATAG ATTCTGGAAG AGCGTTTTTC TTTAGGGAAT ATTCTTTAGG

18001   GAGTTCTGCT GCTGCAATGA ACCCTTCATG GCAGAATTCG GTCACTACAA

18051   ATGAGAGTCC TTCATGATTT GCAGTGATGA TATACGCATG GTATGTAGTT

18101   TTAGGTTGCT CTTGCAAAAA TTTATTTATG AACCGAGTTT TTTTGAGGTT

18151   TTCGAAAGAA TTTTCTGCTT TTGCGGATAC TCGTTCTTTT GTAGAGCATG

18201   CTCTTACGAT AATTTCGAGG TGCGTTTGGT CTATAGATAG GGGGTTGAAG

18251   AGAAGCCTGT GAACAATAAG ATCGATATAT CTACGTATGG GACTCGTAAA

18301   GTGGGTGTAG TAGTCGAGCT TAAGTCCGTA ATGACCTTTA TTTTCTGTAG

18351   AGTAGGAGGC TGTTTTCATA CTTCGGACAA ACTGCGAGTG TAGAACTTGC

18401   TCTAGGGGAT GTCCTGCTGA CGTAGTTTGC AAAAGGTATT GGTAATCAGG

18451   TTCTTGTGTG GGAGTGAACG TGATATCAAA GCCCATGTTT TTTGCCAATT

18501   CTTGGAAGGC GAGTAGGTTT TCATCATTGG GAGGTTCGTG ACTACGAAAA

18551   GGTAGAGAAA CGCCTTGATG GGAGATATGA TAGGCGACCA CTTCGTTTGC

18601   TTTAAGCATA AACTCTTCGA TGAGTTTATG GGAGAAGGTC TGGTGGTTTT

18651   CTATCAGAGC TACGGGTTCT TGAAGATTAT CCAAGGACAT AGTGACTGAG

18701   GGGAGGACAA AGCGAATGCA ACCACGTTCT TCACGGATAT CGGAAAACTT

18751   TTTACTTAGA GTGGCCATCT CATTGAGGAT TTTTGAGAGG GGGTGGGAGT

18801   GTTTCTTTTC AATGATGTTA TCGACTTCAT CGTAGGTCAT ACGATATTTG
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18851   CTTCGAATGA CGCTACGGAA AATCTGGTAA TCTGAAAGAT GACCTGATTT

18901   TGTAAACGTC ATAAATACGG ATACAGCGAG TCTATCAACG TTTGGTTTTA

18951   AGCTGCAGAG ATTATCAGAG AGTGCTGATG GCAACATGGG AATGACTTTC

19001   CCTGGGAAAT ATGTAGAGTT ACAGCGTTTA GCAGCTTCTT TGTCTAGGTG

19051   AGAATGTGGG GTAACGTAGT GGGAGACGTC TGCGATGTGT ACACCAAGAA

19101   TGTAATTGTT ATTATGATCG TAGGTGAGGG AGATGGCATC GTCGAAGTCT

19151   CTGGCTGTGG AAGAGTCTAT GGTGAAACAG AGGAGATCAC GGAGATCTTT

19201   GCGAGAGTGG AGAACTTGGG TAATGTGTTT TTGAGAGAAA AGGCTTGCTT

19251   CTTCAATGAC CTCTGGGGGG AATTCTTCGG CAAGGTTATA TTCGGCTTGA

19301   ATTGCCTGAA AGTCCGCTTT AGCGTTGGTG ATGTGGCCAA TAAATTCGAG

19351   CATTTGTAAG GCTGGAGAGG CTCCTTCTTG GGGTTTATCT ACCCAGGGAG

19401   GAGTGCTCAG AAGAATGCGA TCGCCGATTT TGTAAGTGCG TCCGGGAAGG

19451   AGTTCTACTG GAATTAAAGA TTGGGATCCC GACATGCTTG TGTAGGCAAG

19501   TGCTGATGTG GGACTGACTA GTGAGGTGAT CGTTCCTACG AGTGTTGTTT

19551   TTCCTCTTGC GAGTACTTCG CTGATAGTGC CTTTGAGTTT TTGTCCGTCT

19601   CTTGGATAGG GAAGCACGGA GACAATCACG TGGTCACCAT CTAGAGCCCC

19651   GCGTAAATCT CGGGCGGGAA CAAAAATATC AAATGGGTAT TCTTCGGGGT

19701   TGTCGGGAGA AACAAAACCG AAACCTTTTC TAGCATGAAC AAATAGGGTT

19751   CCTGGAATAA AAATCTTCAA GGATTTACCG TATGTTCTTC TCCCTGGTTT

19801   TCTTTTTGGT TTTTTCAACA ATTGGGCTCC GCCTGTAAGT TTAGGACATT

19851   GAACGAGAAA TCCCGTAGTT TCACTCGTGA ACTGAGTGGC TCAACAAAAT

19901   TTTCCCTTTT AAGTGGGTTT TGTGATTATG AAAGGAGCAG TCTCAAATTC

19951   AAAGCCAATT GTACTAAAGA AGCTCTGTTA TTGCAACTCC TTGATCAGAG

20001   AATAAGAGAA TGGAACTGTT TTCTGTTTAT AAGGAAGTTT CCCATCCTCT

20051   TATGAGGATG GGAATAGAGA AACTTAAATT GAAAATTTTG ATTACTTATC

20101   GTCGTTATCA ATAATTTCTA CATCAGCTTC TTCGATATGG TCTTCTGAAG

20151   AACCGTTATT TGAAGGAGGC TTCGTACTGA AACTATGTTT TTTCAAATCT
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15

20201   TCTGTATTGA TGTTAGGTCC ACCTTTAGCA TTGGCTGCCG ATGATGCTGC

20251   TGCTGATGCA GACTGCGATT GCATAGACTC TCCAATTTTT TGCATATGCT

20301   TGCTTAGGTC TTCAGTAACC TCTTTAATTT TTTCAATAGG AGCGTCATCT

20351   TTGAGTGCGT TGCGCACGTT TTCGATTCGC TCTTCGATTT CTTTAACTAA

20401   AGTTTCAGGA ATTTGCTCCT TATAATCTTT AATAGCTTTT TCGGCTCTGA

20451   AGATCATGCT ATCGGCTTCA TTTTTAGCAT CTGAAGCTTC ACGACGTTTT

20501   TTATCTTCTT CCTTATTAAT TTCGGCATCT CGAACCATTC TTTGGATTTC

20551   ATCTTCTTGA AGTCCTGAGC TTGCTTCGAT ACGAATTTTC TGTTCTTTAC

20601   CGCTGGCAAC ATCTTTAGCT GAGACATGGA AAATTCCGTT TGCATCGATA

20651   TCGAAGGAGA CTTCGATTTG AGGATGGCCT CGAGGAGCCG GAGGGATATC

20701   TGTAAGATCG AATCTTCCGA TTTCCTTGTT ATCTTTGGCC ATGGGACGCT

20751   CTCCTTGGAG AACTACGATG GTAACCGCAG CTGGTTATCA GCAGCTGTGG

20801   AGAAGATTTG TTTTTTCTGT GTAGGGATTG TAGTATTTCT CTCTACCAGA

20851   GTCGTCATGA CGCCTCCTAG AGTTTCGATA CCCAGAGATA GGGGGATAAC

20901   GTCTAGAAGT AGAACATCCT TAACTTCTCC GCCAAGAACA CCACCTTGAA

20951   TTGCGGCTCC AATAGCAACA ACTTCGTCGG GGTTGACTCC TTTATTAGGC

21001   TCTTTGCCGA AGAGTTCTTT TACAGTTTCT TGCACTGCGG GCATTCTTGA

21051   CATACCTCCA ACTAAGAGAA CATCATCGAT ATCCTTAGCG GAAAGTTTTG

21101   CGTCACTGAG TGCTTTGATG CATGGAGATT TTGTTCTTTC GATTAGAGAG

21151   GCTGCGAGTT TCTCGAATTG CGCACGTGTG AGTGTCAATG CAAGGTGTTT

21201   AGGTCCTTGT GCATCCATTG TGATGAATGG CTGATTGATT TCTGTGGAAG

21251   AGACTCCTGA AAGTTCTATT TTTGCTTTCT CAGCAGCATC TTTAAGTCTT

21301   TGTAAGGCCA TATTATCTTT GCTAAGATCA ATGCCTTCTT GTTTTTTGAA

21351   TTCTTCGATC ATCCATTTGA TAATGACTTC ATCAAAGTCG TCTCCACCGA

21401   GGAGAGTATC TCCATTTGTA GATAGAACTT CGAAGACGCC ATCACCGATT

21451   TCTAGGATGG AGATATCAAA AGTTCCTCCA CCAAGGTCGA AGACAGCGAT

21501   TTTTTTATCA CCGACTTTAT CGATTCCGTA GGCAAGAGCT GCTGCGGTAG

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21551    GTTCTGGAAT GATACGTTTT ACATCTAGAC CTGCAATGCG TCCAGCATCT

21601    TTTGTGGATG CTCGTTGAGA ATCATTGAAG TATGCGGGGA CGGTGATCAC

21651    TGCTTCTGTG ACAGTTTCGC CTAGATAAGC ATCAGCTGTC TCTTTCATTT

21701    TCATTAAGAT TTGTGCGCCA ATTTCTTCTG GAGTGTATTG TTTGCCATCA

21751    ACTTCGAAAA CGGCATCACC TTTAGATCCG GAGGTGACTG TATAAGGAAC

21801    GGTTTGGATT TCCGAAGCTA CTTCAGAGTA CTTACGGCCA ATAAAGCGTT

21851    TTGTAGAGCC GAGAGTTTTT TCTGGATTTG TCACTGCTTG ACGTTTTGCT

21901    GGAATCCCCA CTAATTTCTC ATTACCTTTG AAGGCAACGA TCGATGGCGT

21951    GGTTCTTGTT CCTTCGGATG ATGTAATTAC TTTAGCTTGT CCTCCTTCCA

22001    TAACAGATAC GCAGGAGTTT GTTGTGCCTA AGTCTATACC TATAATTTTG

22051    CTTGATTTTT TGTGTTCACT CATGTTTGGT ACCTAATCTC TAGGGGTTAT

22101    TTCTATTCTT TATTTTCTTT GGGAGTAGGA GCTTTAGCGA CTTTAACTTT

22151    AGCTACCCGA ATCGGGCGTT CTCCTATTTT ATATCCCTTT GCAAACTCTT

22201    CTAAAATCGT CCCCTCAGGA ACTTCAGAAG TCTCTTCTGT TTGCACCGCT

22251    TCGTGTAGGA AGGGGTTAAA CTTTTGGCCT ATTGAAGAAT ATTCAATAAT

22301    ACCTTTTTCC TCGAAGATTT GTTTGAATTG GTTGAGAATC ATGTTGAATC

22351    CGAGGGCCCA ATTTTTTACA TCGTCGGACA TTTGTGTAGC AAATCCGAGG

22401    GCTTTCTCCA TGCTTTCTAT GGGATTGAGA AAGTCTATTA AAGTATTTTC

22451    TAAAGCATAC TGCATAAGTT CTTGGCGTTC TTTTTGTAAG CGTTTTCTAG

22501    AATTCTCAGA TTCTGCTAGA GCCATGAGAT ACTTATCGTT TTTTTCTTTT

22551    AATTCGGTTT TTAGGGTGAC GATTTCCTGT TGCAAATGTT CAACTTCATT

22601    TTCGTTTTGA ACATTGCTTT CGTGTTGTTC CTCATTTTCA GGTGGGGTAT

22651    CTGTCATAAC GTCTCCTTAG AGGGTAATAG TTTTATAGAA GAGTACTCCG

22701    TTCTTAAAAT AGGCTCATTC GAAAGCTTAC AGTTAGAGGT GAGTGGTCTT

22751    CTGAAGGATA GTTTAAATTT GTAGAAACTT TGTGTCAGGG TTTCATTTAT

22801    TTTATTCGCA AATAGTTTGA GCAAAGGAAG AGCTTCCTTA TAAGGAAGAT

22851    TGATCGGGCC TAGGATACCT AAAGCTCCGA GTGGAGAGCG ATTCATATAA
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22901   TAGGGAATAG TAATTACAGA ACATCCTGGA TTCGAGGTCC CTAAAATATC

22951   AGAAAGCTCC TTCCCTATGA ACGCTGTAGC TCTTCCTTTA TGCATTCCTA

23001   TATTTAGAAG CTCACACATT TGTCTGCGAT TTTCAAAAG AGAGAGTCCT

23051   AGAGCTAGAA CTTCAGGATC TTTAAACGCT TCGTATTTCA GTAGTTTCGA

23101   CATTCCTGTT TGATAGAGAT CTTCTTCACT AAAGTTGCAG TAGCGTGTTA

23151   GATAGCGGAC AACCACCTCA TTATAGAGGG ACATGCTCAG GTGTTCTTCT

23201   TTTTTCGAAA GTTCCTCATT TGTGGGGAGC TTTCGGATGT AGTTCTGCAG

23251   GAATTTTTCT ATACGTTTGA TAGAAAGAGT ATCGCAAGCT TCAGGCAGCC

23301   ATAGGGTGTC TGTGAAGATC TGACCAAACT CCGTAGAGAG GATGGTGACA

23351   GCTCTTTGCT TATCGACCTG TGTAATTTGA ATATTGGTTA CGGAATCATT

23401   TTCAAAGCGT GGGGAAGAAA AAAACGTAGG CAGGTCTAGG ATTTCTCCAA

23451   GAAGTTCCGT AGCTTTTTGT AGATCCTTGA TAATATTGCG ACTTTCGCTA

23501   GGAAGCTGAC TGATCTTATC AAAAATGGGG GCAGAAATCT CAGCTTCTGG

23551   GCATTCTTCT TGGTGATCTA CATAGTGACG TAATGCTAGG TCTGTAGGGA

23601   TTCTTCCTCC GGAAGTATGA TTTTTTTTTA AGAATCCTTC AGCTTCAAGT

23651   TCTGCAAAGT AATTTCTTAT AGTTGCCGTA CTCAAATCAG AGCAAAAACT

23701   TTCCTTTAAA GTTTTAGACC CTACAGGCTG CCCTGTTTTT AGGTACAACT

23751   CTGTTGTAGC AAACAGGATA TCAAGGATTT TTGAATCTCG CTTTGAGACT

23801   TTGGATCTAG CCATCTCGAG TCCTACTAGA ACAATCGTAA CTGAGAGCAT

23851   TATAGGAAAA GAACCCGAGA AGGTCAAGAG AATTTAGCAC TCGAATTGAA

23901   TGAATGCTAA CTTTTTTACG AGGAGGGCAG CGATCAAAGA GCTAGGCTAA

23951   GTGATTCTGA CACCAAGTAG GGAAGGCCTC CGGGGAGACT GTATACTTTT

24001   CTCCAGATCG GGATTCAATT TCGAATATTC CCGAAGATTG GTAGGACTTT

24051   CCTAAAATAA GCTTATAAGG AATGCCGATA AGGTCACTGT CTTTAAGTTT

24101   AAATCCGAGT CTTTCATCTC GATCATCAAG AAGGGGCTCA TAGCCTTGAC

24151   TTTGTAGCTC ATGATAAATA GTTTCCGCAA GCTCTTGAGA TACAGTGTCT

24201   CCTCCGTTAA AGGCGATAGT GATAGAGAAG GGAGCGAGTG CTTTTGGCCA
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18

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24251   AACAATACCA CGGTCGTCGG CAAGCTGTTC TACACAAGCG GCTAATGTTC

24301   TTCCGACTCC AATGCCGTAG GTCCCCATCC AGCACTGCTG GGTTTGCCCG

24351   TGTTCATCTT GGAAGTTTAC CTCAAAACTA TCGGTATAGC GTGTCCCGAG

24401   ATTGAAAATA TGAGCAACTT CTATGCCTTG ATAAATGCGG TAAGGATGGC

24451   CAGGATTTTC AGGACATGTG TCTCCCTCTT CAGCGAGTAG AAAGTCACCG

24501   TATTGGGGGG GGAGGAGGTC GCGATCCCAG TTTACATTTA CGTAGTGCTT

24551   ATCTTTAGCA TTGCCCGCAC AAACAAAGTT CGTCATTGGG GACGTTGTTT

24601   CGTCTGCGAA AAAGTCTATG GGACAGTTTA GGGGACCGAT GAATCCTTTT

24651   TCTGTGCCTA GAACGCGTTC GATTCTTCA TCAGAAGCTA GAGCAATATC

24701   ATCGGCATTC AGTTTGGAAG CGACCTTCAC TAGGTTGACT TGCCGATCTC

24751   CTCTCATTCC AATGGCAATG AATTTTTCTT CATTTGAGTA GGAGAGTTTT

24801   ACGACAAGGG TTTTTAAAAT TTTATGTAAG GGGATAGAGA AGAAGTTTGC

24851   TAGAGCTTCT ATTGTTGTAA TCCCAGGGGT GGCCACTTCT TCGACGGGAA

24901   GAAACTCGCG ATCGTAGGCA TGCTGTGGAG GAATGGAGAC AGCAGCCTCA

24951   ATATTAGCTC CATAGGAACC GCTGACGCAG ATCGTGTCCT CGCCTAGAGA

25001   GCAAAGGACC TGAAATTCCT CAGACTTTCC TTTGCCGATT TTCCCTCCAT

25051   CAGCTGTAAC GATGACATAG GCAAGACCGA GACGATCAAA GATCTTACTA

25101   TACGCAGAGC GGAGTTTTTC ATATTGCTCG TTCATTTGTT CGGGAGAGTC

25151   TGAGAAGGTA TAGCTGTCTT CCATAAGGAG CTCTCGAGAG CGAATGAGAC

25201   CGAATCGAGG GCGAATCTCG TCTCGGAATT TTGTAGCAAT TTGGTAAAGG

25251   TGGAGAGGAA GTTGTCTTTT TGAGGAGAGC CATTGTGCAA CAAAAGAGCA

25301   GATGACCTCT TCATGTGTAG GAGCTAGGCA ATGAGATTTT CCTTCGCGGT

25351   CTTTGAGAGT GTAGAGCAGT CCTTCCGAAG TAAATGCCTC CCATCTCCCT

25401   GTATGTTGCC AAAGTTCAGC ATTGTGGAGA AGTGGGAGTA GAAGTTCTTG

25451   ACCTCCAATC GCATTAAGTT CCTCTCTAAT GATGTTCATC ATCTTGGAGA

25501   CCACGCGCCA TAACAGGGGT GTATAGGTAT AGACTCCTTT ACTTACTTTA

25551   AATAGGTATC CTGCCTTTTC TAGGAGCTCG TTTGAGAGCA CAGCAGCGCT
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25601   TTTATTTGCA  TTTTTTGAAG  TCTTATAAAA  GAGTTGAGAC  GTTTTCATAG

25651   AGTGGGGCTG  TTATCTTCAG  TGATTGATCG  TCAAGAGTCT  ATAGAAAAAA

25701   TTACAGGCTA  TTGCGATTTT  ATATCGAGAG  TCTTTTAAGC  TAGTAGATTT

25751   AGTTTAGCTA  TGAAGGAGGT  ATCTTAACAC  AGGGATTTTT  CTAGATCAAT

25801   GTTTTGCGTT  GGGTTCTTAA  CTTAACAATT  GGGGTCAGGA  TTATGTATTA

25851   TTTTAATTAT  ATTTTTGTTT  TTATTTAGAA  ATTTAATAAT  CTCAACTTAT

25901   AATTAAGTGT  ATACTTATTA  ATCTTTTATT  TTTGTAATTG  TAGTACTATG

25951   TCGTCAGTAA  ATCAAAGCTC  TGGAACCCCG  AATCCAGAAG  AGGTAACTTC

26001   TCCTGAATCT  ACGGAAGAAA  ACAAAAATGT  TGTTTCTTCA  GATGAGGCGC

26051   AAGCCACGCA  TGCTGTGGCT  CTTCCTATAG  TCACTCAACT  TTCTCTTCCT

26101   GAAGGTGTGG  GGACCTCATC  TGAAGAAACG  GCGAGTAATC  CGAGGGTAGA

26151   CGAGATTGTA  GCTGAAGTTT  CTTCGAGTCG  GGCGGTTGCT  GATCAGATCT

26201   CATCACTTGT  AGAGCGTGTT  GGAGAGCTTT  TAGACGACCT  TAAGGGTGCC

26251   CAGTCCCTTT  TCACTAGCTT  TCAGTCAGAG  TTGAAAAACT  GTCTTCCGGC

26301   ATGGAAATCT  TCAACGAGAA  GACTCGAAAC  TCGAGGTGCT  GGGGATAATG

26351   CGGATATAGC  GAGGCTGGAA  TTATTTCGTA  GCGATTACGA  GGCTGTCTTA

26401   GGCCATGCGA  ACCAGTTTCA  TGGGAAGGCT  CATCTCATTT  TAAGTAAGTT

26451   AACAGATGTA  CATCACAAGC  TACAGGGACT  CAGTCGTGAA  GATCTTTCCC

26501   TGGCGTTTGA  CAATAATGAT  AGGGTTCTTG  AGCATCTGGG  TTCGTTAGGG

26551   CTTGATGTAG  ACGCTGAAGG  TAATTGGTCT  CTTTCTTGTG  AGAGGGGGAT

26601   TCCGCGACTG  GTGCTTACTG  CTGACAGTAT  GCTTGTCCAG  ATCAAGAAAG

26651   TGAATCTACC  TACTGTAGAA  GAATTGCGGA  CTCTTCAGGG  AACAACGGAA

26701   TCTTCGTCTG  ATCCTAGGGT  TGAAGAAAGT  TTGTCTTGCT  GTGAAAGATT

26751   GCTCAATGAA  TTACGTCGTC  TTTGGGCGAA  TTTTGTAGGT  TTTATTTCGA

26801   GTTGCTATGA  CAACATCGTG  TTTGTTTTGA  TGTGGATAGT  GAGACGGATT

26851   AACCTTTTGC  CTGGGCTGGG  GTGTTTGCCT  TTCCATAATC  CCGATGCTTC

26901   TCAAGAAGAC  CAGAGGTCTT  CTTCCGGAGA  GCGTTCTACA  AGGAGAGAAC
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26951   GCCTTTCTCG GCGATCTGAC TTATCTGAGG AAGAGATGAT TGTGAGAGCT

27001   GAGGGAGAGT CTATACATCC TGAATCTCCC CATGGAGATG GCCGTAACCA

27051   ACCTAGTCGA GGTGATAAGC AAGACTCTGA TAGTGAGGAA GAGACGGAGT

27101   TATAATAAAG AATGATCTCT TCTGAGTAGA AACTATCGAA TCAGAATTGC

27151   CAGCTTTTAC TCTCACCCAG TCCTATTTTT ATAGTTCAAA TTGCGGTGGT

27201   TTGTTTATTG TTTTTTTGAA TTTTTGTTAT ATGGTGGCGT CTAATATTGC

27251   CGATTAAGGA GGGCGCCCTT TATGAATAGA AGAAAGCAA GATGGGTAGT

27301   GGCATTGTTC GCAATGACGG CGCTCATTTC TGTTGGGTGT TGTCCTTGGT

27351   CACAAGCGAA ATCAAGATGT TCTATTGATA AGTATATTCC TGTAGTCAAT

27401   CGTTACTAG AAGTTTGTGG ACTTCCTGAA GCTGAGAATG TTGAGGATTT

27451   AATCGAGTCC TCGTCTGCTT GGGTACTGAC TCCTGAAGAA CGTTTTCTG

27501   GAGAGTTAGT CTCTATCTGT CAGGTTAAAG ATGAGCATGC TTTCTATAAC

27551   GATTTGTCTT TATTACATAT GACTCAGGCT GTGCCTTCGT ATTCTGCAAC

27601   GTATGATTGT GCTGTAGTTT TTGGCGGGCC TTTGCCAGCG CTACGTCAGC

27651   GCTTAGATTT TTTGGTGCGA GAGTGGCAGC GTGGCGTGCG CTTTAAGAAA

27701   ATCGTTTTTC TATGTGGAGA GCGAGGGCGC TATCAGTCTA TTGAAGAACA

27751   AGAGCATTTC TTTGATTCTC GGTACAATCC TTTCCCTACT GAAGAGAACT

27801   GGGAATCTGG TAACCGAGTT ACTCCCTCTT CTGAAGAAGA GATTGCCAAA

27851   TTTGTTTGGA TGCAAATGCT TTTACCTAGA GCATGGCGAG ATAGTACTTC

27901   AGGAGTCAGA GTGACATTTC TTCTAGCAAA GCCAGAGGAA AATCGTGTGG

27951   TTGCGAATCG TAAGGACACC TTACTTTTAT TCCGTTCTTA TCAAGAAGCG

28001   TTTCCGGGAC GCGTGTTATT TGTAAGTAGT CAACCCTTTA TCGGTTTAGA

28051   TGCTTGCAGG GTCGGGCAGT TTTTCAAAGG GGAAAGCTAT GATCTTGCTG

28101   GACCTGGATT TGCTCAAGGA GTCTTGAAGT ATCATTGGGC TCCAAGGATT

28151   TGTCTACATA CTTTAGCGGA ATGGTTAAAG GAAACGAACG GCTGCTTAAA

28201   TATTTCAGAG GGTTGTTTTG GATGATTCAT GGATCTTAGA GGTTAAAGTC

28251   ACTCCAAAAG CCAAAGAGAA CAAAATTGTA GGCTTTGATG GACAAGCTTT
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28301   GAAGGTCCGT GTTACCGAAC CCCCAGAAAA GGGTAAGGCC AATGATGCTG

28351   TAATTTCTTT ATTAGCAAAA GCTTTATCCT TACCGAAGCG TGATGTCACT

28401   TTAATTGCAG GAGAAACTTC TCGAAAGAAA AAGTTTCTTC TTCCTAACAG

28451   AGTTCAAGAC ATTATTTTTT CTTTGCATAT AGACGTATAG CCTAACTCAC

28501   AGCTACGTTT TTCCCTTTCT CAGATTTTTC CAATTTTTTG CTTTTAAAAG

28551   ATAAGAACTG GTTGCGTTCT GTTTTATGAA GCTTGATTCC TAAGTACTTG

28601   ATGATATCTT CATTAAAGGT GGTTGTAGGT GACAGGCGTT GAGCAATGAT

28651   TTTACGCAGG CTGTCCACAT CGTGATTGTT ATAGAGTAGG TGGTGCACAA

28701   TTTTTGCGAT TTGTTTTCCT GATTTTTTGT AATCCACGCT ACAGGCAATG

28751   CAGGCTCCTT CGGAAATTAA GGAGGTATCG TCGGTAATGA TAGGGATTTT

28801   CTCTTTGAGG ATTTCCTGAA GGAATGCGGT GCCTTCTTTA TGAGAAAGTG

28851   GGGAGAGGGG AATGAAGATA GCTGAGGGGC GCTTGTCGAT AGCCTGGCGT

28901   ATCCGGGTTT TGAATGTACT GCTTGTAATA GAGATCTCAA TGACCTCAAT

28951   TCCTGAAGCA TGGAGTTTCT TAACAATTTC TTTTTGGAGA TCTGAGGGGA

29001   AAGGTTCGGA GGGTTTTAAA TACACGATAG ATTGTGCATT GGTAGCTACG

29051   GCTTGTATAG CAAAGCAGTA TTGATTGATG TCTAGAGTGT CATTCACTCC

29101   GTAGATATTC ATTGTGTTTT TAGGAAGGGT TAGGCTTTCG CGATCAGGAA

29151   CAGCGGCATA GATCACAGGT TTCTGTGTTT CAATGTGGCT CATGACCTTC

29201   GTAGCAATAG TTCCTAAGGT GACAATCGCC ACGACATTTT TATCGGTATG

29251   TAAGGAGCGA GCAATTTTCC TAGCCTTTAC GATACTGTCT TCAGCATTTA

29301   GGACAACAAT TTCAGGAAGG TTCTCAAAAT CTTTCAAGGT TTCTATACAG

29351   CTTTTACTGC AATCTTCTAA TAGGGGATGG GGAAAGGATA AGAAAATTGC

29401   GATTTTAGGA GAGGAGACGC TATCTGGTTG AGAACCACAA GTGGCTACAT

29451   AGATGAAAGA GCAAACAGA GAAAGAAAA ATAAGTACTG AGAGAGTTTA

29501   CGTAGAATTG TCATGCAAGA ACCATCGTTT CTTTTAGTGA AGCGGTACAG

29551   AGGCGGTCAC AGGCTAAAGC GATATTTTGT GGTTGTGTCA GAGCGGAGAA

29601   ACGAACAAAT CCTTGTCCAC AGGAACCAAA ACCGTGGCCG GGAGTCACTG
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22

29651 CAATATGATA CTGATGTAAG AAGAAATCAA AGGCTTCTTC ATCAGAGATT

29701 CCTTCAGGGA GTTCTACCCA AAGGTAAGGG GCATGATCGC CACCATGAAC

29751 TGAGAATCCT GCAGTTTCTA AGCTTTTTTT AAGTTTCTGA GCATTGGTTA

29801 GATATAAAGA GATGGCGGGA GGTGTCGGAA ATAAATCTAG GCCGTAATAC

29851 CCTGCTTCTT GCATGAGGAG AGATGCTCCG TTAAATGTAG TCGCAAAGAG

29901 CCGTTTCCAA TCGTTGATCA TAGGTTCGTT ATTGTCATAG GTGAGTTCTT

29951 TAGGGATCAC GTTCCAGGCA AGGCGCATGC CAGTAAAGCC TAATGATTTA

30001 GAGAAAGAGT TGATTTCTAT AGCACAATAT TTTGCTTCAG GGATTTCGAA

30051 GATGCTTTTA GGTAGGCTAG GATCTGAGAC AAAGGCGCTA TAGGCCGCAT

30101 CAAAAATAAG AACGGTTCCG TGCTGATTCG CGTAGTTCAC AAGTGCTTGG

30151 AGTTGTTGAA AGGTTAGAAC TGTTCCTGTG GGGTTGTTAG GATAGCATAG

30201 ACAAAGAATG TCTAGGGATT GTTGGTTCGG AAGTTCTGGA ATAAACCCAG

30251 TTTCTTTTCT GCATGCTAGG GGGATAATGT CGCGGATTCC TGTAATGTGG

30301 GCAATGTCTC TATAAGCTGG ATAGACAGGA TCCTGTAGAC CTAGAGTCTT

30351 TTCTGAGCCA AAAAAAGAAA AGAGACGGAA GATATCAGGT TTGGCACCAT

30401 CCGAAATAAA AATCTCTTCA GGGGAGATTC TATTTTCATA GACTTCAGAG

30451 GCAATTTTTG TGCGTAATTT TTCTAATCCG GTTCTGGGC CGTACCCACG

30501 ATAGGTCTCT TGTTTCTCTT GAGAAACGCA GAACTCTTTG ATTGCCTGAG

30551 TAATAGAGCG GCAGAGAGGT TGTGTCGTAT CTCCGATAGA AAGATCTATG

30601 ACAGAGATTT CTGGATTCTC CTTGCGAAAC TGAGCAAGCT TTTTACTAAT

30651 TTCAGAAAAT AGATACTGAG GCTTGAGAAG AGAAAAGTGG GGATTTCTAC

30701 GCATAGCGTG CTCCAGGTAA GGGCGTGATT CACTTGGAAG ACATCTTAAG

30751 AAAGCCCCAG CTTTTTGGAT AGCCATTTTC TGATTTTTCT TTAACCGCCT

30801 CTATAAAGGC AAGGAGTGCT CTGTAGTTTC GGTTAATTAT TAAGATATAT

30851 TTATAATTCT GTTTATTAAA AGTTTTTTAA ATCTTTTCTA ATTTGCTCAC

30901 TATAATTAAA GGATAAGATT TGAAAAAATT TTTTAGGTAA TTATGATAAG

30951 GGTCAATCCT TATGGAAGTT ATAGGGGTAG GAATCCTTCT CCAGAAGATG

23

31001   GGAAAAAGGA TGTACCCCTT TCAGGGAACT CTCGCTTGCA TCGTCGTGGT

31051   GGGATTCGTA GAAAGCATAA GAGTGCTTCA GTTGGGGTGA CCTCGGGTTC

31101   TAAGACGGGG AAAGCTTCTT TAGAGAAGAA GGTCAAAGGC ATTTCAGAAG

31151   CCCATTTCAA ATAATCCAAG ACAGAAGGTT CTCATTCGAA GACAAGCAAA

31201   GGATTCGTTG GCAGATTTGT TCAATGGATT AGAACGTTTA CAGGACGTGG

31251   AAGCAAGAAG CGTTCTCCCT CAAGTTTTTC TCCAACGCAC CCTTACATAC

31301   GTTTGCGAAC TTACACACGC AGTCCAAAAC AGAGTGGTGT AGAGAGAAAA

31351   CAAGAAGATG CTGAGACCTC ATTTATAGAG ACACCCAAAG GGATCTTGAA

31401   AAAGCCTGGA AACAAAGACC CCAAAGGCAA GCACGTCCAT TGGAAAGACA

31451   GCTAATCCGG ATCAGAGCTG AGATCCCTCC TTCTCTTCAT TAAGAGGGTT

31501   CAGAGTTTTA GGTCTCTGCG GTAGAAGGGA GGGAATCCAT AAGGAGAAGA

31551   CCAGTGGATT TTCAACGGAG ATTCTAGAAG GAAACAAGCT GATTCTACAT

31601   GGAGATGTTT GTAGGTCTGT TGTGAATTCC TCTCTTCACA GATCGGAAAG

31651   ATCAATGAAA AGAGTTAGGG TCTCTTAGTT TTAAGAATTG CTATACAATA

31701   TTGCGAAATA AATACTTTCT TCTCTATACA CTGTCTTTAC GATGAAGACA

31751   GCTTTTCACT CTTGCTATTC TTGGTTTTGT TGGCTCTTTA GCTTCTTGGT

31801   ACTCTTTGTG GGTGGCATCG CTGGGGGAGA GCCTTTGTGC CCCGATTGCA

31851   AATACGAAAC TAAGTCTGTT TTACGTTCGG ATCAGCTGCC GGATCATCTC

31901   TGGAACTATG AAAACGACTG TTATCTTACA GGTTATGTGC AGTCTCTTTT

31951   GGACATGCAT TTTTTAGATA GCCGTACGCA AGTTGTTATT GAGAAGAATA

32001   GAGCGTATCT TTTCTCTTTG CCTGTAGATT CGAGTTTATC AGAAGCCATT

32051   ACCAACTTTG TTAGGGATCT TCCCTTCATA TGTGCTGTGG AGATTTGCGA

32101   GCGTCCTTAT GGTGAATGCA TAACGAGATC TTCTGCGGAG CGTCCCTTAC

32151   TCCCTAAAGA GAAAACTTTA GGAATGCCAA TTTTCTGCGG CAAAGAAGGG

32201   GTATGGTTAC CTCAAAATAC CATTTTGTTT TCTCCTTTGA TTGCAGATCC

32251   TCGTCAGGTT ACCAACAGTG CTGGCATTCG TTTTAATGAG AAGGTCGTGG

32301   GGAATCGGGT AGGTGCTACC ATCTTTGGGG GAGATTTTAT TCTCCTGCGT

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32351   CTTTTTGATG  TTTCTCGATT  CCATGTAGAT  TGTGATTTCG  GAATTCAAGG

32401   AGGAGTCTTC  TCAGTTTTTG  ATTTAGATCA  TCCTGAATCG  TGCATGGTAA

32451   ATTCAGATTT  CTTTGTTGCC  GGACTCTGGT  CAGGGGCTAT  AGATAAATGG

32501   AGTTTTAGGT  TTCGATTGTG  GCACCTCTCG  TCCCATTTAG  GAGATGAGTT

32551   TATTCTTACG  CATCCAAATT  TCCCAAGATT  TAATTTGAGT  GATGAGGGCG

32601   TCGATCTCTT  CATTTCGTTT  CGTTACACAC  CACAGATCCG  CTTGTATGGC

32651   GGCTGCGGTT  ATATTGTAAG  TAGGGATCTT  ACTTTTCCTG  AGCGGCCGTT

32701   TTACTGTGAA  TGGGGTGCGG  AACTCAGACC  TTTTGGTCTG  AGAGAAGGAA

32751   ATCTCCACGC  ACAACCGATT  TTCGCGATGC  ATTTCCGTTG  TTGGGAAGAA

32801   CAGAAATTTG  GCTTGGATCA  AAGCTATATT  TTAGGCATGG  AGTGGGCCAA

32851   ATTTCAAGAA  ATCGGAAGGA  AAATCCGTGC  TGTTTTAGAA  TATCATCAGG

32901   GATTTTCTAA  AGAAGGCCAA  TTCATTCGTG  AACCGTGTAA  TTACTACGGT

32951   TTCCGTCTTA  CCTATGGATT  CTAAACGATA  ACAAAACCAT  CTTCAGGGAC

33001   AGGGTGTTCA  GGTCCTATGG  GCAGCGTATG  ATTGAGATAT  CTGCGGAAGA

33051   TTGCAATGCC  TGCCTTTGCT  GAGGATAGGC  AGAATAGGCA  GTTGTGTACC

33101   CATTCAGAAC  CTCGAATGGT  TCCTACAGCA  TGATTGGAAT  TATACAAAGC

33151   TGTGATCTTG  GATTTCCAAT  AGTCTACAGG  TCCGATTAGG  AAGACGGGAA

33201   CAAGAGCTTT  TTTCCCTGTT  TTGAGACTAA  TAAGCTCCAG  AAGGAGTTCG

33251   AAATCGGTTC  CCATGCCTCC  GATAACAAAT  ACAGCAAGGT  CGACATGGAA

33301   GTCGGCCTGA  CGTTCTAAAA  GATCAGGAAT  AGCATAGCTC  ATTTTAGCTT

33351   CTACATAGGC  ATTCGTGGTA  TCCAAGCTAA  TTAGATTCCC  ACAAGAGAGT

33401   ATGGAGAGTT  CTGTAGCTAC  ACGATTCGCG  AGTTCCATAG  CTCCAGAACC

33451   CCCTCCTGTA  AGGATTGCTA  ACGGTGTCTG  TGGTGGAAAT  TCTGGGATCG

33501   TGAATTGCTG  AGAAAGAGTA  TGCATTCCTG  TCAGGAGCTC  ACGGAGAAAC

33551   TCATCATAAT  CCCCAGCGAT  TAGGCAGGAA  CCATGAATTC  CTATAAAGTA

33601   GGATTGAGCA  AACTGTTCAG  CTTGATGTTT  AGGGACAAAC  ATGCCCACAT

33651   CTTTATTTCT  GCGTTTGATG  TATTGTAAGA  GTCGTTCGA   TTCTAAGTCT
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33701 GCCCAAAATA CAGAAATTCC TGCAAAATAT AGATCGAGAA GGAAAGAGCG

33751 ATCTCGATTC GAGAAAAACT CTCCAGAAGT GGGAGAGGGA ATCTGAAAAT

33801 AGATATGTTG CAGGTAATAG CGAGAGTAGT TAGAGAGGAA CATGCCCTTC

33851 AGCGATGCTG AAGGGAAGTA GCGGGAAAAT AAAACTCCTT GGCTTGTGAT

33901 ATGATCTGTT TCCATGGCTT TTAAAAAAGG GAAACAAGGT TGGTCTTCAA

33951 TGTGCTTTTG AATTTCCCTA GCATGTCTTT CATCTGATGG GGAGATTCGA

34001 GGTTTGATGA TCCAAGAGTC TTGGGAGAGC TCAAGCAGCT CACTACCTTT

34051 GGAGATAAAC ATCGCAGCTT GATCTTCGCC TTCCGGTATG GATTCAAAAA

34101 CACGAAATAC CTCTTGAGGA GATTCTAAGG TTTCCTGGAG CATATCTCTA

34151 TAGAAGAAAA ACGAATGCTC TTTGTAAGGC TCAAGAGTAA AAAATTCTAA

34201 AGGTATTCTC TCAATAGGTT CTGAAGTGCT GCCGTAGAAT TCATAAATAT

34251 CTCCAGATTC TTGTGTGGTA GGTTCGAGAA TATCCGCTGC GGTGTGACGA

34301 AGCCCTTGGG GGAGTAAGTC CTGAACGACT CTTGCAAATA CGGTTCGGAT

34351 GTGCAGAGGC TCTGTCTTTA TGAGAAGAAT TTTATGATCT TCGGGAACGG

34401 GAGGACGATC TGTTACCATT TGATACAAAG GAAGAAACTT ACGTATTTTT

34451 AAATGGGGAC GCGTGAGTGA TTTGCTCATT AAGGGAAGGA ACCCATAAAT

34501 TGTCTCTTCG TAACAGATTG TTCCTGGAAG GATCGGAAGG AAGACAACAA

34551 GCCGATCATT AATGATCTCT AGAGTGATGA AGTGCTCAAG TTTTTTCCCA

34601 AAGCGTAGGA GCGGAGATCC TGTACGGTCT GTGTGCGTAA ACATCCTGTT

34651 GAGATAACAA GGCGAACGTA CGAGTCGGCG ATCATCAGCA GCAAAGAGCT

34701 TGCAGACAAA ACTTCCAGGC TCTAGGAGCT CCAACATAGC AGTGGCTATA

34751 GGATCTTGGC TCATGAAGAG AACGTGTAGA CGAGCTTCTT TTCGGGCTTT

34801 ATTTAGCTCC AAGTGGTTTA AAACGGCTTC GACACCTAGT TGGGCTAAGG

34851 AACTTTTTAA ATTTACTTGT ATACACTGTT GAGGCAGATG AAATCCAAGA

34901 AAGTACGCAG GAATATTCTC AATGAGGACC TCTCCTTCGT AAATGTGGGG

34951 CGAGAGTTTT TTCAAATGGG AAACGAGTCG TCCGTCTGGG GAGGCTGCAT

35001 CATGATGCGC GTGGAGTAGG TTATACATAA TTCATCGTAT TTTAAAGTTA

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35051    AAAGCAATAG GTAAGGTCCC TCTTTGCGCT TCTAAGACTA GCGTTTCCAG

35101    AAGAATTTCC TACAAGGACT TCATTCTGCT TGTTGTTATA ATTTTGTGCA

35151    ATTTGTCAAG GAGGGGGTCT TGGAACGAGA AAATTGTGTT GTGGAAGGGA

35201    ATTTTAGGAA AAAAGTTTCT TAGAAAATAG GGCAGAAACT TTCTCTTGGA

35251    GAGATTGAGT AAAATGTAAA GAATAGTCTT TGCAATTGAG AATTATTTCT

35301    CTCTGGTTAC AATGGAGGAT TGGCTAAGGA GGATAGTAGG TATGCAGATT

35351    CCAAGAAGCA TTGGTACTCA CGATGGTTCT TTCCATGCGG ATGAGGTCAC

35401    AGCGTGTGCT CTCCTTATTA TTTTCGATCT TGTGGATGAA AATAAAATTA

35451    TACGCTCTCG AGATCCTGTC GTATTATCGA AATGTGAATA TGTTTGTGAT

35501    GTCGGTGGTG TTTATTCTAT AGAAACAAG CGTTTTGATC ATCATCAAGT

35551    CTCTTATGAT GGATCTTGGA GTAGTGCAGG TATGATTCTG CATTATCTTA

35601    AAGAGTTTGG TTATATGGAT TGTGAAGAAT ATCATTTCCT TAACAACACT

35651    TTGGTACATG GTGTGGATGA ACAAGATAAT GGCAGATTCT TCTCTAAGGA

35701    GGGATTTTGT TCGTTTTCTG ATATTATTAA AATTTATAAT CCTCGCGAGG

35751    AAGAAGAAAC TAATTCGGAT GCGGATTTTT CTTGTGCTTT GCATTTTACC

35801    ATCGACTTTT TGTGTCGGCT AAGGAAGAAG TTTCAGTATG ATCGAGTTTG

35851    TAGGGGGATT GTCAGAGAAG CCATGGAAAC CGAGGATATG TGTTTATATT

35901    TTGATCGTCC TTTAGCATGG CAAGAAAATT TCTTTTTTTT AGGGGGAGAG

35951    AAGCACCCTG CAGCTTTTGT TTGTTTTCCT TCCTGCGATC AATGGATTTT

36001    ACGAGGGATT CCTCCGAATT TAGATCGCCG TATGGACGTT CGTGTTCCTT

36051    TCCCTGAGAA TTGGGCAGGT TTGTTAGGTA AAGAGTTGTC CAAAGTATCA

36101    GGGATTCCTG GGGCTGTGTT CTGCCATAAA GGTCTTTTCC TTTCTGTATG

36151    GACAAATAGA GAAAGTTGCC AACGTGCTTT GCGGTTAACG TTACAAGATC

36201    GAGGGATCAT ATGACAGTAT TCAAACAAAT TATCGATGGA TTGATAGATT

36251    GTGAAAGGT ATTTGAAAAC GAAAATTTCA TAGCTATAAA AGATCGTTTT

36301    CCTCAAGCTC CTGTTCATCT TCTTATCATT CCTAAAAAAC CTATACCACG

36351    ATTTCAGGAT ATCCCAGGGG ATGAGATGAT TTTAATGGCA GAGGCTGGAA
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27

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36401  AGATCGTGCA AGAGCTTGCT GCAGAATTTG GAATTGCCGA TGGGTATCGT

36451  GTGGTTATCA ACAACGGTGC TGAAGGAGGA CAGGCGGTAT TTCACTTACA

36501  TATTCATCTT TTAGGTGGGC GTCCTTTAGG TGCTATAGCC TAATTTTCTT

36551  TTGTTTCTGT GGATCCTTGT TCGGCTCGGA GTCCCTCCGT TATCAATTGT

36601  TGATCCAAGA TTTTGCAAAA GTTTCAGAAG AGGGCATAGG CCTTTTGGAG

36651  TCTAAAGAGT ATTCTTTACT TCAGGCTAAG CTAGTTTTAA GGGCTCTGGC

36701  TCAAAATTCT TCTTTTGATG ATTGGTTTAG AAGTTTTAAG AAGTGTCAGA

36751  TTTCCTATCC AGAGTTAGCT CATGATCGCG ATGTCTTAGA AGAATTTGGG

36801  ATTCAAGTTC TGCGTGAGGG AATCGAAAAT CCTTCCGTGA CCGTTCGTGC

36851  TGTGAGTGTC CTTGCTATTG GGCTTGCTAG AGATTTTCGC TTGGTCCCTC

36901  TCCTGCTCCA AAGTTGTAAT GATGACAGTG CTATTGTTCG ATCTTTGGCT

36951  CTTCAGGTTG CTGTGAACTA TGGCTCTGAA AGTTTAAAAA AGGCCATTGT

37001  AGAGCTTGCC CGTAATGATG ATTCTATTCA TGTTCGGATT ACAGCATATC

37051  AGGTGGTCGC TCTTTTACAG ATAGAGGAGC TATTGCCATT TTTAAGAGAG

37101  CGTGCTGAGA ACAAACTTGT AGATAGTGTA GAACGTCGAG AGGCGTGGAA

37151  GGCTTGCTTG GAACTCTCTT CTCAATTTCT AGAGACGGGT GTAGCTAAGG

37201  ACGATATTGA TCAAGCGTTG TTCACTTGTG AAGTGTTGCG TAACGGTATG

37251  TTGCCAGAGA CTACTGAGAT TTTTACAGAA CTCTTATCTG TAGAGCATCC

37301  TGAAGTGCAG GAGTCTCTCT TACTTTCTGC TTTAGCTTGG AGTCATCAGC

37351  TACAGAATCA CAAAGAGTTT CTTAGTAAAG TGCGCCATGT GATGTGCACT

37401  TCTCCATTTG CAAAAGTACG TTTTCAAGCT GCTGCACTTC TCCATCTGCA

37451  TGGAGACCCT TTGGGCAGAG ACTCTCTGGT TGAGGGCTTG CGCTCTCCTC

37501  AACCTCTTGT GTGTGAGGCA GCTTCGGCGG CTCTCTGCTC TTTAGGAATC

37551  CATGGAGTCC CTTTGGCAAA GGAGCATTTG GAGAGCCTTT CTTCTCGAAA

37601  GGCTGCTGCG AACCTCTCCA TTTTGCTTCT TGTGAGCCGT GAAGATATTG

37651  AAAGAGCTGG AGATGTGATT GCTCGCTACC TCTCCAATCC TGAAATGTGC

37701  TGGGCTATAG AGTATTTCTT ATGGGATGCA CAATGGAATT TACGTGGTGA
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28

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37751   TACCTTCCCT CTATATTCGG ATATGATTAA ACGTGAGATT GGTAGGAAGC

37801   TCATTCGCCT TTTGGCAGTA GCTCGCTATA GCCAAGCCAA GGCTGTAACA

37851   GCAACGTTCC TTTCAGGACA GCAAGCTCAG GGATGGAGCT TTTTTTCTGG

37901   AATGTTCTGG GAAGAGGGAG ATGTGAAAAC TTCTGAGGAT TTGGTTACAG

37951   ATGCTTGCTT TGCAGCAAAG TTGGAAGGAG CGTTAGCCTC GCTATGTCAG

38001   AAAAAAGATC AAGCTTCCCT ACAGAGGGTC TCTCAACTTT ATAATGACAG

38051   CCGTTGGCAA GATAAATTAG CAATCTTAGA GAGCGTTGCT TTTTCTGAGA

38101   ATCTTGATGC TGTGCCTTTT CTTCTAGACT GCTGCCATCA CGAAGCTCCT

38151   TCGCTGCGAA GTGCAGCAGC GGGTGCTCTT TTCTCTATTT TCAAATAAAT

38201   ATTAATAAAA TTATTCAAGA TATAGAAGAA AAACCACGCA GTTGTAATTT

38251   CTATTTCTTA AAAATAATTT TTCAGACTGA CTTTATTCTT TCATTTTTAA

38301   GTCTTTGGAG ATAGAAAACT TTGTTATAGA TTTTTATCTG GTAGCTTTTA

38351   TAATTTATGA AGAGCGTAAG CTCAGAGCCT GTATGTCATG CACAACCTGT

38401   ATATAAAATC AGATTTGTTT TTTGAATCTC TATTCTCGTT AAGATTTCGT

38451   TATTCTGGAC GTTATCTCCA TCACCACTCC TAATTTTCCT AGCATTTCTA

38501   TCTTTAAGCT CAGCACCGTA GCTTGCTTAA AGGAAATATT TTTCATTTAG

38551   GTTGTGGAGT TCTTTATTTT ATGAATTTTT CATTATTTTT ATTTTTCCTG

38601   ATAGCTATTC AGGGAATCTG CTTGTACGTG GGACGTCGTG GTAGCAAAAA

38651   GGTAGAAGAT CGCGAGAGCT ATTTTCTTGC AGGAAGGAGT TTAAAAATCT

38701   TTCCTTTGAT GATGACATTC ATTGCCACCC AAATCGGTGG CGGTGTACTT

38751   CTTGGGGCTG CTGAAGAGGC CTTCTGTTAT GGTTATGGGG GGATTCTTTA

38801   TCCTTTAGGA GTCGCTTTAG GGTTGATTTT CTTAGGAATG GGGCCCGGGA

38851   AGCGGTTGGC AGAGGGATCG TTAACGACCG TAGTCTCTAT CTTTGAAGTG

38901   TTTTATGGTT CTAAAAAGCT CCGTAAGATC GCATTTTTAT TATCCGCAGG

38951   TTCCTTATTT TTCATCCTGG TCGCTCAGGT GATTGCTTTA GATCGGTTGT

39001   TTAGCAGCTT CCCTTTTGGC AAGTACGTAA CCGTAGCATT TTGGATTGTC

39051   TTAGCATCCT ATACCTCAAC AGGAGGGTTT CGCGGGGTCG TACGTACTGA
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39101  TGTGATCCAA GCAGGATTTC TTCTTATTGC GGTGCTCGTC TGTGGTGTTT

39151  CTGTATGGCT CTCTGTCCCT AAATCCTTGT CTGTGTTGGA TCCTTTCCAA

39201  TCACTTCCTT GTGCGAAGCT TTCCAATTGG ATATTCATGC CTATGCTCTT

39251  TATGCTTGTT GAGCAGGATA TGGTGCAAAG GTGTGTGGCT GCCTCCTCTC

39301  CAAAACGCTT GCAATGGGCG GCTGTAGGCG CAGGCCTTGT TCTTCTTCTT

39351  TTTAACTTTA TCCCTTTATT TTTAGGTTCT TTAGGAGCTA AAGCAGGCCT

39401  TAAAGCAGGA TGCCCTCTGA TTGATACCAT TGCATATTTT TGCAATCCCT

39451  CACTAGCAGC TGTGATGGCT GCTGCCATCG GCGTTGCGAT TCTCTCTACC

39501  GCGGACTCTC TTATGAATGC TGTAAGCCAG CTAATCGCTG AAGAATACCC

39551  TACGTTGAAA GCCCCTTATT ATCGTTATTT AGTATTGGGT TTGGCGGTTG

39601  CAGCTCCTCT TGTTGCTATT GGTTTTACAA ACATCGTAGA TGTCTTGATT

39651  TTAAGCTATA GCCTGTCAGT GTGTTGTCTT TCAGTCCCTG TGGGTTTCTA

39701  TCTTCTAGCT CCTAAAGGTC GCCGTGTGAG CGGAGCTGCT GCTTGGGCAG

39751  GAGTGCTCGT TGGTGCTCTG GGCTATGGAT GGGTTCAGAT AGTCTCTTTG

39801  GGGATGTTTG GGGAGCTATT GGCTTGGGTA GGTTCTCTAG TCGCCTTTTC

39851  CTTTGTAGGA TTTATTGAGA TCACTTGGAA AAACAAAGTC AAAACGCAAA

39901  CTTAGATAAC CACTGCATGA GAAGATATAA CTAAAATAGA TCCTGAGTTG

39951  TTTAGGTTTC TCTTAGATCT GATAGGTTGC GCTTAGTAAG AGATCGTCAG

40001  TTTTTTAAGT TGTGTTTAGA ATCTGATACC TCTCCTTCTT TTCCAAGAAG

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40101  GTTTTAACTG ATAGAGCAGG TCGATAAGAG AGGAGAGCAG GGCTTGATAG

40151  AGCGTCTCTT CAGAATGGTG AAGAGTGCCC TTAAGAAGCT TTCTGCAATA

40201  CTTTAATAGC CAATACAGAG CGCAAAGTAA ACACTGTAAA AGGTAAAATT

40251  TACACGCTTG TTTTATCATA AACCTCCAAA GAAAGACGCG TGTTGGCGTT

40301  CTTCCAATTG GCTGTTAGAT AGTGAAAATA GTATTACTA TTCAATAAAA

40351  ATATTTATAT TAAATATAAT AAAACAAAAT TTCTAATAAA CTTTTTAAAA

40401  GTATTTGGCT AAGTTTAATT TAAGAGTTCT CAAATAAAAG ATTTTTTAGT
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40451    CTCTTTTATT TGAGAATCAT CAACCGATTT CAAGAAATCG CATGAGCCCG

40501    TGATTCTGAT GGGCAGAAGT GCTTTTTAGC AAATAGGTGA AGCTCCTCGG

40551    GCGTGATCTG TTGCTTCGCG TCACAAAGAG CCTTTTCAGG GTGTGCATGC

40601    ACTTCGATCA TCAGACCGTC GGCACCTACC GAGAGACCAG CAGAGGCGAG

40651    AGGAAGAACT AGAGAACGCT TCCCCGCTGC GTGGGAAGGA TCTACAATTA

40701    CAGGGAGAGA AGAGATCTCT TTAAGGAGAG CCACGGTATT GAGATCTAGC

40751    GTGTAGCGCG TAGAGTGCTC AAAGGTACGA ATTCCTCGTT CACAAAGGAT

40801    TACCCCAGGA CAGGAGGGAG AAGAAGCAAG GATGTACTCC GCTGCGCATA

40851    GCCACTCTTC AAGAGTAGCT GCTGGACTGC GTTTTAGGAT AATCGGACGA

40901    TGTGATTTGC TGACCTCTTG TAAAAGAGGG GTGTTATGCA TGTTTTTGGC

40951    TCCGATACGG AGGATATCCA CATGTTCGGC AGTAATTTCA ACATCTCGGA

41001    CATCTAAAAC TTCGGTTTCT GTAGGGAGAC CATGGATGCT CTGTGCTTCC

41051    TTATGCCAAA GCACACACTC TTTCTCCCAT CCTTGAAACG AAAATGGGCT

41101    TGTCCGTGGT TTTCTGATTG ATCCTCGGAA TACCTGAGCT CCTGCTTCTT

41151    TAACTGTAAG AGCTGAAGAG ACTGTATGCT CGTAACTTTC TAAGGTGCAG

41201    GGGCCTGCGA TCAGTATTGG CGATCCTTCT CCAAACGATA GATTTGGAGA

41251    AATAGGAACG GTATGGACCT CGTCAGGATG CTGTTTGAGG GTGCGCGGTA

41301    GGGGATAGGT AAACGTAAGA ATAAGTACCT CATGCAAAAC TAGGGATTTG

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41501    TATTTTCTTC TGAGACAGTA TCTCGATCAG ACATGATCAG ACAAACAGCA

41551    AACGGCTGCA AAGGTACAGT AGTCATAGCA GCGACGTCGT TAGCCTCAGC

41601    TTGCTCTTTG ACGTCATCCA AGATATCACC GAGTTCATTA GAACTTAGGG

41651    AGTGGAGGTA GCCTATCAGT GATTGTCTAA AACCAGAGCG ACAGAAACCA

41701    TCAGATGCTG TGACCGTGTT TTTTAAGAGA TTACAAATCA ACTGATCTCG

41751    AGCTCTAGAG TATTGATTTA TAGTCGCTGT AGCTAGAGGG AAACCGTATT
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41801  TTAACGAAAG TAAAAGCTTA TCTTTTACTT GTGTAAATCT ATGAGAAGCC

41851  TCTCTTTGGA AAGCGTCTAA TCGAGCAGCT AGCGGAGTCT TTTTTTGTAG

41901  AAGTTTAGGG TAGTTGTTAA GGAAACAAAA GATTAAAAAA GATTTCGAAA

41951  ACTGATCACT TAAAGCTGTG GGAGAAGAAG GCGAACCCAG TTTTGATCCG

42001  AAGAGATTTA ACCGTGTTAA AAAAACGTTC CACCCATTCC TAAAGGTACT

42051  TTCGATTTCT TTTTCTAAGA GTATGGCCTC GGTTTCCAGT TGATAATTTG

42101  GGAAAGTAGC TCGTAGAAAC TGCATACAGT TCTTTTCAAG TATGGGATCT

42151  AAAACCATCA CTTCAGGATG TCGTGACCAG AACTTGCAGA ACGTCTCTTT

42201  ATCTTTATTA GAAGGGGTTG AAGGATAGCG TGCTGGAGGC TTGAGTACTA

42251  GAGACCCTAG AATGGAACGT AGAAGTTTTT GGAGTTTCTT TTCGTTTTCT

42301  ACTTTTTTAA AGGCATATTG TAGAAAAGGA AGTAGAAGCA TTTTTAACTC

42351  TTTAACGGCA TCTTTAGTTT CTGGACGATT ATTCACTTGA GGATGCTGTA

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42451  TGTGAGAGAC CACTGCCTTC ATCACGCGTT AAACGTAAAC TTCTTGCCGA

42501  GCAGACAGTA TTGAAGTGCT CTTTTAATTC AAGCTTACTA TGAATTGCGA

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42801  TATTTGTAAG ATCTCTTGTA TAGAGCGTTG GGGGGGCGCG GACGCTATAA

42851  TGATATCCTC TAATGATTTG TAGAAAGTAG CGCAGAGTTT GTGAAATCTT

42901  ACAGAGGGGC AGGTACATAG AAAAGCAAAG AAAGAAAGAG CTGGAGACCA

42951  AGGGAGATCC CCAGATCGTC TGTTTTCTAT AGTTGCAAGA AAGCGAGAGT

43001  ATTGACATCG GATTGCTTCA GGGAGGTGAT CTTTGACTAT AGCATTGAAT

43051  CTCTCAGTAT CCCACCCTGA ATCAGCAATG CGTCGACTCA GCTTAGCAAA

43101  AGCCTCTCGT ATTTCTCTTT CATATTGCTT TCGAAGTTGT TGATCTTCTG
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43151   GAGACATCTT TTGAAGCTCT GCATCAGTAA GAAAGAGAGC GGGCAGATGT

43201   TCCAAGAGAA GAAAGAGTTT GTCTCTAGAT TGCATGTAAG GAAGTGCGGA

43251   ATGATCAATG AGATTTTGGA ACAATTCCGA ATAGGGACGA TTTGCAGCAA

43301   GAAATTCCAG AACACTGGGG AGGAGATCGT CCTGCATATC AGAAATAAAT

43351   AAGGCTCTCG CTGTTTCTTC ATTACTTGAA GCTGCGATTT GTTGGCGAAT

43401   CGCATATGCA GAGAGTTTTC TTAGAAAGGC TATCAGAGTT GCAGTGTGTT

43451   TCTGAGAAAG AATCACCCCG TCATAGAGGT CTATGAAGGA GCAATAAGTA

43501   CTGCATAACT GAAGGAGTTC AGCCATTTCT GCACAAAGAT TCGCATTTGC

43551   CGGAGAAGAG GAGGCGAAAG GCAGGTCAAG GAGACGTGTG GCTTCCTGCT

43601   CAAAGACAAT ATCATTTCTG CTGCTCTCTT CGTAGAGAGC AGATAGCCAT

43651   CCTACAGCAT AGGCACGATA AAAGCAGTTC CCATCTCCCG GTACATTCAC

43701   AAGGTAGTAA TTGTCATTTA GATAGAGAGC CTGTTCAAGA GAGAGTTGCG

43751   CAAGTCGCCG GTGTTGTTGA GGAAGATCCG GATTTTGTGC GATTTTCTTG

43801   AACTGTTTTA TTTGGAAATA CATCGGTTCG TTATCAATCC GATTGGGATA

43851   GGAAGCTACG AAATGAGGGT TAAAGTCGCC AAGTATTGGA TCAACTTGCA

43901   TGGCAGGAAG AGGCAGAGGC GCTCGTCTTA GTACCATGCT CACCATGCGA

43951   TTTAAGCATT GCCAATAGCC TTGACTAGAT GGGCGGAGAG GCATGGGGGT

44001   AGCCACCCGT ACGGGAGGAG GAGGGGCCTC TGGTGGTGGA GTCGGCTTTT

44051   TATCAGCAGG TTGTTTAGGG ACTTTTGGGC TCGCTGGTGA AGGAGCTTTG

44101   GGGGGAGGCG GGGGTGTGTC CTCTGGGGGC GGCGTGCCCG GCTTGGGAAC

44151   ATCGGGTTTT TTGTCTTCAC CATCCTTAGG CGGTTGTTTG GCAATTTCTA

44201   TAGTTTTTGG CTCTGGTCCT TTGGGAAGAG TGGGAGGCGT TGGCAAGCCT

44251   TCTTTTCTGA CAACCCGATG ATGCTTGTAG TAGTGAATCA GAAGAAGCAA

44301   ACCAAGAGTA ATGATATGGA GCAGAACGTA TCCTATGGTA CGTAGAATTC

44351   TAAGTAACAG AGGGTCTTTA GTATCAGTCG TTAAGTGGTA AAAATTATTC

44401   TTGTTATTGG GCGGGCAATG TGGTGGGGAA TTGGATACAT ACGTTCAAAA

44451   ATTGCTCGTT TTTTAATCAA AATTATTCAA AGTTAAAACT TTTTCGAGTT
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33

44501   TGATGTATTT ATTTTTTTAT GTAAACTTTA ACACATGATA GAATTTAGCG

44551   TATAGAGCGC AAACTTTCAT GATAAAACAA ATAGGCCGTT TTTTTAGAGC

44601   ATTTATTTTT ATAATGCCTT TATCTTTAAC AAGTTGTGAG TCTAAAATCG

44651   ATCGAAATCG CATCTGGATT GTAGGTACGA ATGCTACATA TCCTCCTTTT

44701   GAGTATGTGG ATGCTCAGGG GGAAGTTGTA GGTTTCGATA TAGATTTGGC

44751   AAAGGCAATT AGTGAAAAAC TTGGCAAGCA ATTGGAAGTT AGAGAATTCG

44801   CTTTCGATGC TTTAATTTTA AATTTAAAAA AACATCGTAT CGATGCAATT

44851   TTAGCAGGAA TGTCCATTAC TCCTTCGCGT CAGAAGGAAA TCGCCCTGCT

44901   TCCCTATTAT GGCGATGAGG TTCAAGAGCT GATGGTGGTT TCTAAGCGGT

44951   CTTTAGAGAC CCCTGTGCTT CCCCTAACAC AGTATTCTTC TGTTGCTGTT

45001   CAGACAGGAA CGTTTCAGGA GCATTATCTT TTATCTCAGC CCGGAATTTG

45051   TGTCCGTTCT TTTGATAGCA CCTTGGAGGT GATTATGGAA GTTCGTTATG

45101   GGAAATCTCC GGTTGCCGTT CTAGAACCCT CGGTAGGACG TGTCGTTCTT

45151   AAAGACTTCC CTAATCTTGT TGCAACAAGA TTAGAGCTCC CTCCTGAATG

45201   TTGGGTGTTG GGCTGTGGTC TCGGCGTAGC TAAAGATCGT CCTGAAGAAA

45251   TACAAACGAT TCAACAAGCG ATTACAGATT TAAAGAGCGA AGGGGTGATT

45301   CAATCTTTAA CCAAGAAATG GCAACTTTCT GAAGTTGCTT ACGAATAGAG

45351   GGTATTCTTA TGGCAACCTC TGTTCCTGTA ACTTCATCTA CTTCTGTAGG

45401   AGAGGCTAAC TCCTCCAACG AAAGATTTAC TGAACGAACA TCGCGAATGT

45451   ATTACGCAGC TTTAGTCCTA GGGGCTTTGA GCTGTTTAAT TTTTATTGCT

45501   ATGATTGTCA TTTTCCCACA GGTCGGATTG TGGGCTGTGG TCCTCGGGTT

45551   TGCTCTTGGA TGTTTACTTT TAAGCTTAGC TATCGTTTTT GCTGTCTCCG

45601   GTCTCGTTTT AGGCAAGACT TTAGAACCTA GTCGAGAAGC GACTCCTCCA

45651   GAAATTGTTG CGCAAAAGGA GTGGACTACA CAACAAGATG TCTTAGGGAA

45701   TGAGTATTGG CGTTCCGAGT TGATTTCCTT GTTCTTACGA GGGGATCTCC

45751   ACGAATCTCT GATTGTTGAT TCTAAGGATC GATCTTTAGA TATTGATCAG

45801   AGTTTACAAA ATATATTGAA ACTTGAGCCC CTATCTACGA CACTTTCGCT

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45851    GTTAAAGAAA GATTGTGTCC ACATCAATAT CATTTTACAT TTAGTGAGAC

45901    AGTGGAACTT ACTGGGAGTG GATCTTAGTC CTGAAGTCAC TGCGCACGCC

45951    GAGGAACTTC TACTCTTTTT GATAGAAGAG CAGTATTACT CTCCTGATAT

46001    TTTGAAATTG ATTCGCTACG GAGATGCTTT ACAAGCAACG TCTCCTTTGA

46051    TGGATTGGGC AGATTCAGGT TCCTTTAGTG TAGACGCAGA CGGGGTATTT

46101    AGCTGTCGCA GAGAAGAATG TTCTCCTGAG GATGCTTTGG CGCAATTCGA

46151    TCTTCTTTTG GCGTTGGAAA ATCCCGACAG ACGCTTCTTA AAGGATTCTT

46201    TTCTTACCTA CATTTGGTCG TCTTCATTTT TTGAGAAGTT TTTACATCGC

46251    CATCTAGAGA GCTTGCAAAG AAAGCTCCCA GAGACAGCGA TCGATGTCGC

46301    CCGCTATGAA GCACAAATAC AAACATTTCT CTCTCGCTAT TTTCAGAAGC

46351    TCGATTTGAT AAACGCAATG TCCTTAGATT GGGGATATAA CTGTGCTGAG

46401    GGAGAAAAAT GTTATGAGAG CGCAAATCAA AGATTAGACA ACCTATTTAT

46451    TGCTTTTTCT TCTTCTGTTC CTGCTATGAA GCGGCTCTTT GACAAATATG

46501    GTTCTGTGGT ACGGGTAGAT CGTAGGCAGA TTCGTGAGCA GATTCTTTCG

46551    AACACTGAAA TCTTAGAAAA TGAGTCAGGG TTCCTCTGCA GTTTGTATGA

46601    ATATCCTTTA TCCTATTTGA TAGATTGGGC TGTTTTGCTA GACTGTGTTC

46651    GCGGTACCGA AATCTCTCTA GAAGATCAGG CCGATTACAC CGTTTGTTTG

46701    CAAGGCTTGG ATTCTATGTT ATCTCAATTT GCGAGTCGTT TACAGTCTGG

46751    ACAAAAAGTA TTGAATCCTA GAGATGTTTT AAGTGAACAG GCTGCGGTTA

46801    TGCTTGTTCA TGGCTTGGCA GCACAGGGCG TGTCGTTTCA AGGATTGAAA

46851    GCTTTGATGT ATTTGACAGC CGTTCCCCAA AGAATGTGGT TAGGAGCATT

46901    GCCTTTATTT GAATCTTTTC CTGTCTTTAA TCGGATGAAA GAATTTCTTG

46951    GGGAATCTCT GGGAGACTAG GTGAATTTGT ATCAAAGAAG GAACAAGATT

47001    GCATGTTAGG TTCTTTGCCA TGTTATCCTG GTGCTGGCAA TATTGAAGAA

47051    TACAAAAATA GGTATTTCTA TTGTCAGTTA TGTGCTGAGG TCGTTAGTCC

47101    CTATGTTGTT CCTGTTATTG TAGTTGATGT GCAAGGGGCT CCTCCTACAG

47151    GTATCTTGCA GGTCTTGCGT TGTAAGCAAC ATAAATTTCA AGGCCTACCC
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35

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47201   GTACATGGCC CCATTACTTC TTTATGGGCT TTGGAGCCCG TGGGTAAGGG

47251   AGCTCCGCAG CTGGAGTCTG CAATGTACGA GCTCTGTTCT CAAGTAAGGA

47301   ATTTTGACAT CTGCTCTATT GTGAGTTGGG TCTTTGGTGG GTTGTGTATT

47351   TTTGCAGGTC TGATTGTCGG GGTAATGGTT GAAGCCCCTT TGATTGCGGG

47401   ATTAAGTGCT TGGGTGATTC CCTGTATCAT TGGAGGGGTT GGTGCCATTT

47451   TATGCTTGTT TGCGATCTTG ATGGCGTACT TGGGAAGAGG GAGAGTCCGT

47501   GAGTGGCTCA ATCTTTCACA CGAATATATA ACGCAATGTC ATTGTCGTCA

47551   GATACAGGCA CATTCTCAAA ACTATTCTGT GATCACAGAG TATCCTGCAA

47601   CCTGTGCATT ATCTCAACCG ATTACAAAGT TACCTAATGG ATCACGCAGA

47651   GATAACTAAG CGTGTTCGTC AGTTATTTCT CACATTTTCT CATGAATCTT

47701   TTACTGCGCT GCACGAGATC CCTCTCGAAA ATTTTTAAGG ATAGATACTT

47751   GGAAACTATG GTTTAAAAAG CTATAGAGGA TTCTAAATTG GGGTTCTAGC

47801   AACTTCTTGA CTTTAAGATC CAAAGTTAAG AGACTGACTA ATTATTTTTG

47851   TTTGCTTGTG TTTCCAGATG AGCAATTGGT ATGGTAAGAG ATATTCAGAG

47901   TGAATCTATA GGGAAATTAG TATTTTTAGG CACAGGAAAT CCCGAAGGAA

47951   TTCCCGTGCC GTTTTGCTCA TGTAGAGTGT GTCAAAACAC AGGGATTCAT

48001   CGTTTACGAT CTTCGGTACT CATTCAATAT CAAAACAAGA CTCTAGTGAT

48051   TGACGCAGGC CCTGATTTTC GTACGCAGAT GTTAGTTGCA GGGGTTTCCG

48101   AGCTCGATGG GGTATTTCTG ACCCATCCCC ACTACGATCA TATCGGTGGT

48151   ATTGATGATT TACGTGCGTG GTACATAGTC ACGCAGCGTT CGTTGCCTTT

48201   GGTCCTTTCT GCAAGCACCT ATAGATTTTT AAACAAGGCT AAAGAGTATC

48251   TCTTCGCCAC TCCGAATGTA GAGTCTTCAC TTCCCGCAGT TTTAGAGTTT

48301   ACAATCTTGA ATGAGGACTG TGGGCAGGAG GAATTTCAGG GCATTCCCTA

48351   TACTTATGTT TCCTATTATC AAAAGTCGTG CCATGTAACG GGTTTTCGTT

48401   TTGGAAATCT TGCTTATCTT ACAGATCTCT GTAGCTATGA TGCAAAAATT

48451   TTCAGTTACT TAGATAATGT AGAGACATTG ATCTTGTCTG CGGGTCCATC

48501   GGAAACTCCT ATTCCTTTTC AGGGACACAA ATCTTCGCAT CTTACTGTAG
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36

48551   AAGAAGCCAA AGCTTTTGCG AATCATGCAG GGATAAAGAA TTTAATTATT

48601   ACACATATCA GCCACTGTTT AGAAGCAGAG CGTGACCAGC ATCCAGAGGT

48651   CACATTTGCT TATGATGGCA TGGAGGTCCT TTGGACACTA TAGATACGCC

48701   CGGGGAACAG GGTTCTCAAT CTTTCGGAAA TTCGTTAGGG GCCAGGTTCG

48751   ACTTGCCTCG TAAGGAACAG GATCCCTCTC AAGCTTTAGC TGTGGCTTCC

48801   TATCAAAATA AGACAGATTC TCAGGTCGTT GAAGAACATT TAGACGAGTT

48851   GATCTCACTT GCGGATTCCT GTGGTATTTC TGTTTTAGAG ACCCGTTCTT

48901   GGATTTTAAA AACACCCTCA GCTTCCACCT ATATCAATGT GGGGAAGTTG

48951   GAGGAGATCG AAGAAATCTT GAAAGAGTTT CCCTCTATAG GGACTTTGAT

49001   CATAGATGAG GAGATCACTC CATCCCAACA ACGGAATTTA GAGAAACGCC

49051   TTGGCCTTGT CGTTTTGGAT AGGACGGAGT TAATTTTGGA AATCTTTCC

49101   AGCCGTGCCC TTACTGCAGA GGCAAATATC CAAGTCCAAC TTGCACAAGC

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49201   AAAAATCTGG GGGAGGTAGC GGAGGCTTTG TTAAGGGGGA AGGAGAAAAA

49251   CAGATCGAGC TAGACCGTAG AATGGTCCGT GAGCGTATCC ATAAGCTGTC

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49351   AATCTCGACG AGGAATTCCT ACCTTTGCTT TGATAGGGTA TACAAATTCA

49401   GGGAAGAGCA CCCTATTAAA TTTGCTGACG GCTGCTGATA CGTATGTTGA

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49751   AAGTATCCCT ATGAAATTAC GTTTGCTCTC TCCTCTTCCT GTATTGATTT

49801   CAGCAAAAAC TGGGGAGGGG ATCCAGAATC TTCTTAGTCT TATGACGGAA

49851   ATCATTCAGG AGAAAAGTTT GCATGTGACT TTGAATTTTC CTTATACAGA

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50001 CAAAAGAAAT TTCGTCCTTT TATTTCTTAT GTTTTCCCTG AAGATTGTGG

50051 AGATGACGAG GGTAGAGGGC CCGTCTTGGA GAGTTCTTTC GGGGATTAGG

50101 TAGTTTTCTT CTAGGACATC GAATCTTTGT TAGTGAGAAA AAGAGTGATA

50151 TTTTAAAATA GCCACTCATC GCTAAATCTA TTGAAGTCTC TAGAGGTATA

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50851 CGAATTTCCT CTATAGATCC TGATGATATC ACTGAAGATC TGCACCGTGC

50901 CATCACCTCA TCGCGTCACA CTTGTCCTTC GTCACACCTT GTTCTTCAAT

50951 CGGGGTCGAA TTCAATTTTA AAGAGAATGA ACCGGAAGTA TTCTCGCGGA

51001 GATTTTTTAG ATTGTGTAGA GAAGTTCCGT GCTTCTGATC CTCGCTATGC

51051 CTTTACTACA GATGTGATTG TCGGATTTCC TGGAGAGAGT GATCAAGATT

51101 TTGAAGATAC TTTGAGAATT ATTGAAGATG TAGGCTTTAT TAAAGTGCAT

51151 AGTTTCCCTT TCAGTGCTCG TCGTCGTACT AAGGCATATA CTTTTGATAA

51201 TCAGATTCCC AATCAGGTGA TCTATGAGAG GAAGAAGTAT CTTGCTGAGG

38

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51251   TTGCTAAGAG GGTAGGCCAG AAAGAGATGA TGAAGCGTTT AGGAGAGACT

51301   ACAGAGGTGC TTGTTGAGAA AGTAACGGGG CAGGTTGCTA CGGGTCACTC

51351   TCCTTATTTT GAAAAGGTTT CTTTCCCTGT TGTAGGAACG GTAGCTATCA

51401   ACACTCTAGT TTCTGTGCGT CTTGATAGGG TAGAGGAAGA AGGGCTGATT

51451   GGGGAGATTG TATGATAGAT ATAATGCAAC ATTTTAAGCC CTATACTATG

51501   GTCCCAGGAC AAAAACTCCC TATTCCTGGA TCTTTGTTAT ATGCTCAGGT

51551   ATTTCCTACC CTGTGGCGTC TATTTTCTTC GAAACACGAA ATCTTAAATG

51601   AGCAGACCTT ACAGGTGCAA GGGCCTTTAA AACGCTTTGC TGTTTTCCAA

51651   GATTTACATC GTGGGGGGCT TGCAGTGACT TCTGAGCGCT ACAAGTATTA

51701   TCTCCTTCCC TCGGGAGAGT GCACACAATC TATCAAAGGG AAACTGCCTT

51751   CGGCAGCGCA AGCAGGGCCC CTGTTATCTC TTGGGGTGCA TAAGCATGCA

51801   GATTGGCAAA AGGTCCGTTG TCGTCGTGAT CTTAAAGAAA TTCTTCCCCT

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51901   AGACGACGGC TATCGGTAGC TTGGTAAAGA CTGCCCATCA AAGAGTTTTA

51951   CATAGGGAAA CTACAGAGAT TGCTCCTGCG TTACTCTCCA TAGCCCTTGC

52001   GGGATTTTCA GAGTGCTTTC TTCCTAGGAG CTATGATGAA GAGTTCCAAG

52051   GAATCCTCCC CCAAGATGGA GATCCAGAGG GGGGAGTTCC TTTTGAGCTT

52101   CTCTCGTATA GCTTTGGTAT GATCCAAGAT ATTTTTCTGA GACACCAGGG

52151   ACAGCTAGTA GAGATCCTTC CTGCATTACC TCCTGAATTT CCTTGTGGCC

52201   GCTTGATTCA TGTTGCCCTT CCTAATCTTG GGACTTTGTC TATCGTCTGG

52251   ACTAAGAAAA CTATCCGTCA GGTCGAGCTC CATGCAGAAT ATAGTGGCGA

52301   GGTATTTTTA AAGTTTTGTT CTTCACTATG CAGTGCGCGC CTTCGGGAAT

52351   GGTCGGAGCG ACGTCTCTCT GGATCTAAGA GACTTTCTTT AGGAGAAACT

52401   CTGGAGATAA AAGCAGGAAC CACATATTTA TGGGATTGTT TTCATAAATA

52451   GATAGCCTTC CATGGTTGAT AAACTGATCC ATCCTTGGGA TCTTGATCTG

52501   CTCGTCTCAG GACGACAGAA AGATCCCCAT AAACTCTTAG GGATCCTTGC

52551   TTCTGAAGAT TCTTCAGATC ATATTGTTAT TTTTCGTCCA GGGGCGCATA
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39

52601 CGGTTGCTAT TGAACTTCTA GGAGAGCTTC ACCACGCTGT AGCTTATCGT

52651 TCGGGGCTCT TTTTCTTATC CGTTCCCAAA GGAATCGGAC ACGGGGATTA

52701 CCGTGTGTAT CATCAGAATG GACTTCTCGC TCATGATCCC TATGCGTTTC

52751 CTCCTCTGTG GGGAGAAATT GATTCTTTTT TATTCCATAG AGGAACGCAT

52801 TACCGCATTT ATGAACGCAT GGGGGCAATC CCTATGGAAG TTCAAGGAAT

52851 CTCAGGGGTG CTCTTTGTTC TTTGGGCTCC CCATGCGCAG AGAGTCTCTG

52901 TAGTCGGAGA TTTTAATTTT TGGCATGGCC TTGTCAATCC TCTACGTAAA

52951 ATTTCCGATC AGGGGATCTG GGAGCTTTTC GTCCCAGGCT TGGGAGAGGG

53001 AATACGGTAT AAGTGGGAAA TCGTTACCCA ATCGGGGAAT GTGATTGTAA

53051 AAACAGATCC TTATGGGAAG AGCTTTGATC CTCCACCCCA GGGTACAGCT

53101 CGTGTTGCGG ATTCTGAGAG CTACTCTTGG AGTGATCATC GTTGGATGGA

53151 GAGGCGCTCG AAGCAGAGTG AAGGGCCCGT CACGATCTAT GAAGTGCACT

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53251 GCGCATCGCC TTGCTAGCTA TTGCAAGGAA ATGCACTACA CTCATGTGGA

53301 GCTTCTTCCC ATTACGGAGC ATCCCCTGAA TGAATCTTGG GGCTATCAAG

53351 TGACGGGATA TTATGCTCCA ACATCAAGAT ACGGGACTCT CCAGGAGTTT

53401 CAGTATTTTG TAGACTATCT ACATAAAGAA AATATTGGTA TTATTTTAGA

53451 TTGGGTGCCG GGACATTTTC CCGTAGATGC GTTTGCTCTT GCCTCTTTTG

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53551 CACTGGAATA CGTTTACCTT TGACTACAGT CGTCATGAAG TGACCAACTT

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53651 TACGTGTGGA TGCTGTGGCC TCTATGCTGT ATCGTGATTA TGGCCGTGAA

53701 GATGGAGAAT GGACGCCTAA CATCTATGGA GGTAAGGAGA ACTTAGAGTC

53751 TATAGAATTT TTGAAACACT TAAATTCTGT AATTCATAAG GAGTTCTCTG

53801 GAGTGCTCAC CTTTGCAGAG GAATCCACAG CGTTTCCAGG AGTCACTAAG

53851 GACGTAGATC AGGGAGGTCT GGGGTTTGAT TACAAATGGA ACTTAGGTTG

53901 GATGCACGAT ACCTTTCATT ACTTTATGAA GGATCCCATG TATCGTAAAT

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53951  ACCATCAGAA AGATCTGACA TTTAGCCTTT GGTATGCCTT CCAAGAGTCT

54001  TTTATTCTTC CTCTCTCGCA TGACGAGGTG GTCCACGGTA AGGGCAGCTT

54051  AGTGAATAAG CTTCCCGGGG ATACCTGGAC CCGATTTGCT CAAATGAGAG

54101  TGCTCTTGAG CTACCAGATC TGTTTGCCTG GGAAAAAGTT ACTGTTCATG

54151  GGTGGGGAAT TCGGACAATA CGGCGAGTGG TCTCCTGATC GTCCCTTAGA

54201  TTGGGAGCTT TTGAATCATC ACTACCACAA AACTTTGCGA AACTGTGTCT

54251  CTGCATTGAA TGCGTTGTAT ATTCACCAAC CCTATTTATG GATGCAAGAG

54301  AGCTCTCAAG AGTGCTTCCA TTGGGTAGAC TTCCATGATA TAGAAAACAA

54351  TGTCATTGCC TATTATAGAT TTGCAGGCAG CAATCGTTCT TCGGCGCTTC

54401  TCTGTGTCCA TCATTTCAGT GCGAGTACTT TTCCTTCCTA TGTTTTAAGG

54451  TGTGAAGGTG TAAAGCATTG TGAACTCCTT CTCAACACTG ATGATGAGTC

54501  TTTTGGAGGC TCAGGGAAGG GAAATCGGGC TCCTGTGGTC TGTCAAGACC

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54601  ATCTATTTAG TTACTTTTTT CTAAAAATTT AAATACTTTA TTTGTAAATT

54651  GTTGTGGGAT TGTTCTATTT TGTGGTGTAG TTGATATTAA TAATTTATTT

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55101  GAGCAGAATC AAAAGTGCTT TAGCTGTAGG GACTGGATTT ACTGTCATGG

55151  GTTTGGTCAT GAAGGTGGGG GCGAATTTTG TTCCTGGAGG GTATGGGGGT

55201  CTCGTGGGTA GCTTGGGATC CAGTGCGTAT TCCCGGGGAA GCCAAACCAC

55251  ATTAGCAAGC TTCAGTCATT ATATTTATAC TAAGTTTTTC CGTTCTGAAA
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41

55301   AAGTTGCTAA AGGGGAGAAG CTTACAGAAG CAGAAACTAT AAAAGAGGCG

55351   AAAAAATTAC ACTATATCAC GTTGTCAATT GCCACTATTG GCGTTGGTCT

55401   TGCGGTTTTG GGGATTCTCC TTGCCATTGC AGGAACGGTA TTGCTAGGAG

55451   GCGCTCCCGC AACGATTGCT ATTATTTTAG CTCCCCCTTT AATTTCTATA

55501   GGGCTTACGA CGGTTTTGCA AACGATACTC CATAGTAGTA TCGGAAAGTG

55551   GAGAGCCTTT CTGCTTACTC AAGAAAAAAA AGATCTTTTT GTAGACACCT

55601   CCCTGAAAGA CATTCGCTTA GAAAAATTGC CCCCAGTGA GGTGGAAGAG

55651   AGTGAAACTT CCCAATCTGT GATAGAAGTT CCAGATTCAG AGGGGATTGC

55701   AGAGACGAGG ATCTCTGCGG AAGAAATCGA TACGAGGCTT TCCCTGACGA

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56501   AGGCCAGGTC CTTGAATGTA AGATCCTCGA GCTTTGGGAG CTTGTCTGCC

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56601   AATCAGCATT CTTTTTGTTT ATTTTAATTT ATATTTTGTT TTTAAAATAT

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56651   TTTTTATTTT AACATTTGTT TAATAGTTTT TATTAAATAA TTTATCATTT

56701   TAAGGTTCAA TTATGGCAGT TGGTGGCGTA GGCGGCTCAA GATCTCCTTC

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56801   AAGACAACTT AGGGGAACAT ACAGTTAGCA GTAGTGACAG TAGTCTTGCA

56851   AGTCAGGGCC CTACAATAGA AGAGAGAAAA GCCCAGTTAG GCGGGACTGA

56901   TAAAATTCCT TTGCCATCTG TCAAAGAACC CGGAGATTCT CAAACTTCAG

56951   GACGTTCTGG GGTACTTCAG AGAATTTGGA AAGGCGTTAA AGGGGTCTTT

57001   AAAAAAACCC CTCAAGCGCG TCCTGAAGTT TCTAGTCCAC GTCTTCCATC

57051   CCATGTGCAA CATGGCCAAC GTCTTCCTGG ACTCGAGGGC TTTAGAGATC

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57251   GTTCTTCCTT CTTATCAGGA GTTCGAGGAG CGGTGTCTAA AGTTCATGGT

57301   GCCCTAGGTG ATATTAAAGG AAAGTTCCAG CGTTCTGCTT CCGAAGATGA

57351   TTTAACAACT CAGGGCGAAG ATTCTGCCGG CGATACTGTA AAAGAAAGGC

57401   GTTCCGAAGA AGCAGAGGCT TCTTCGAAGA GTTCTTCTTT TTTATCAGGA

57451   GTTCGAGGAG CGACGTCTAC AGTTCAGGGA GCCTTAGGTG ACGCTAAAGA

57501   GAAGGTTTCG GCGTTCGGAG AGCAGGCTGC AGGTGCAATC AGATCAGCAC

57551   CAGGGAATAT CAGAACTAGA TTCCAACGTT CTTCATCGGA AGGTGATCTT

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57651   GGAAAAAGTA GCTCCAGAAC AAGTGTCACC AGAGGTGGCT TCTAGGGTGC

57701   AATCTCTTCT TGCACGCATG GAGCAATTGA CTCATCAGGA ACCTCCTACT

57751   GTGGAGGATC TTATTACTTT CGTAGAATCC AATGTAGGTA GTGATTCTGT

57801   GGAGTATGCA TCCATCGTAC CTCAAGATGG ATCGCAAGCC CCAGCAGAGA

57851   CTGCGGAAGC TCCCGAAACA GGTGGGGTAG AGGGATCTGC AGCGCAGGGA

57901   GCATGGAAAG CGTTACGGGA TTTTGTAGTT AGCATATTCC AAGCGGTAGC

57951   GAGCTTCTTT AGGGCAATTG CTTCAAGATT AAGTTCAGCA CGACGTGAAT

43

58001   CAGCTGTAGA TGATCTTGCA TCAGAAAGTA ATACACAATG GTTTGTGGAG

58051   CAAGAGGGCG TTTCAAATCC ATCGGCTGCA CCTAGCTTAT CTTTTGCGGA

58101   AGAGATCGCT CGTAGAGCTG CAGAAATGAG TAACAGAAAT GCCCAGAGTC

58151   TTGAAAAATT GGAATCAGGC AATGTGACTG ATCCTGTCAT TCAACAAGGC

58201   TTAGGATTAG CTAGATCATT TGCTCCAGAG GGACAGTAGT CGTTATCTCA

58251   CTGTTTCTCT ATGCGCAAGG GAAACTTGAA GAGTTTTAAT TAAAACTCTT

58301   CAATATGTTG ATTATTTTAA TATATTTAAA AGCATTTTTG TTGTTTTTA

58351   ATAAAATTAA ATTGTTTCAG AAAAAAGATT ATTCTTTTTA GGAAGTGTTT

58401   ATGGCATCAG GAATCGGAGG ATCTAGTGGA TTAGGAAAGA TTCCACCTAA

58451   AGATAATGGG GATAGAAGTC GATCGCCCTC TCCTAAGGGA GAACTTGGCA

58501   GCCACGAGAT TTCCCTGCCT CCTCAAGAAC ATGGAGAGGA AGGAGCTTCA

58551   GGATCTTCGC ATATACATAG CAGTTCCTCT TTTCTACCAG AAGATCAGGA

58601   GTCTCAGAGC TCTTCTTCGG CAGCTTCTAG CCCGGGATTT TTTTCTCGCG

58651   TACGTTCTGG GGTAGACAGG GCCTTAAAAT CATTTGGCAA CTTTTTTTCC

58701   GCAGAGTCTA CGAGTCAAGC GCGTGAAACG CGACAAGCTT TTGTTAGATT

58751   ATCAAAAACC ATCACCGCGG ATGAGAGACG GGATGTCGAT TCATCAAGTG

58801   CTGCTGCTAC AGAAGCCCGA GTGGCAGAGG ACGCGAGTGT TTCAGGCGAA

58851   AATCCTTCTC AGGGGGTTCC AGAAACCTCT TCTGGACCAG AACCTCAGCG

58901   TTTATTTTCT CTTCCTTCAG TAAAAAAACA GAGCGGTTTG GGTCGGTTGG

58951   TACAGACAGT TCGCGATCGC ATAGTACTTC CTAGTGGGGC TCCACCTACA

59001   GACAGCGAGC CTTTAAGTCT CTACGAGCTA AACCTCCGTT TGAGTAGTTT

59051   ACGTCAGGAG CTCTCTGACA TACAAAGTAA TGATCAGTTG ACTCCAGAGG

59101   AAAAAGCAGA AGCCACAGTT ACCATACAAC AGCTGATCCA AATTACAGAA

59151   TTCCAATGCG GCTATATGGA GGCAACACAA TCTTCGGTAT CTCTAGCAGA

59201   AGCTCGTTTT AAGGGGGTAG AAACTAGTGA TGAGATCAAT TCCCTCTGTT

59251   CAGAACTGAC AGATCCTGAG CTTCAAGAAC TCATGAGTGA TGGAGACTCT

59301   CTTCAAAACC TATTAGATGA GACTGCCGAC GATTTAGAAG CTGCTTTGTC

59351   CCATACTCGA TTGAGTTTTT CTTTAGACGA TAATCCAACT CCGATAGACA

59401   ATAATCCAAC TCTGATTTCT CAAGAAGAGC CTATTTATGA GGAAATCGGA

59451   GGAGCTGCAG ATCCTCAAAG AACTCGGGAA AACTGGTCTA CAAGATTATG

59501   GAATCAGATT CGCGAGGCTC TGGTTTCTCT TTTAGGAATG ATTTTAAGCA

59551   TTCTAGGGTC CATCTTGCAC AGGTTGCGTA TTGCTCGTCA TGCAGCTGCT

59601   GAAGCAGTGG GTCGTTGTTG CACGTGCCGA GGAGAAGAGT GTACTTCTTC

59651   TGAAGAGGAC TCGATGTCGG TGGGGTCTCC TTCAGAAATT GATGAAACTG

59701   AAAGAACGGG CTCTCCGCAT GACGTTCCAC GCAGAAATGG AAGTCCACGT

59751   GAAGATTCTC CATTGATGAA TGCCTTAGTA GGATGGGCAC ATAAGCACGG

59801   TGCTAAAACC AAGGAGAGTT CAGAATCAAG TACCCCGGAA ATTTCGATTT

59851   CTGCTCCCAT AGTGAGAGGT TGGAGTCAAG ACAGTTCCGT CAGTTTTATT

59901   GTTATGGAAG ATGATCATAT TTTCTATGAT GTTCCTCGTA GAAAAGATGG

59951   AATCTATGAC GTTCCTAGTT CCCCTAGATG GAGTCCTGCG CGAGAGTTGG

60001   AAGAGGATGT TTTTGGAGAT TATGAAGTTC CTATAACCTC TGCTGAACCA

60051   TCTAAAGACA AGAACATCTA CATGACACCT AGATTAGCAA CTCCTGCTAT

60101   CTATGATCTT CCTTCACGTC CAGGATCGTC TGGAAGCTCA CGTTCTCCGT

60151   CTTCAGATCG CGTACGAAGC AGCTCACCAA ATAGACGGGG TGTGCCTCTT

60201   CCTCCAGTTC CTTCACCTGC TATGAGTGAG GAGGGGAGCA TTTATGAGGA

60251   TATGAGCGGT GCTTCAGGTG CAGGTGAAAG TGATTATGAA GATATGAGCC

60301   GTTCCCCCTC TCCTAGAGGC GACTTGGATG AACCCATATA TGCTAATACT

60351   CCTGAAGATA ATCCATTTAC TCAGAGAAAT ATAGATAGAA TTTTACAGGA

60401   GAGGTCAGGC GGTGCTTCCG CTTCTCCTGT AGAGCCTATT TATGATGAGA

60451   TCCCATGGAT TCATGGCAGG CCCCCTGCTA CACTTCCAAG ACCCGAGAAT

60501   ACATTGACTA ATGTTTCGCT TAGAGTGAGC CCAGGGTTTG GACCAGAAGT

60551   AAGAGCCGCT TTGCTTAGCG AGAGCGTGAG TGCTGTTATG GTCGAAGCAG

60601   AGAGTATTGT TCCTCCAACA GAGCCGGGGG ACGGAGAATC AGAATATCTA

60651   GAGCCCTTAG GGGGACTTGT AGCTACAACG AAAATCTTAC TACAAAAAGG

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60701  ATGGCCTCGT GGAGAGTCGA ATGCTTAGGA TTTAAGTAGT TCTTTCGAAT

60751  CTCTAGTGAG GATGTATCGG GTTCTTAATT TTTATGGGGG AAACGTATCT

60801  GTGGATTTCC CTTAGCTTCT CCCATAAGAT TCATGATGGT AGAGAGTGTT

60851  CACTACTCTC TATTTGGTCT TTACAGGTTG CATTGTCTAT ATAACATGCT

60901  TTTAAAACTT AAAGGTCGTT CCTGCGTGAA GGTAATGTGT CGTCGTTGAT

60951  GAGGATACCG AGCCTTGATA GTCTAAGAAC ACCGAAAGTT TAGGGAAGAT

61001  AAAAATTTGG TTTCTTCCTT TAAAAGCAAT GGCATTGCGA GCAAGGGTGG

61051  TTCCTGATAG GAGCCATGAC GATCCACTAG ATTCTAGACT CACGTTGATC

61101  TCAGGATTTT GTTGGTAGAG GACAGGCTGA TAAGCAAGCT CTATGTTCCA

61151  ATAGGTAGGA AGACGGAACT TGGATTCCCA AGCGCTCTGA ATTCCCAGAG

61201  GGACTGTCAG GTTATATAAG GGTTATGAA CAGAAAATTT TCTAGCTTTA

61251  TCTCCACTTT CTTGAAACGC AGTTTGATTA GAACGAACGG CAATTGCTTG

61301  GATAAAAGGA GTGAAGTGGA GAGGTCGTGA TCGCCATTGT AGAGATAGAG

61351  AGCAAGAGAG AGCCGCCCCT AATGTCGTAC TATAACATTT GCCTTCCGTT

61401  TGTATTTTTC CAGAATATCC AGATGCTTTG ATATGGTGGT TGCTGTAGCT

61451  GTAGGCTAGA GATGCAGATG TAGAGAATCT CTCTTGCAGC CAAGGATTAT

61501  TGATCTGGAG CGCTACAGTT GTCGTATGCG AAGCCACGGA ATTGTCGGAG

61551  TGGCTCTCGT AGAGATTACT GAAAAGTTGG GAGAAGTTTA CACCAAAGCT

61601  ATGATTAGAA GCAGTGTTTG AGGTTGTTCC CAAAGAATAA CCCGTAGCTT

61651  CCATATGGAA TCCTTTCGCA TCATTGTTGC TATTTTGATG CACGAAGAGT

61701  CGAGTAGCTT CTCCAGAAGC TGTAGGTGCT ATTTGGCCTT GCTGTGTTTG

61751  ATAACGTAGT GTCGCAAATA AGTTATGGAA AGATTGCCAG AAGGCAGATA

61801  GGGCAATGTC TCCTTTGTTT TCTGGGTTTA CCTTATATCC TGTAGGTGTC

61851  CAATCACCAT AAAGCTGGCG ATGTAAAGTA TTCACAGTAT CTTCAGAAGA

61901  GGTATCAGAA GTTGTGATTG TTTCGATCCA GTAAGGGGAC CAAACGCCTT

61951  GGTAGCCGTA GTGTTGAGTT GTATTTAGAC CCTCAGGGTA GAAATTATCC

62001  GTATTAATAT GTTTAGCTGT GACGTCTAAG AGATACAGAA GAGGAACTTC
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62051   TGCGATAGGT TGGGCAAGGT CTGCAGTATC ATAGGGATCT AGGTTCTCGT

62101   CATCCAGTAG GCTCAAAGGT CCTGAGAGAT TGATTATAGG GTTATTATCT

62151   TCGCTATAGG GTGCTGATGA ACCTGTGGGG CGAATCCATA GCTTGGGAGC

62201   AACTCTGTTG CCTAAGATAG AGGGAAGGTT AATTGCAAGA TTATTGATGT

62251   TAATTACAGA ACCCACACTA CTGCTACTTT GTTCTTCGTC TGTTGTAGAA

62301   AACACAGCTC TACTGCCTAA CCGTAGAGTC CCACCAAATT GATCAAATTT

62351   ATAGACTTTC CACTCTGCTC GATCTTCAAG AGCGAGTGTG CCGTTGTACA

62401   GTCCAATGTG GTTTCTGAAA TGTGAAATGA AGTCATCACG AGAAGTCGAT

62451   GTATCCGGAA TATATGTTGA GGAGAACAAG ATAGTTCCGA GGTGTTCTGG

62501   ATTAGGATTA AATTTTTGGA TAGAGTTTTG TATAGTATAT CTTTGTAGTA

62551   TGGGATCATA GAAGGTAGCA GAATGACCTT GACTTGCTCC AACTGTTAAT

62601   GAGACATTAC GCGTGCAGTT TACAGAAACA TGATTGCTGA AAGTATCTTT

62651   GAAGTGTCTA TTATTATAAA AAATAATATC TCCCTGATCA GCAAATAAAG

62701   TGCATGCACC ATCTTGACGG AGCATGATAG CGCCGCCCCA AGTTCCCTGA

62751   TTGTTTGTGA AATAGACGGG ACCACTGTCT TGTATAGTTA GAGATTGTGT

62801   ACAGATAGCA CCTCCATCTC GTGCTGCAGT ATTATTATCG AAGGCTGCAA

62851   TTCCTGGGTT GTCTTTTATA GAACAACTAA TGCAATAGAT AGCCCCTCCA

62901   GAGGAATGGT TAGCAGAGAT GTCCGCTTCC ATGGCAAAAT TATTGTTGAA

62951   GATCACAGAA CCGGTATTCT TTGTAAGAAT GCACTCTTGA TGTACTCTTA

63001   TTGCACCACC CAGACCTGAT TGGTTATTCA AAAAATAGAT AGGCTGAGAA

63051   TTATTCTCAA TTCTACAAGC ATTAGCGAAC AACGCGCCCC CCGCTGTTCC

63101   GCCTGCAGCA TTATTAAAAA ACAGGCAAGG GCCAGTGTTG TCCTTAATGT

63151   TTATGATTGC AGCTTGGATT GCTCCTCCTG AAGATTTGC CTTGTTGTTA

63201   ATGAAGTATG CGGTTCCTTG ATTTTTTGAG ATTGTAACAT TTTTCGAACA

63251   TAAAACAGCT CCCCCTGTAC AAGTATCAGC GAAATTACTT GCATTAGGAA

63301   AGCTTAAATT CCCAGAGAAA ATGATGGAAC CATGATTCTC AGAAAGATCG

63351   AAATTACCAT TCACATACAT CGCACCAGCT CTTTTAATAG CAAAGCTATT
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47

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63401    TAGGAAAAGA ATTTGGTTTT TTGTATTCGT TATGGCAAGT GATTTGCAAG

63451    AGAGAGCACC GCCGTCTTGA GAGAAGTTTT CGAACCAGCT TTCTATGGAA

63501    TTCTGGTGAT CGAGGACAAT GTCTTGGTTA GTGTCATCCC TAACTCCAAA

63551    AAGTGTTGCT CTATGAGAGT AGGGAGTCAT GTTAGTAAGA GTATCAATTA

63601    GAGGGAAGAG TGTTGTGAGT TGATTTGCTT GATTATCAAA ATAGTCAGAC

63651    AACGGAGTCG CATTAAGGAG TATTGTAGTT TTACCTAAAA TTAAGGCTCC

63701    AACAAAGAAG GAAGATTTAC TAAGGGATCT GTTATTTTGC ACTGTTTATT

63751    CCTTGATGTT TTCTTTGTGG TTAAAATGTG CAATGACTCT CAGCTTTAAG

63801    GTATTGACCT ACAGTTGACG AGGAGACTTG AGCTGAATAA TCTAAGGATA

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64151    AGCGCAGAGC AATGGCACTG ATAAAGGGCT GGAGTTCGAG AGTGCGGGTG

64201    ATTCTAGCTG GTAAGAATGT GCAGTCTAGA GAGGCTACCA AAGTGTGGTT

64251    ATTAAAGAAG GCTTTGGACG ACCCTTTTAA GATTTCTGTA TAGTGGCAAA

64301    GCATATGGTG ATCTCCGTAG CTATAACCTA GGGATAGCCC TGTAGAGATG

64351    AAGTCCCTGA AGAGGAGACT GTCGAAGCGG AGTCCTGCAA AGTAGTTGTG

64401    GGAGGAAGTC GTACTTGGAG ATTGACGTTC TCTAGTTTTG GAGAACATTT

64451    GTGCGAATCC TAAAGAGAAA CTATGTCGTG CTGCAGTTTT TGCTGAGGTT

64501    GTTGCTGCAT AGCCCGTAGT ATGGTTTCGG AAGCCTTTGC GTCCCTCGCG

64551    ATTATGTTGG TTAATTAGAA GCCCGAGTCC TTGCAGAGAG GCTTCAAGGT

64601    CATGCTCTTT GAGGTTTTGT GGAGGTAAGA TGCGGATTCC TAACAGAGCG

64651    TTATAGGCAG ACTGCCATAA GGTATTAGCA ATAAATTCTC CGTGACGTTC

64701    CGGGTTAGGG CGGTATCCTA CAGGAGTCCA GTCTACGTAG AGCTGCCTGT
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48

64751   GGTTTGTATT GGTCTGTTCC GGTACTGTAG AGCTTGTTGT AGTCGTAGTT

64801   TCCATCCAAT AGGGAGACCA GATTCCCTGA TATCCATAGT GCTCATCTAA

64851   GTTCATGGCT TCTACAATGA GATTCGAAGT ATCGATTTTT TTTGCAGTCA

64901   CATCGAGGAG GTAGAGGAGG GGGGATATCC TTTCGAGGTT CAGAGAGATC

64951   TAAGCTATCA TAGGGGTTTT CATTTTCATC GTTTAGAAAA GTCAAGGGTC

65001   CTGAGAGAGT GATAGTAGAA GAAGTGTCTT CAGAATAGGT GGATCCTGTT

65051   AATGTAGGAT AAATCCAGAA CTTTGGAGCT GAGGCTTCTG ATTGTAAAAT

65101   AGAAGGAAGA TTGATCGCGA TTGCATTAAA ATTTATGGAG CTTCCCGGGC

65151   CTTTCGTCCT GATTAATGCT GCGTTTCCTA AACGTAGAAT GCCCCCAGTT

65201   TGCGATAGGG TTTTGCAAGA AATAGCAGCC CGATCTTCAA TAGCGAGCAC

65251   ACCCCTTTCA AGTCGTGAAG AGTTAGAAAA TTTTGATAGG AAGTTCAATG

65301   GATTTGTTGC GTTAGAATCT ACATTGATTC CGGAAAACAA CACGGTGCCA

65351   AGGTGATGGG GTTCATAATT AAATACTATA GGATCTGTTG TCGTCTGATC

65401   GTGATCTATA GGATCATAAA AGAGAATTTT ATAACCCTGT CTTGCTCCTA

65451   GTTTTAAGTT AATCCCCGGA GCAGCATAGA GTGCATTTCT ATATCCGGGT

65501   TGAGGAGAAG AAGATGTGAT TGTATTATTG TTAAATAGAA TATCGCCGTA

65551   GTCTGCAGAG AGGAAGAAAT TTTGAGGAGT ACTTCCTATA CCAGAAAGAT

65601   TGATGAGAGC CCCTCCTGAA GTCGCAGAGT TATTAATAAA TGCTGTCGGA

65651   CCGTTATTTT GGAAGATGAA AGATCTCGTG TGTATAGCTC CGCCGCTAAG

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65951   CGGCTCTGCA GAAGATGCCT CCTCCAAAGC TGGAATCTTC TAATGTTTGA

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66051   CCCAACATAG ATAGCTCCTC CTCTATTTTT AGAGACATTA TCTAAGAATT

66101   GTCCTTCTCC TAAGTTATTT GTAATATAGC TATCTAGTGC ATGTATAGCC

66151   CCACCAAATC CTGAAGTTGT AGTAGTAGCT AAGGAAGCCG CATTTGAAAT

66201   AAACGAGTAG TTCTGATTCT TAGAAATCCA GCATTCCCGA ACACTGTAGA

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66351   GTAGTGGTAG TTATAATCTA TAACAGAATT GATAGAGTTT CCTGTAATTG

66401   TGATGTCCTG GGTTATATCG TGACCGAATC CATTAAGAAG ATTAGAGGGA

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66701   ATATTTAAAT ATGCTTATTA ACATGTTGAA TATTACAGAG TTAGTAAACT

66751   CATATATTTG AATGATTTTC TATATTTAAA TTTTGAGGGA GTCCTCTACC

66801   GATTGGGCTA ACGTAGCTCA TCGGATAGTT GTTAATTCTA AAGATTTCAA

66851   TTTTATCGTT CTTTTATTTT AGAATTTTAA GGTACTTCCT GCTTGGAGAT

66901   GGTGCGTAGA TGTCGAGGAG GAGACCGATC CTTGGTAATC CAAGAATAGA

66951   TCGAGAGAAC GGAAGAGCGC AGTTTGATTG TGGACTTTGT ACCCTAAAGC

67001   ATTGCGAACA TAGTTATGGC CTAGGATATC CCAGGAACCT CCGCTCGCAA

67051   GTAGCGTGAC ACCGATTTGG GGATTTTGTT GATAGAGTAC CGGTTGGTAA

67101   GAAAGTTCTA GAGTCCATTC TGTAGGTACG TGGAATTTTG ACTGCCATTT

67151   TCCTTGGATT CCTAGAGGTA AGGTCAGATT ATAGAAAGGC TTTTGAGAGA

67201   CAAACTTTCG GGGATTGTCA CCAATCTCTT CGAACGCTGT TTGGTGAGAA

67251   CGTATTGCAA TTGCCTGAAC GAACGGGCTG AGGTGAAGAT AGGATTTCTG

67301   TTGCCAAGGG AAAGAACAGC CGATAGCTGC TGCTAATGTA TGGCTATAAC

67351   ACGTCCCTTC TGCCTGTTCT TGATGTGAGG GATGTAGGCT GTGGAGGTGA

67401   TGGTCCCCAT AGCCATACGC TAACACTGTG GATGTTGCAA AGGCCTCTTG

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67451   GAACCACGGA AGCTCAACAT AAAGTGAAGA GACTGTATTG TGAGCCGAGA

67501   CGTTGTTGCT TGATCCGATT TCTTTAGTGC GGGTGAAGAA CTGTGCAAAA

67551   CCTAAGGAGA TTTTCTGATG TAAAGAAGTT TCGGAGGATG CTTGTAAGGA

67601   ATACCCTGTA GATTGGATAC GGAATCCTGG AGCCCCGGGG ATGCTATTTT

67651   GATGAACAAA GAGGCCGTCG GCAATCCCTT GAATTTCTAA GAAAGGCCTC

67701   TCGATATCAG AATCACCAGT TCGATTATAA CTTCTTAATA GAGAGAACAT

67751   AGTATGAAAG GATTGCCATA GGGGAGTCGT AGCAAGATCT CCTTGGTATT

67801   CAGGATTGAC CTTATATCCT AAGGGAGTCC AATTGGCATA CAGAGCTCTG

67851   TAGAGGGTGT TTGCCGTCTC TATAGAAGCG TTATTTGTTG TTGTTATCGT

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68251   TTGATGGAGT CTCAGAGTTG GCAGTTGTTG CAATACTCGC CGCATGCCCT

68301   AATTTAAGGA TACCTCCTTT TTGAGTGAAC TTATAGAATT GCCATCCCGC

68351   ACGATCCTCG ATAGAGAGGA CACCATTGCG AAGTTCAGAG GTATTTTTCG

68401   AGCTGCTAAT GAAATTATTT TCGTAGTCAG AAGCTTCTGG GATATAGGCT

68451   GAAGAAAATA AGATCGTTCC CTGATGGTTC GCATTGGGAT TAAAGATTAG

68501   AGGATTTGTA GTTGGATGTT GGTGTTCTAT AGGATCAAAA AAAGCAGTCG

68551   TATACCCCTT ATTAGCTCCA AGTTGTAAGT TGCTATTTGG TGTACAATGT

68601   ATGGCGTTGT ATCTACCAAA TGTGGTGAGG AAAACCTCAT TATTTTGAAA

68651   TGCGATATTT CCTTGTTCCG CGAAGAGTAG GCAGGTGCTG TCCTGTAGGA

68701   GCATAAGAGC ACCTCCCCAG TTTCCTTGAT TGTTGGTGAA ATATACGTGG

68751   CCACTATTTT TGATTGTCAA AAATTGTGTA CAGATAGCTC CGCCATCGCG
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68801   AATGCAGTAG TTATTATTGA AAAGAATAGT TCCAGGGTTA TCGTCTATGG

68851   ATAGGTTTGT TGTATAAATC GCCCCTCCTG AACCATTTCC TGAATTTATC

68901   GAACCAGATA ACGCTGTGTT GTTATTGAAA ATCACCGACC CGGAGTTATT

68951   TTTTATCGCA ACAGTAACGC TTGTTTGAAT GGCCCCGCCA TTGTTCCCAC

69001   AGTTGTTCTT AAAATAAATA GGACGCGTGT TATCAGAGAT CGTTGTATTT

69051   TCACTACGAA GCGCACCCCC TCCACTAGGG GCTGTATTGT TAAAAAAGAG

69101   TAGAGGTGCC CTGTTGCTTT GGATGCGGCA GTGTCCATTG GTGGAGAGGG

69151   CTCCTCCCCA GTTGTTGACG GAATTGTTGA CAAAGTAGAA AGTCCCTTGA

69201   TTTTGAGAAA TCGTGAAGTC TCCATTACAG GCAATCGCAC CCCCACGAGT

69251   TTCTCCTCCT GTACTCGCAT TGTTAAGACC TCGATTGCTG AAAAAAATAA

69301   GGGGTCCTCT ATTCTTCGTG ATTGTGCAGG CTCCCTGGCA AGCAATCGCG

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70001   ATTTCTGTGA GCCAGACTAG GGGAACTCGG TGGTGGTTCT TCCAAGAAGC

70051   GCGGATTCCT ACAGGGAGGG AGACGTCCGT TAGGGGGCGG TGTAGGGAAA

70101   ATTCCCGAGC ATGGTCTCCA GATTCTTGAA ACGCAGCAAG ATTTCCTCGG

52

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70201   TTGAGGTAAG   AAAACACAGG   AGAGAGCCCC   TGCTAAGGTA   TGGTTGTGGA

70251   AAGATCCCTG   AGAGTTCCCT   TCCAGGAGAC   CCTGATACAT   TGTATGGGTA

70301   TGTTCCGAGG   TAAACATATA   AGCAAGAGAC   ACAGATAGAC   GTATCCACTC

70351   TTTGAAGAGA   GTATTTTCTA   TGCACATTCC   AGAGAAATAG   TGGTGAGAGG

70401   ACGTGCTATT   TTGAGATTCA   TGTTCTTTAG   CTTTGGAGAA   GAACTGAGCA

70451   AATCCTAAAG   AGAAATTCGG   ACTTTGAGAA   GAGGTTGCTT   CGGTGGTAGC

70501   ACTATAACCT   GTCATATGAC   TACGAAATCC   CTTAAAACCG   TTTTTGTCTT

70551   TTTGATGAAC   CAGAAGACCA   ATGCCTTGTA   GGGAAGCTGC   ATGACCCTTC

70601   TCTTCATCCC   AGGAGGAGAG   GGAGTGGAGT   CCTGCAAGAG   CCGTATATGC

70651   CGATTGCCAC   AAGGCATTCG   TAATGAATTC   TCCTCGACGT   TCGGGATGAG

70701   GACGGTAGCC   TAGAGGAGAC   CAGTTTGCAT   AGAGCAGCTT   GTGTTTTGTA

70751   TTCGCGCCTA   GTAGAGATGT   AGGGTTCGTG   ATTGTTGTAG   TTTCTACCCA

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70851   TGGATAGATC   CAGTTGCGAA   GAGTTAATTT   TTTGTGCAGC   GACATCGACA

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71001   TGATTGTCGG   GTTGGAATCT   TCAGTATAGG   TAGATCCTGT   TTTTGTGGGG

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71101   GTCAATGGCA   ATGTGATTTA   AAGTTATAGT   ACTTCCTACT   GTCGTTGGTG

71151   TTGAGGATGG   TGTGGGAATC   GTTCCTGCTG   TCGTGATCAC   CGCACCTTGA

71201   CCTAGAAGTA   GAGTGCCTCC   TCGTTGGAAG   AACTTATAGC   AGGCCAGCCC

71251   CGCACCATCT   TCAACAGCAA   GGACTCCTTG   ACGTAGTTCC   GAAGTGTTCC

71301   TTAAATAGGA   AAAGAAATTC   ATTTCATCGG   TAAAGTTCTG   GTGTACATGT

71351   TCCCCTGAAA   ATAAAACTGT   ACCTGTATGA   CCGGTTTCGA   AATTAAAGAG

71401   TATGGGGAAG   GAGGAAGGGA   GCTCATGTTC   TATGGGATCA   TAGAACAGCA

71451   CTCGATAGCC   GGGACGGGCT   CCTATTTGCA   GATTCATATT   AGGAGTCGAG
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53

71501 TGAATGGCGT TTCTGTATGG AGGATTGAGG GCATGCTTGG AGGCCGTATT

71551 ATTGTTAAAG ATAATATCTC CATTATCTGC AGATAAGATG AAGCTTCCGT

71601 TTCCAGAACC TGCTGATAAG TTGAGGAGAG CCCCTCCCCG AGTTGCAGTG

71651 TTATTTAAAA AGTATACAGG ACCATTTTCT TTGATAATGA TAGATTTCGC

71701 ATGAATGGCT CCACCGTTGC TCTGGCTTTG GTTATTGTTA AAGAGTACCC

71751 CTTCTCGGTT GTTCAATATC GTGCAAAAGG TGGTAGTAAG ACCTCCTCCT

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71851 GATTTCTATG AGTTTTTTAT TCGAGGAGAT CGTGAGTGTT TGGGTAGAAA

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71951 GAATTTCCCT CTATATTTAG AGAGTTCCCA CTATAAATCC CTCCTCCTAA

72001 ACTGTCCGAA TTTAGTGCCC GATTCTGCTT GATTATGATC GGGCCTTTAT

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72101 AAAGCGAGAT TGTCAACGAA AGTTCCCTGT CCTAGGTTAT TAGTAATAGA

72151 GCAATTTATG GCAAAGAGAG CTCCACCCAA TAGTGATCCC GCAGTGGCTG

72201 TAGGATTGTC AGAGACCAAG TTTGTAGTAA ATGCATAGTT CTGATTCTTG

72251 GAGATCGTGC AATTTTGAGC AGCATAAATT GCCCCGCCAG AATTGGGACA

72301 GACATTCTTC TCAAAGAAGA CATTCCCTAT ATTTTCAGAG ATCAGAAGAT

72351 TCTTACAGGT AAGAGCACCT CCATTCGACC GATAGTACTT ATAGTCCAAG

72401 ATGAAATCAT TGTGATTCCC GACAATTGCG AGATCTTGAT TTTGGTTATG

72451 AGTAAACCCT ACTTGAGGGG CTGCTTGATA TTCAGGACTT AATGTAATAT

72501 AGGTCTCCAA AGGAAGTTGG AGACCTTCAT TAGCCAATAC AAAAGTAAAA

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72601 AGAAATATTC TGAATAAATC AATGCTAGAT TTTTTGTCTA TAATTTGTTT

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72701 GATTTTAATT TCCTTTTTTC ACAATAAAAT GCGAGTCCAA GAGTTTTAGT

72751 AAACGTACAT CATACTTTGG AAAATGGCGG CAAGTAGTCA GAGGATCAAG

72801 CTCTTTGCAT ACTTTGCTTA GAGCAGTTTT TGGTTCTCAG GGTCGTTTGC

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72901   GGGGATGCCC TAGGAACTCT TCCGAAACAC CGAGGGTCTG TTAGAGATAA

72951   AAACAAAGGA CCATCGGGGA GACTTGTACT CATAAGAGCC ACTTATCTCT

73001   ATTCCTATAG ATTTTTGCTG ATTTTGATTA TTAGAAAATA ATAGATTTTT

73051   TCTGTTTTTT AAAGTAAAGT ATTTTTTAAA AGACTCATTT TTAATGAGTT

73101   ATTACTTTTC TCTTTGGTAT CTGAAGGTGC AACAGCACTT TCAAGCAGCA

73151   TTTGATTTTA CTCGCTCCCT GTGTTCACGA ATTTCTAATT TTGCTTTGGG

73201   AGTGATTGCA TTGCTTCCTA TTATTGGGCA GTTGTATGTA GGGCTGGACT

73251   GGCTCCTCTC TAGGATAAAA AAGCCAGAAT TTCCTTCCGA TGTGGATCAG

73301   ATCGTGCGAG TAGAACACGT CGTGGGTCAC GACCATAGAA GTCGAGTTGA

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73401   AGGTTCACGG AGATCTGCCT TCAGCTCCTT TTTTTTGATA TCCAAAGTCT

73451   CAAGTTCCTA CAGTTGTTCT CTGAGGGGAC AGCTCTAAAT TTATTTCGTA

73501   TATTTGCTCC ACTACGCAAC CGTGTGACTA CAGAATACAG TCGTGCTAGG

73551   CAACCCGACC TACATAGAAT TGCCATCGTC TATATAGGAG TTCTCGATTC

73601   AGAAAGTTCC AAGATCCTAG AGCGGCTAAT CTCTTATATG AGTTGTATCT

73651   ATTCTGAATC GCAAATGTAT TTAAGATTCT TTATGGGCAA GAATGTAAAT

73701   CAAAGTGCTG TACTCTCAAA ATTACATGTA GAAAATCTGC ACATCCGTTG

73751   TGGGTTTTTC AGCGAGGATG CTGTTCCAGA GAGTGAGCCC TTCGATCTCT

73801   CCATCTACGT GCACACAGAT CGTAGCTGTC CTCTCCCTAC GAAAAAACGG

73851   AGCAGCTCCT GGGAACTCCA AACTGTAGAA CTCCCAGAGT CAATATATCC

73901   ACAGTCGGAA TTCCTATTGA TGAGACCTCG AATGCTTTCG TAGACTCTAT

73951   GATGAAACAA GGAGTCGGGC AGGATGCTAA AGAGCTATAC ACATTTCTAT

74001   CTCGTGGGAA TGAGCATTAC CAACCGTGTC TATGGTTCAG TCTCGAAGAG

74051   GAACTCGGAT TCCTTTTCGA TGAAAAAATG CTCTGCGCCC CTCTATCTGA

74101   GGATCACTAT TGCCACTCGT ATCTTGTAGA TCTAGTGGAT CAACATTTAA

74151   AGGATTTAAT ATTATCGATG TTTTTAGATC CTCAGAATAT CTCAGCAGGA
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74251   ACAGAAAGAT TTCCTCTCGA TGGTCTTACG TGATGAAACG GGAAAAAACG

74301   TCGTCGTGGT TTTTAAAGGA GTTCTCTCCT TACCCGCAAC CCAAGTCTGC

74351   AAATTAGTAG AGGAATTGAA CTCTAAGGAC TACTCCTACC TCAATATATT

74401   TTCTTGTCAC GGAGATAGTA GTCCTCAGCT TTTATTCCGT AAGGAATTAG

74451   AGGGAACTTC AGGGCGTTAT TTTACAGTGA TTTGCGCTTT ATATCTAGGG

74501   GATACAGACA TGCGTAGTTT ACAACTTGCT TCTGAAAGGA TCATGGTCTC

74551   TAGAGAGTTT GATCTTGTAG ATGCCTATGC TGCAAGATGC AAGCTCTTGA

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74651   TTCGCAGATG CTGTAGACGT ATCAGCAGGA TTTAACTCAA GAGAATTTAA

74701   ACTGATTACG CAGGCGAATC AAGGGATCCT AGAGTCTGGA GAACTCCCGC

74751   TCCCTTCAAA AACCTTCTGG GAAGGATTCT TAGCATTCTG TGATCGAGTG

74801   ACTGTCACGA GACACTTCAT TCCAATGTTA GACGCCGCTA TAAAGCAAGC

74851   GGTATGGACT CATAAACATC CCAGCTTGAT AGATAAAGAG TGTGAAGCCC

74901   TAGACTTGAA AACACAGTGC TTGCCATCTA TCGTATCGTA CCTTGAATAT

74951   GTCACAAACT CTCACGAAAA AACATCGAAA GGCCCGTTCA TACAAAAAGA

75001   GATTATCGCA GACTGTTCTC CTCTTAAAGA GGCGCTCTTC CCAGGTTCTG

75051   ATGAAGATGT TCCCTCTACC TCTGAGGATC CTTCAGATGA TCATCCTTCG

75101   GATCTTGAAG ACTCTTAATT AGTTGCGATA GAATTCAATT TTTTATATAA

75151   AAACTATCGT GTTGTTCTTA TTAAAGATA GTTAATTTTC TATCTTTTTT

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75251   CCTATGGCAT GCTATATTTC TATTTGGATA TCTACAGTTA AGCAGCATTT

75301   TATTAGGGCT TTTGATTTTA CACGTCCTCT TGGTTCTCGG ATTACAAATT

75351   TTGCTTTGGG GGTCATCAAG GCTATTCCCA TTTTAGGATG CGTTGTTATA

75401   GGGGTAAGTT GGCTAGTTTC CACATGTTCT GCACGAAGGT TTGGGAAACC

75451   GGCATTTACT TCTGACGTTG CTAGTATCGT GAAAATAGAA AAAACTCGAG

75501   GTTATAATCC CCTTGCTTGG GTGGAACAGT ACTTGAGACA GCTTAGGGTT
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75701   ACCAAGGCGT ATCAACGAGT CACTCCTCTG GAAGTCCCTT GTCTTACGCT

75751   CGTCGGTTTT GACATTTTAG ATCCCGAAGA TCAGGTGAAT TTCGTTCGTC

75801   TGGCTAACGG CATACAAACT CAGTACCCCC AAACTCAAAT AAAACTTTAT

75851   TTAATCTCTA TCCAAAGAT ATGGAATCAG TGTGACGGTA CGATTTCTCA

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75951   GTGTGTCGGC CCCCGCTCTC CTGCTCCAGA AATATCTTCA ATCCGAGAAC

76001   TTGCCTTCCT GTGATCTTCT CATTAATTAT TACGGGAAAC AACAGTCCGT

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76151   TATTTCTTTC CTGGTTCTCA AGGAGGAACG GCACCCGATC AGAGGATCCC

76201   TTGGAGTGAG CAGGAGCATC TTCAAACGTA TACCACCCTG TCTAACCCTA

76251   GATGTGATAG ATATGCTGTT CACTTGGGAA TGGAAGATTT TGCCTCTGGA

76301   GTATTTTTAG ATCCTCTTAG GGTTTCGGCT CCTTTATCTG GAGAGTATTC

76351   CTGCCCCTCA TACCTCTTAG ATTTAAAAAG TGAAGAGCTT CGTTGTTTCT

76401   TGTTATCCGC TTTTATAGAT CCCAACAATT CTGGTCAGGG AAATCCGCGT

76451   CCTATGTCCA TAAACTTTGG AAACTCTCCT TTGGGTCAGA GGTGGTCTGA

76501   GTTTCTATCT CGTGTTCTAC ATGATGAAAC AGAAAAGCAT GTGGCTGTAG

76551   TCTGCAATAA TCCACAACTT ATAAAAAAGA GTTTTCCCTC ACATTCTTTA

76601   TCTCTATTAG AGAACGAACT GGAAGAGTCA GGTTATTCTT ATTTGAATAT

76651   CGTTTCAGTG AGTCAGGAAC GCACGTGTGT TAAGGAACGT AGAATTTTAA

76701   GTTCTGATCC TTCGGGGAGG TCATTCACTG TAATCCTCAC TGATCTTCCT

76751   GAAGGGAGTT CGGATATCCG CAACTTGCAG CTAGCGTCAG ATAGGATCTT

76801   AGTTTCTAGT GCTCTCGATG CTGCTGATGC CTGTGCTTCT GAATGTAAGA

76851   TCTTAGAATA TGAGGATCCC GAGCAAGAGT GGGCGCAACA GTATGCGTCG

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76951   AGGAGAGCCT TTAGGGGTCT CAGCATCTAC GAGAGTAGTT TTAGAAAAGG

77001   ACATCGTATT CAATCTCAAT GCGGTAATCC AACAGGCCAT GTGGAAGTTT

77051   AAAAAACGGG ATCTTTTGC TGTAGAAAGT CAGGCTTTAG GAGATGACAT

77101   GCGACGTGCT TTAGAAGGTT ATATCGGCAG CAGTCTCTTA GTTGAGGGGA

77151   CTATACAGCC TCAAGTCGCA TGTAATGTCA ATGTGAGTTT TGCTACGTTA

77201   GACGAGGCTG TGTGTGCAGC TTGTGACTCA GCTCAAGATG CACCTTCTGA

77251   GGAGAACAAT ACAGATGACT AAAGATCGCA ATCTTGTGAA CGAAATCGCA

77301   GATTGATGGG AACTAATTAG ACACACCTTT CTAAGGTGTT TGTTTTGATG

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77601   TTATTTGTTT TAATGTCTTA TTTGATTAAA ATAACTTTGT TAAAATTTTT

77651   ATACATAAAT TTCTATTGTG GCTTGTCCAA GTATTTCTTC TTGGTTTACT

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77801   TAGGACACAT TGTCATGGGA ATCGAGTGGT TGATTCCTG GATTCCCAGA

77851   CACACCGTTC GTCATGGAAT GTTTACTTCT GATGTCTCTA GTGCTATTAA

77901   AGTAGAACAA ACACGGGGTC ATAATTGTTT AGCTCCCCTA GAAGCCTATT

77951   TAAGTAGCTT GAGAGTCCCC ATTTCCCAAG AAGATCTAGG CAAAGTACAC

78001   GGGAGAACCC CAGAAGATCC CTTCGTAGAT ATCACACCCA CAGAAATTGT

78051   CCAACTTCTC CCTGATGAAG AACTCTCTAC TGTAGATGAG GCACTGCAAG

78101   GCGTTCGTAG TAGGTTAACC TATGCCTATA GGTCCGTAGA GAAACCTATG

78151   ATTCAAGATC TTGCTCTTGT GGGTTTTGGT CTCCGAGATT CTGCGGACCT

78201   CATAAATTTC GTGCGTCTTG CTAATGGCGT GCAGAATCAC TATCCCCATA
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78251   CTAAAGTGAA GCTCTATTTA GCGAAGAACT TGGCAGATGT CTGGGACTGT

78301   GAAATTTCTG AAGAGGAAAA AGGGCAACTC CGAGCTCTAG GTTTAGACCC

78351   TAAAATAGAG AGTATATCCC TTACGAGTGC AGGTCTTCCT TCAGTGCCAG

78401   AAGTCGCTAC TGTCGATTTT ATGATTACCT GTTACGGGAA AGATCAGGAA

78451   GTCCAAGATC CCTAGGTGAT ACAACATCTT CTAAACTTTG CTCTAGAAGA

78501   GACCCCTTCC ATTTCCGTGC AATACCAAGA ACAAGAGAAG CTCTCTCCGT

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78601   TCCTTCTCCA CGTATTGTTC TCTGTTTATG TCTGTTAAGG ATCATTATAA

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79401   TAATTAAACA GGCCGGTTGG AGATCACAAG AGAAACTCAA TTTATTTTAT

79451   GTTGAAAGTC AGGCTTTAGG AAGAGAAATC AAAGTCAGCT TAGAGGAATA

79501   TATTCAGAGT ATGGTCGGGA TTTTGGGATC TCAGAGAACC AAGAAAAGCT

79551   TTAAGTTTTC TGTCGACTTT ACCCCTTTAG AGCAGGCTCT ACAAGAAAGA
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59

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79651   GGCAACAGCA TCTCCGACTG ACATGCACGA AGATGAGTAA CGTTTGTCTG

79701   ATACCTTAAA AGTTCCTTGC AAAGGGCTCC CTGAAAACTA AATTCCCTCA

79751   GAATCTCGAA TTCTCCTGAC TCTGAAACAA TCTTAGGTTT CCTGAATAG

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83551 CAAAAAACAA TTTTAGCGGC ATTTCTGAAT CCTAAGGAGT TGAGCAGTAC

83601 CATACTGCAA CCTATATCTC TAAATCTTAT CTTAAATAGC AAAACTTACT

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83751   GCCAAGCTTC CAACACTTTA TTATGGAGCT AGAGTGTCGA GGGTATTCGC

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84851   ATATTCTCGA ATTACCCACT TCGCTTTAGG GGTGATTAAG GCCATCCCCA

84901   TTGTAGGGCA TCTTGTTATG GGAGTCGATT GGTTGATCTC TCATTGCTTC

84951   GAGAGGGGAG TCTCACACCC TGGGTTCCCT TCAGATATTG CTCCTATACT
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85051   AGCTAAAGAG CCTTAGGAAA ACTATCGAGG TTGAAGATCT AGATAAAGTC

85101   CACGGGCAAT ATCAAGAGAA TCCTTATGCA GATATGGCCT CTAGTGAGGT

85151   TCTTAAACTC GATAAGGGAG TTCATGTTAG CGAGCTTGGC AAAGCCTTTT

85201   CTAGAGTTCG CAATCGCATC ACCAGATCCT ATAGTTATGC CCCTACTCCT

85251   CAGTTGGACT CTATAGCTAT TGTTGGTATA GATCTCGTCA GTCCTGAAGA

85301   ACAAGAGAAT TTAGTACGCT TGGCGAATGA GGTCATTCAA CTCTATCCCA

85351   AATCAAAGAC AACTCTATAT CTTCTTATCG ATTTTAATAA GGAGTGGGTA

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85651   CTCGGCTTTC CTTACCTATA AATACCGAAA AGGATAAGAC AGAGCTTTAT

85701   AAAGAGATTT CTCGTACACA CCATCAGTTG CATACTTTGG GAATGGGACT

85751   TGGAGCCCAG GATTCAGGAT TGCTCTTAGA CCGGCAACGA CTCCATGCTC

85801   CTTTATCTCA AGGGTCTCAC TGCCATTCCT ATCTTGCAGA TCTCACCCAT

85851   GAAGAGCTGA AAATTTTGTT ATTTTCAGCA TTTGTGGATG CTAAGAACAT

85901   AAGTAAGAAA GAGCTTCGTG AGGTATCTCT AAATTTTGCT AACGATACTT

85951   CCGTAGAGTG TGGCTGCGCT TTTTACTTTT AGTGTCCTAT GATGAGAAGG

86001   AGAAAGACGT AGTTGTCGTT TGTAATCATT CTGAACCTAA TATCCTCGGC

86051   CTGCCTCCTG AAGCAGTCTC TCAGCTTATT GAAGAGCTTA GCGATGAAGG

86101   CTATAGCTAT CTGAATGTAG TGCGTTGTGA TCTCTCCGGG GAGACTACGG

86151   TTCAACAACG TCTGCTATTG AATGCCGATG AAGGGAGATC TATGACGGTG

86201   GTGATCTCAG AGCTTCCTGA AGGGCACCCC GATATTCGGA ATTTGCAGTT

86251   GGCATCCGAA AGAATTTTTG TTTCTCGTGA AAAAGAAGCT GCTGATGCCT

86301   ATGCTTCAGG ATGTAAAGTG GTCGCTTTCG ATGATGAGCA TCTCCCTTGG
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86351 GTCTCCAGTC ATATTGCCTA CGCGGAGGAG ATCAGAGAGA AACAAGAACA

86401 AACAATGCAA GGGTCTTTAA CTGAAGAGCA GTTAGGAGCA CTCCTCTGCA

86451 ACACAGTCTC CACAGAGAAA AATCTAGCCT TTGCTCTAGA CGCCGTGATA

86501 AAACAGTCTG TGTGGAGATT CCGCAATCCG GATCTTTTTG CTTATGAGAG

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86601 ATTTAGACAT GATACCGTAC ACAAGTTCTC AGGGCATAGT CATAGAAGAT

86651 AGTAGTATCG TCCGTACCTC TCAAGAGCAT ACACTCATTG TGAACTGTGC

86701 AGCATTCGAT AAGTTAGCGA GCCAAATAGA GTTCTTATGC CCCAGTGACG

86751 TGTTGCCCAT TTCTGGTAAA GACCCTTTGA TTTCTGATGA TGAGGATGAG

86801 GAACTGAATC CTAAAGTTTC ATCTGCTGCA GACTCTAAAG ATAAAACCTA

86851 GGGAGTGAAT TCTACACGAG AATCGAGAGG AGAGCGAGTC TTTCAAGGAT

86901 TCATAATCCT TGTTAACGTA TGCATAAACA AGTGAAGCCA TTGCAACGTG

86951 AAGTAATCGC ATTGATGAAA GATGCTTTCC CTAGGGATGC AAAGCAGATC

87001 GTATTCCCTT CTTTCCAAAA CAGACTATAG ATTCAAAAGA TATTCTTTCT

87051 TTTCAAATAG ACTTGAGAGA GGGGGGGGGG TTCTCATAGA GTGAGAATCT

87101 TGGCCTTCAT TGCTAAGTTC TTCGATGATG GATAGAGGAT TCTAAGACGA

87151 CCGGGGCTAC AGAAAACTCT AAGCAGAGCT TAGAGTTTTA AAATGTGGAT

87201 TTTAGTCCTG TAGACACTCG GTGGTTTGTA AATCCATTTT TCCCGTCAAA

87251 GGTATAGTTT AGAAAGGCCT GAGTGTCCTC GGTGAGATCT ACTACATCAT

87301 GGATTTGTAC AAACAAACCG TGGCGGCGTA GATTTGCTCC TGAGATCGAA

87351 GTGCTCTCTT GGTTTGAGAC GACAGTCACA ATATTGTGAG GGTTGACACG

87401 ATAGATATCA GGCTTGTAGG CAAGTTTGAT GGTCAGTGTA GAAGGAGCCT

87451 TCTTAAATGG TGTGAACCAT TGAGAAGAAC ATCCTATCGG TAGGGAAACA

87501 TTGTACCCTT TACCTCTACT AAAGCTACGT TGCAGATCTC CAGTTTCTGT

87551 GAACTTACTT TGCCAACCAC CTAGGAATTC TGCGGAAATA AAACCTGAAA

87601 GATCCCAAGC TTGAGCCAGA GGTCTTGTAA GAAGACACCA GTTTAGGAAA

87651 GGATGTTCTG CAGAAATAAG AACATAGTAA CTATTGTTAT GCCATTGCCC

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87751   TTTTGGAATA ACCATAAGCT GCTTTCCAGG AAATTAAGGC CTCGCTCTTT

87801   TGAGTCACGA TAGGGAATTG ACCAAAGAAC GAGAGTAAAT ACATTTGTTC

87851   TGAGCAACGT GAATCGTAGG GGTTGGCGTT AGTTTTTCCA TAAAGCTGCC

87901   CGAAAGAAAG TCCTAACGTA GTGTGGTCCG TGTAGTTCAT AGATAGCGCA

87951   GCTTGGTAGC CTCCATAGCG ACCTGAAAAG CCCTCATGTC CTTGTCTTGG

88001   TGTGTGTTCG ACATAGGCTC CTAAAGCTTT CGCGGTTATG GACAACCCGG

88051   GATGATCTAT CAAAAGAACA TCTTGGAGAA TATCAGAGAA TGCCTGATTT

88101   CCTAAGAAGG AAATCCATAA GCTGTTGCTG ACAATTTCTC CGTAACGCTC

88151   GGGATCTAAG ATATAGGTAG AACGCACGAG AGTGTCTGAA TTCCATACAG

88201   CATAGAGAGT ATTTGCGCTA GGAGAGGGAC CTCCAGGAAA TCCTCCATCA

88251   GGAGCTGGAA TTAACAGGGG ACGGGACCAT GTGTAGGACC ACTTTCCTTG

88301   GTAGCCGTAG TGGCTTGGAG TCGCAATCTC CCCATCAGGA AATCCTGTCT

88351   TAGTAACGGT TGCTCCTTTG AAAACAGCGA TAGGAATTGC TACTGGAGTT

88401   TGTAATGACA CCATATCATA AAGATCTGTA ACGTCATGTT CATCAAGAAC

88451   CAGAGCTCCT GTTAAAGTGA CGTTTTTTGT GCCTGCATTT ACTGATGCTG

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88551   ATCGTAAAGT CTACAGCGGC AGGTGCTCCC GTGGGTGTTG CCAGCCCTAA

88601   GGTTCCTCCA GAGCCCAGGG TAAGCTGACC TGAGCCCTGA GTAGCGAAGC

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88701   ATCTTGACTG TTCCTAGAAG TATAGTTGTC GTGTTGGCAG GCAACAGGAG

88751   TTCTGTAGAG GAGAGTCCCT TACTTGTAAA GACTACAGAT CCTGAAGCGC

88801   CATTAGCGTT GATTGTAATG TCTTTATTAG ACGGACTTGT GGTTGGGAGG

88851   CTATGTGTAA TGGGATCATA AAATACAAGA CGTGAGCCTC CTTGTGCAGA

88901   TAGAGACACA ATCTCTCCCC CTGCTTCTAC AGTGATGGCA TTGCGGATTC

88951   CAGGTTTTGT ATTGAGCATG TTTCCTTGGA ACGCAATATC ACCTTCGGAA

89001   GCCAAAATCG TAAGTGTCGA TGTTTGCTTC GCAGGGTCTC CAACAGAGGG
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89051 GCCTATGAAA ATAGCTCCAC CCTTCTCCGC GCGGTTTCTA GAGAATTCAA

89101 TAGGACCGCG TCCTTGAATA TTGAGCACTT TAGCACAGAT GGCTCCGCCA

89151 TTTCTCGCTG CAGTGTTGCT ATCTAGGAGC AAGGCACCCT GGTTCCCTAC

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89251 TATAAGAGAA GGTGCACTTC CCCTGATTGT TTTTTAATTC GAAAGTTCCC

89301 GTAGGGATGC AGATGGCTCC GCCACTTCCT AAAGCATAGG TTCCTGATGA

89351 AGGGGTGACG CCTTTTAAGC TGTTCACACA GGAGTTGGCG GTGAAGATGA

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90001 CTTCACCCTG ATTCGTAATT GGAGGAACAA AGTTCCCTCC GAGTCTAGTC

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90101 TGAAGATTTG AAAGAAAGAG GCATGCCTCA ACCCTGTCGT TAAATAAGGT

90151 TTAAAATCGT AATTTGCTTC CTATATCTAG AGTATATTGA CGGGAGGTTC

90201 TGCGAATATC ACATCCACAG TGCCCGAAGA TCTCTAGAAC ATCATTTACT

90251 GAAGTATGGC TGGATGCTTG TACTAGCAAA GTACTTCTGG TTAGATTATT

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90351 CAGGATTGTG ACGATAGACA TCAGGAGCAT AGGCTACGAT TATAGTGTAA

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90451   TGCAACGTTG AGTAGATGAC CGTGTCCAAA AATCCTCCCC TCGGGGGTAT

90501   TTTCTTGGAT GCCCCCATGA GTCGCGTAAG CAACTTCAGC TTTTACAAAG

90551   GGAATGATCT GCTTGAGGTT TAAGATGCGA GAAGAGAGAG TGATGGGAAG

90601   GTTCCCTTCG AGTTCTCCTA ACCAGCAATT GTTACTCCAA GAGCAGCGCC

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90701   TAGGTAACTC GAGAAGTGCC TCCTGAGAAG AATCTCGATG ATCCAAACAG

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91351   AGTGAGAGCT CCATTGGTAC TCTGCACATT AACGACAGCC GCTTTAGTGC

91401   CATCCAAAGA ATCCAGATTG ATTACAAGCT TGTTTAAGGT GATAGCACCG

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91601   AATGTAGATG TAGCATTTGC AGGGGTTGCT GCTTCGGTAG CAGTGAGGGT

91651   TTCTCCTGAA AAGACAATAG TCCCTGAATA CGCACCATCT GCACTGGCTT

91701   TGGGATTGAC GACCACAGTA GCGGCTGCGG ATGCAGCAGA TAAATCATCA
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91801   AGTGGCAAAC TTGGCATCTT TTCCGAAGTG AATACTATTG CGAGTAGGTG

91851   TCCCACTAGT GATGCTGAGG TTCTTGTTAA AGAGGATATC ACCTTGATTT

91901   GCGGATAGAG AGAGCTCCCC AGATTCGGGA ATAGCAATAG CGCCTCCTTT

91951   TCCAGCTGTA TTTCCAAGAA ATATTGTAGA TTTATTAGAA TCTATAGAGA

92001   TCTTTTTGCC ATAGAGGGCT CCTCCTTGTT CGGAGGCAAT GTTTTCTAGG

92051   AATGTAACGC TGTTTTCTCC AGATATAGTC AGGCTAACAC CTGTTGGTGG

92101   GGGGGTAGCT GGAGGAGTAC AGAAGATGGC GCCTCCATAT CCTAACAAAG

92151   GAGTGACTGC TGGTGGTGTA GGTGGAGGTG TAGGTGCAGG TAAGGAGTTT

92201   TGTGGAGATG CTGTATTGTT TTGGAAAGTC AGGTCGCTGT TATTAGAAAA

92251   TGTGACATTT CCGTTAGCAT AGATAGCGCC TCCTGAGCGC GAGCTATTAT

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92651   GTATCTGAAG TCAAAGATTC ACAGTTATCG AAGATCATCT GACTAAATCC

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92851   AGAGGTTCTG GATATGGCAT TATCAAGATT CGCAATGTAG AGATCCCCTG

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92951   ATCTTCCCAC TCGATCCATC AAAGTTCTCG GAAGGCATGA TAACTTCTAC

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93051   ACTTACGAAT AGACGTTTTC ATTTGCACGT AGAGATGAAA CCAGATTATC
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93151  TTAATCTCTT AATTTTGACA GCTTTAAGAT TACAGGATAT TTTAAAGGGC

93201  ATTTTCCCAT TTCTTACATT GCTTTCTTAG AAGAATACTT GATAGAAAAT

93251  GGCGATTCTA TTTTTGAAAA ATCTCAAGAA ATTCTCCCAA ACGAAGATGT

93301  TTTAGAGAAC CTGTAAAGTA GAAAATGGCG CTACGCCCGA GACTCGTGAA

93351  CATGTGTGCA TAGAGGGACC TATCTCTGAA TACAGATAGG TCCCAAAATC

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94151  TAGGTTCTTA AACTGTGCTC CAGATTGCAG ATGGATGGAG TTGTGTATTG

94201  TATTTCCGTC TTGTGATGCT GTATTTCCTT TGAAGATGAG ATCTCCGCTT

94251  TTCACGGATA TAGAGATCGA TCCTCCAGGA GCAATGGCAA TGGCTCCTCC

94301  ATTACTATTC ACGTCATGAT AAGCATGATT ATTTTCAAAA CACGAAGGTC

94351  CTCGAGTCGT GAGTGTGAGA TTGTGGGTAG ATATGGCGCC GCCATAACCT

94401  TGGCTCACAT TGTCTCTAAA CACCAGGTAG CGGTTCCCGC TGAGATTTAC
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70

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94501   CTCCACTCCA CGAAGAGTAG TTCCCACAGA AAGTCACTTC CTCACTATTT

94551   TCGATCATCA CGGAACCAAG ACTATAAATC GCTCCTTGTC CTTGAGGTAG

94601   TAGAGGTGCT GAGGTGAACG CTAAGTAAGA AAAATTAGAG AGAGTGAGAG

94651   TGGTGTCTCC AACGCGGTTC GAAATGGCAG CGCCAAAACC CTCGGTCATA

94701   AGGTTGTGAA AAGTGAAGTT GCAACGGTTG CCCATGAAAA AAAGATTCCC

94751   AGATCGATTT ATAAAAACCC CAGCATCTTC TTGATCATGC TTAACGTTGG

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97001 CTTCCGGTTG TTGTAAGGGT ATTTCTTACA AAGGTAATGT TTCCTGTCTC

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97201   TACGTTTGAA GCAAAGATCA GAGTCTTATT GTTAGAGATT ATCAGTTCAG

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97401   TAACATAACC TGTGTTATTT GCTATGCGAG CGCCTGCTGT AGTAGCAATT

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97501   AGTGCCAGTT AAAAGGAAAG ACGCTCCTTT GATAGCTCCA CCATCTGCAG

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97701   TTGCTGTTGT AGATGCAGCA GCACCTGCAT GAGTGCCAGC ATCTATAAAG

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97951   TTCCTCGTTA GCTAGTGACT GTAGGTGACA TGAGAAAGCT AACACGGAGG

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98051   AGAGAACTAT TCGCATCAAT ATAGAAACAA AATAAGTAAA TCAAGTTAAA

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98151   ATTTTATATG ACGCAAGTAA GAATTAATA ATAAAGTGGG TTTATGAAAT

98201   CGCAATTTTC CTGGTTAGTG CTCTCTTCGA CATTGGCATG TTTTACTAGT

98251   TGTTCCACTG TTTTTGCTGC AACTGCTGAA AATATAGGCC CCTCTGATAG

98301   CTTTGACGGA AGTACTAACA CAGGCACCTA TACTCCTAAA AATACGACTA

98351   CTGGAATAGA CTATACTCTG ACAGGAGATA TAACTCTGCA AAACCTTGGG

98401   GATTCGGCAG CTTTAACGAA GGGTTGTTTT TCTGACACTA CGGAATCTTT

98451   AAGCTTTGCC GGTAAGGGGT ACTCACTTTC TTTTTTAAAT ATTAAGTCTA
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73

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98551  ACAGGATTTT CGAGTCTTAC TTTCTTAGCG GCCCCATCAT CGGTAATCAC

98601  AACCCCCTCA GGAAAAGGTG CAGTTAAATG TGGAGGGGAT CTTACATTTG

98651  ATAACAATGG AACTATTTTA TTTAAACAAG ATTACTGTGA GGAAAATGGC

98701  GGAGCCATTT CTACCAAGAA TCTTTCTTTG AAAAACAGCA CGGGATCGAT

98751  TTCTTTTGAA GGGAATAAAT CGAGCGCAAC AGGGAAAAAA GGTGGGGCTA

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98901  AAACTGTACA ATTACAGGGA ATACGTCTCT TGTATTTTCT GAAAATAGTG

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99101  GGGGGGTATC TCCTTTTCTA ACAATATAGT CCAAGGTACC ACTGCAGGTA

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99251  ACAAACTACA AAAGAAATT CTATTGACAT AGGATCTACT GCAAAGATCA

99301  CGAATTTACG TGCAATATCT GGGCATAGCA TCTTTTTCTA CGATCCGATT

99351  ACTGCTAATA CGGCTGCGGA TTCTACAGAT ACTTTAAATC TCAATAAGGC

99401  TGATGCAGGT AATAGTACAG ATTATAGTGG GTCGATTGTT TTTTCTGGTG

99451  AAAAGCTCTC TGAAGATGAA GCAAAGTTG CAGACAACCT CACTTCTACG

99501  CTGAAGCAGC CTGTAACTCT AACTGCAGGA AATTTAGTAC TTAAACGTGG

99551  TGTCACTCTC GATACGAAAG GCTTTACTCA GACCGCGGGT TCCTCTGTTA

99601  TTATGGATGC GGGCACAACG TTAAAAGCAA GTACAGAGGA GGTCACTTTA

99651  ACAGGTCTTT CCATTCCTGT AGACTCTTTA GGCGAGGGTA AGAAAGTTGT

99701  AATTGCTGCT TCTGCAGCAA GTAAAAATGT AGCCCTTAGT GGTCCGATTC

99751  TTCTTTTGGA TAACCAAGGG AATGCTTATG AAAATCACGA CTTAGGAAAA

99801  ACTCAAGACT TTTCATTTGT GCAGCTCTCT GCTCTGGGTA CTGCAACAAC
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100751  TGTTCCTGAT CTTATCCGCA ATGATCCCAA ATGCACTACA GCACTTGTAA
100801  TCAGCGGAGC CTCTTGGGAA ACTTATGCCA ATAACTTAGC ACGACAGGCC
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101151  GGAAATTTTT TAATAGAAAC CCGTTCTTTA AAATACGTTT CTTTAATTCT
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101301    GGTACGTCTC TTTCTTTTTT AAGGGAAGGG GTGTTGTTAC ACCCATCCTA

101351    AGATTTGTGA GATTCCCCTC AGGCAGTAAC TTTTACAATC GTACTTTATG

101401    TTTTGATCTA GCTGTTTTCT TGTCTTTAAT TTATTCAACC ATCGAGAAGA

101451    GAGATCCATG AGTGGAAATG TATTTTATTA GGATCATCTC TAAGGATGGA

101501    AATGATGAGC CCATTCCAAC AACCTGAGCA ATGTCATTTT GATGTTGTGG

101551    GAAGTTTCTT ACGTCCTGAA AGTCTTACAC GAGCACGCTC TGATTTTGAA

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101751    CATGGCGTGG ATCGTCGCAG GGACTCTAAT GACCCTGAAA TTGGAGTGTA

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103851   CTACAAGCTG TTGTATGGAG CGCACATCAA CAAAGGATCC CCATAGCGTG

77

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105201    TTAGCGATAG ACTGATAGAG CTGCCTTGGA GGGCGCCTCC ATTGTCATTA
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106401  AGTATAGCGA GTATCCATAT CATTTTAGT GTAGCTGTAG CTTAGCTGGG

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107651  TGTCTCCTTG ATTTGCAGAG AGACTTAAAG ATCCAGAGTC GGCAATTGCA

107701  ATAGCGCCGC CCTTGCCTGC AGCTGTGTTC CCGCATCTAT TATTTGAAAA

107751  TAGGGTAGGG CCAGCAGCGG AAAGATCTAG ACCATGGGCA CAGATTGCTC

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109251   TGTGGTTGTC TGTATGGAGA TAACTGAATT TAGCATCGAA CGATAAAGGA
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111951   ACGTAGACCA CGAGGTGCCA TTTGTTAAGG AGGTCAGGCA GTGAGGGTGA

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112101   TGACCAGATG GCTAGCGTCA AAGATACGTG GATCAGCAGC AACCTCTTGG

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112701   CGATCTCCTG CTGTATAGAA TGGATGTTTA CATAAGCATT CCAAAGGCTA

112751   TTAGGAACTA AAGTCGCACG AAGCTCTGGT TTAGGAGTGT ATCCTAACGC

112801   TTGCCATTCC GCGACCAAAG TCACCTTCCC TCCAGCTCCT ACTTTAGGAA

112851   CCAGAGTCCA ACTCCCTTGA TACCCATAAT CCGGAGCAGC CATGCTAGAA

112901   GGAATCGGAT TGAAGTCGTC TAAATTTACA GTTCCTGAAG TAGAAGAAAG

112951   ATCTAAGAAA GGAAGATTTA AGTTTGCTTT CAACCCAGGA TTGTCATAGA

113001   AACTTCCTTC ATTGTTATGG AATTTCAGAT CCCCTGAGAT TTTTAATCCC

113051   CCACTTGTGC TGTTTACGGC AATCGTTATC ATACGCTTGC CATCTAAAGC

113101   ATCCAGATTT ACAGAGAGAT TCTTTAGATC GATGCTGCCA TCTGTATTGT

113151   TAGTTGTCGT GGTCTCTAAG GTCGTTCCTG CATCCATGAA TACTGTAGAA

113201   TCAGGCTGCT GTGTGAAGGA ATATACTTGT AGGGTGGCTC CTTCTTTTAA

113251   AACGACATTT CCTCCTGCTA AGTTGATCTT CTGGTTCAGT ATGGTGGTAG

113301   TATTTGCAGG AATCGAGGCA TCTTGACTGG GGAGTTTTCC AGAAGAAAAT
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113351  ACTATAGTTC CCGTGTTTGG GTTTGCAGGT GCTACAGGGA CTACAGGCAC

113401  TGAAGCTATA GGACCATTTT TTGGTTGGGG AGGAGGAACA ATAGCTTTGA

113451  CAACAGGATT GATGACTAAC TCCTCTATTG TTCCTCCAGA TGCAGGAGCT

113501  TCCATCGTAA TAGGATCATA AAAATAAATC GTATGACCAG GAGCTGCTGC

113551  AAGCTTAGTG ATCTTAGCCC CTGCACCTAA ATGGATCGAG TTGGGAGTTG

113601  AAGTTCCCTC AGTCGCTCGG TTCCCTGAGA AAGTAATATC CCATCAATA

113651  GCCTCTAAGG AAAGTTCTCC GCTATCGGCT ATATAAATGG CGCCTCCCTT

113701  GCCTCCAGAA TTATTGGTAA AGGAGACAGG ACCGTTAGCT GTAATCGAAA

113751  GGTTTTTCGA ATAAATCGCT CCTCCCGAAG TTTCAGCAGT ATTGCCATCA

113801  AAGTTTATGG ATTCACTGCC TGAGATTACA CACTTAGGAG CATAAATACC/

113851  ACCACCACTT CTTTTTGCCG TATTGTTAAT GAAACTTAAA CTCTCATTTT

113901  CAGTAAGAGT TAAGCTTTTT GTAGCTATGT CAGACTCTGA GATATTACAG

113951  AGGATCGCTC CACCACAACC TTCTTGATCT GTAGTTGTTG TTGCTGTTGC

114001  TGTTGCTGAA TTTCCAGAAA ATACAAGAGC CTTATTTTTG GTAAAGGAAG

114051  TATTTCCTTT AGTATGTAGA GCCCCTGCTG TCTTTGCTGT ATTTGTGCTG

114101  AAGGTCACGG TTCCCGTACT TCCCGTAAGA GTAAAATCTT CGGTTTCTGT

114151  ATAGATCGCT CCTCCTGCAG TTTCGGCAGT ATTGCCATCA AAGGTAAGAG

114201  TCGTGTTTCC ATGCAGAGCA CACTTGGTCG CATAGATCGC ACCGCCACTT

114251  ACTGTTGCAG TATTACCAGA GAGACTCACG TTTTCGTTAT CTTCAATCCA

114301  GAGTCCTTTT TTAGTACTTA CAGATGCTGA CTCAAGAAAC GATAGGATTG

114351  CCCCACCGCA ACCCTCTTGA TTTGCTGAAG AATTACTCGG GCCCGTAGCT

114401  TTGTTCCCTG AAAAGAGCAG GTTGGTATTA CCAGACAGAG AGTTGTTGCC

114451  TTTAGAATAT AAGGCGCCGC CTGTCTTTGC TGTATTTGTG CTGAAGGTCA

114501  CGGTTCCTGT ACTTCCTGTA AGAGTAAAAT CTTCAGTTTC TGTATAGATC

114551  GCCCCTCCTG AAGTTCCAGC AGTATTGCCG TCAAAGGTCA GGGAGCCGTT

114601  TCCAGTTAGA GTACATTTGG TAGCATAGAT CGCACCACCA CTTACTGTTG

114651  CAGCATTACT AGTGAGGCTG ACTTCTTGGT TGTTTGCAAT CGATAGTCCT
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114701   GTTTTATCGC TTACGGATCC TGAATCAATA AAGGCTAGGA TTGCCCCACC

114751   GCAACCCTCT TGATTTGCTG AAGAATTACT CGGGCCCGTA GCTTTGTTCC

114801   CTGAAAAGAG CAGGTTGGTA TTTCCAGTCA GCGAGCTGTT TCCTTTAGAA

114851   TATAAGGCGC CGCCTGTCTT TGCTGTATTT GTGCTGAAGG TCACGGTTCC

114901   CGTACTTCCC TTAAGAGAAA AATCTTCAGT TTCTGTATAG ATAGCTCCGC

114951   CACATCCTGC TGTCGCAGTA TTCTGATCGA AGGTAAGAGT TGTGTTTCCA

115001   TCCAGAGTAC ATTTAGTAGC GTAGATCGCT CCACCATTCG CAGTTGTTGT

115051   ATTACTAGTG AAGCTCATTT CTTGATTCTG AGAAATGGCT AATCCAGTTT

115101   TGTCTGTTGC TGTAGCAAGA TAACAACAGA TTGCCCCACC ACAACCTTCC

115151   GGGTTATTTG CCTGTGCTGC TGAGCCGGTT GTTTTATTTT CCTGAAAAAG

115201   TACTTGAGTG TTGCCGGTAA GAGCAAGATT GTCATCAGAG CTCCAAGCAC

115251   CCCCCGTCTT TGCAGTATTA GATTTGAAGG TAACGACTCC TGTATTGGCA

115301   TCTAGCGTGC TATCCTTTTC TTTTGAGTAG ATCCCCCCAC CTTTATCTGT

115351   AGCAGTATTT GAGGAGAAGG TCACCGTTCC TGAGTTTCCT TGGACTGTAG

115401   TGTTTGCTGT ACTACAGAGG GCCCCGCCAT TTTTTGTGCT AGTATTTTGA

115451   TCTAAGAGAG CTGCTGTCGT AGTCTTAGCA AGATCGATGC TGTAGGCAGA

115501   AACTGCAGCT CCATCTTTTT CTGAAGTATT TTTTTGGAGG GTGACACTGG

115551   CATTGTCAGT AAAAGTCGCA GTACCTCCCT CTGTATTTGT CACACAAATA

115601   GCACCCTTGC CGCCCGAAGT TCCTGTTGCT GGAGCTGAGT CGATTAAGAG

115651   TGACGAGAAT CCTGAGAAAG AAAGAGCTGT GTTGGTATTG TTAATTGCAG

115701   CACCATCATG CGTAAGCGCT ATGGTTTGCA GAACCAATGA GTGATCAGCT

115751   CCAACAAAAC TCAATGCTCC TCCTGTGTTT GTAAACAGC TTTTATCTGC

115801   AGGAGTAATT GCAGATACAT TCGTAATAGA AACATCGCTA GTGAGAGTGT

115851   AGGTAGTTCC TGAAGCATCC GAAGTTTCCT TGGCAGTGAA TGCTGCGCTA

115901   CCACTACTAC CATTTTCATA GTTATCGGAT GATGAGAGAT CCGTGTTAGC

115951   AGCCATTAGT GGATGTAGGG AGAAAACTAA AGCCGAAGAG GTAAGTAGCC

116001   AAGGTAAAGA ATATTTCATG TGTCTTTGGG GAAAAGCTTT TTATCAAAAA
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116051  TACTCCCATA GCATGTGGCT TTAGGAGCAT GGTGCACCAA TAGAGAATAC

116101  AGTTAAATAA ATCAAGTAAA TGCTCTGGAG AAGACTCTCA GTTATAGAAG

116151  TTTCAATCTT GGGAGAGAAG CATTTAAGGT ATTTTTCTAT ATTTAAGAGT

116201  CCCTTAAAAC ATAAGGGAAA TGCTTAAGGG TAGGGGAGAA GGTGTACAAG

116251  CGGTTTTGCT TTTAGACCTT CTTGAATTTT AGAAGGAGAG AGTAAGGAAG

116301  ATGGTTATCT AAACCACGGA TCCTTATTTG TTCTTTCTGT GTTTCCGTTT

116351  TTCTCTTTCG TCATAACCGT CAGAGAATGG ATTGGAGGGG CTGAGGTTAG

116401  CCGTGCTTTT TCCGTCTGGA GGCGGAGTTT TAAGAGATTG ATTCGATTTC

116451  CCGCTTTTCT TCTTAGATTG CTGTTTCTGT TCTTCATCTT GATTTTGCTG

116501  TTGCTGCTGT TTATCTTGGC GATCACGAGG GGAACGGCGG GAAGATGAAG

116551  AAACTCGAGG AATTGAGGGT TCTTTTCCTC CCTTAGGGTA GACCGGCTCA

116601  GGGTGTAGAA CCGTCCCCGT GGAGAAATTA GGAGAGCGGG AACTTGCAGG

116651  CATTATGGGT GTAAACGCAC TGCTCGCTCC ACTACCGAAT GAACTGCTTC

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116851  AGAAAGATCC TTGAGCCTCC CGACCGATCC TACGATGACG GGCATCTTGG

116901  CGTTGTGAAG CTTCGTGTTC CTCCATGCGG GCAGATGCAG AAAGATCTTT

116951  TTTCTTTTCC ACTGCGATTT TTTTTGCATC GTCGGCGGAT GGAGTCACTA

117001  GAATAGGCTC CGCGGTCTCT TGGGTTTTCT TTTCCATCCT CAAGAGGTGT

117051  TCCCTACGGA AATAATCTAA GGTGAGCTTA TTCAAGGACA TGAAGTATAG

117101  CCCCACCGTA ATCAATCCCA TGACAAACAT AGGGTTGGCA AAGACTAACA

117151  TCGTCCCACT AGAGGCAACG AAAGCCCCTG CAATAAGACC CGCAGCAATC

117201  GCTAATACAA TGATAGGAAC GACGATAGCA GTGATTGCCT CACCGATTTT

117251  CTTGGCCTTC GGACTGTCCA GAATATCAGA AATAAGTAGA GTAACTCCCA

117301  AAGCTCCCAG GGCAAGTGCC GGAGCGAGAG CATAAAGCAT AAGGCTGTTT

117351  CCTGAAGCAG TCAGGAGAAT CGAAAGGATC GCAATTGCCG CAAGGGCAAT
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117401   AATGCCTGTG TCATAGACAT AGCGCATTTT AGGATATTTA TCAGGAATAG

117451   TAATAAATCT TTTGAATAAC CCTGTGGATG ACGTTTTTAA ACGTTTTACC

117501   ACGCTTGGCT GCCCTGATGG GGATGCTGCT GCAGGAACTT GAGGTTGACC

117551   TAAAGGGTTT ATAGGGGGTT GGCTCATACT ATCAACTTAC TGTAATTATC

117601   ATTAGGCCCA TGAATTTTCA TTCATAGGAT ATATTTCATA CTATTATAAG

117651   ATTTAATAGG ATTTAGTTAG TTCTCTTTTC TTCTGAGTCT TAACTTTTTT

117701   ATTAAATAAA GTTTATTTGT TAAAATCTTA ACAGATTTTT AACTAAAACT

117751   TTAAGTTATT TTTATTTGGA ACTTTTAGTC GAAATAAGAC TCGCTTATGA

117801   GAGGGACATA CTCATCAGCA AATGGAGGGG GCGTGTGAGG TCGTGAGGGT

117851   GGAGGCTCAT ACGGGGGGAA AAGATTTTTA TGCACTTGGA AGAGGGTAAC

117901   GCTAGTAGTT ACAGACATGA GAAGCCCCAA GGAGATAAAG ACAACTGGAG

117951   GGGGGATAAA GACCAGACTA AAGACCAGAC CGATAATCAC AGCAATCGTA

118001   AGAATGTGGA GGAGCCAAGC CATAGCATAC GAAGCAAGAT GTTGGCAGCT

118051   TTTTGTTTTT ATAGCGTTAA AGAGAGCCCG TAGGGGTAGG GTCAAGGCAG

118101   CATATGTAGA AGCGCAAGGG ATCAGGATAA CCTTAAGAGC TCCTAAGACC

118151   GAGGATACCA GTACTTCTAT GGTAAGAGCA GTTCTGGGAT AGCTCTTCGC

118201   ACAGTTTTTT AATTTTCGAG CTAGTATTCG TTCCGGAAAA ATGCCATTCA

118251   GGTATAGCTG AGAGCCTTGT TTGCAGATAT TTTTGAATCC CATATCCGTT

118301   TGAAAGAGAA TATTTTATGA AAAATTATGT AAAAATTCTA AGAGGATAGT

118351   GGTTTTTAGA CAATCGAAAT TCCTGAAAAG GCAGGAAAAT GAGAGACACA

118401   AGTAGACAAA ATCTCCTGAA GTTTTTGTAT GGGCCTGTAA AAAAATCTTT

118451   CTGGAAACTG GAAATTAGAA GTTCATTACA GCGGAACCAC CGAAAAATGC

118501   GGAGGTTTTA AAAGTATGGG ACGTTTATT ATTGTTGTGA TCATCAGCTA

118551   TCGAGATATC ATTCCCAATA GACCAACCGT AAAATCCCTT AATAAAACTT

118601   CCCGGCCAAG GGGTGAGCTT CACGTTAGCT TCGATTTCAC GTCCTTGATA

118651   TTCAAAGATG CCGCGAGAAG AAATTAGGTG ATTTTTGTGA AGTTTTTTTC

118701   GGAATCTTGT AAGGCGGTAA GCAAGCCCTA AGTTACAGAC AGATGTCGAG
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118751   CGGTAATCAA TAGAAAAATT CACAGGATAG ATGCAATTGA GAGTTAGTTG

118801   GTCGGTAGCC TTGTAACTAA CACCTACTAA AGGCCAAGCC TTCTCTTGAT

118851   GGAGGCCTGT TTCATTAATG ACGCCAAAAA TAGCAGAAAG CTTCTCAGTG

118901   GCCTGGTATT TTCCAGAAAG AACTCCTTGA TAGAGTCCAT AACCCATCTC

118951   AATATTTTTA GGATCCACAA GCCCAGAAAG AATGATAGAC CACTGCCAAT

119001   TTTTTAAGGA GAGTGTATAA GCTCCTAAAG AGAGGAGAAC ATAGTTATAA

119051   AAAGAAGTAT CTTGGAAAGT CGCCCACCCA AGTCCATTAG GATCTGTCTC

119101   CGAAATAGGA AGTGAGCTTT TCCATTGAAT ATCCGCACCT ATATAGCCAG

119151   TAGAAAACAG TAGCCCAGAA TGCTCTGTAA TCGGAAGTGT GCAGAGAAAC

119201   GTTCCATCGT ATTGACGATA GCCTATAGTT TGATGAGGCA GCTTTTTAAA

119251   TTTAGCATCG TTCACCTTTA GGTATTGTAC CTGAGCAGAG AAAGGACGTG

119301   GAGGAGGATT TTTACATGCT TCTTCATCAA TTCCACAAGC ATCTTGAACA

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119401   GAGCAGTTTG AACATGTTCT GTAAGATTCT CCAACGTTAC TAGAGATTGA

119451   AATGGAATAT ACGTAATTTT TAAATTACTA TCTAATAATT TTCCTACTCA

119501   GGAGGGACTT TCAAGAAGAT TTCCCTAGAT TTAGGGGGAT GAAAGGACTA

119551   GAATTTTTCT AATCAGCAAT CGAACAAAAT TACAGGGTTC TTGGAGAGGT

119601   GCTTAATACT ACGCATAAAT GATTTCTGAG ATGATTTCCG TTTCGGCTGT

119651   TTCTGTGCTA ACTTGTTTTG GCACTCAGTA ATTTTAAGCT CAAGATTTTG

119701   GATCGATTCC TTTTTCGCTT CAATTTCATT TAAAATTCTT GTTTTTTCTT

119751   GATTTGTGT TGTCAGCTCT GGAAGATGCA CGCTTTTAAT TGTAGAGAAC

119801   ATCAACCCGT ATCTCTGAAC AAATCCTGAT CCTATAGAGG AAATGTCTTG

119851   AGATATCTCA TCAATCAGTT TTGTTCCTGT CTGCTTATTT TTAAGAGGGA

119901   TTGCTAGAAG AAGAGCAAGA ATCAGTGTGA GTACGATAAT TCCCAAGCCG

119951   ATGCCACAGA TGATCCAGTT TCCAGTATAT CCTGCGTAAC CTGCTGAGAT

120001   CGTTCCCCCT AAGGTTAACA GTAGTGTTAA GGCAAAACAG AGCGTATGCT

120051   TTGTGGAAAG TTTGGAGCGA AAGGTCTCCC AAGGAGCCGC TGGAATCGGA
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120101  TGAGGCTGCG  TAATATAAGC  ATTAGGAAGA  TTGAGAACTT  CTGTAGCATG

120151  AGAGAGAGGG  CTGCTCTCGG  GGACTGGTGA  TGGGGCTACG  GAAGTTGCCA

120201  TGTTGTTTCC  TCGAATCGTT  GCTAACTAGT  TTTGATTTGT  CTTTTCATTC

120251  TTGTGAGAAA  GCTCAAAACG  TTTTTGATAA  AGAGTTGATT  GCAGTTTGAA

120301  CTCTTTTGT  GAGAGGTCGC  AGAGTTCTTC  GTATAACTTT  AGCGTATCTT

120351  GAGTGGTTTT  TCTCTGTGCA  TTGGTTACAA  GCTGTAGAGA  GGATTCAGGT

120401  CGAATCTTCT  CCCTGATAAA  TTGTACTGTC  GTATGGAGCT  GCTGAGGGAG

120451  CTGCCGGATG  AATTTAATAA  ATCCTACCAA  GGCTTGTAGG  CAGAGAAGAG

120501  TCAAAATAGT  AAGAACAATG  CCAACGGCAA  TCAACAGAAT  GCTTTGGCTA

120551  TAGCAACCCA  AACAGATAAT  AGCGATTCCA  GCAAGAGCTA  CAATCACTAA

120601  GATCGTAATC  GCAGCAATAT  GCATAGGAAT  GGAGTGGGTG  AGAAAAACAT

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120751  CACAAAGAGA  ACTCTATTAT  TTGAGGAAAT  AATTTAAGAA  AAATGGTATT

120801  TTTAGTCAAT  TAGTAAGCGA  GTCATGCCTC  TTAGTTATTC  AAATTTTTAA

120851  AACCTTACCC  TTCCTATGAG  GAGACAAGTA  AGAGAAATTA  TGCAACAAAC

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121001  TGGGAAGAGG  ATCGCGACGG  CGGTCTCAGC  TCGACTACTA  AAGATTATGA

121051  TGATGTCGAG  AGGGTCTGTC  TTCAGCTCGA  TATACAGTAT  TACACCGTAT

121101  CTTTTGCTAA  AGAATATAGA  GAAAGAGTGT  TCGCTCGTTT  CCTCAAGGAA

121151  TACTCTTTAG  GCTACACTCC  TAACCCCGAC  ATTCTTTGTA  ACCGAGAAAT

121201  CAAATTTGAC  CTTCTACAAA  AGAAAGTCCA  GGAACTTGGC  GGAGATTACC

121251  TCGCTACAGG  GCACTACTGC  CGATTAAATA  CCGAGCTCCA  AGAAACCCAA

121301  CTCCTTAGAG  GTTGCGATCC  TCAAAAAGAT  CAGAGCTATT  TTTTATCAGG

121351  AACTCCTAAA  AGTGCTCTTC  ACAATGTGCT  CTTTCCTCTT  GGGGAAATGA

121401  ATAAGACTGA  AGTTCGTGCG  ATTGCAGCTC  AAGCAGCTCT  TCCCACAGCA
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90

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121451    GAAAAAAAAG ATAGTACAGG CATTTGCTTT ATAGGGAAGC GCCCTTTTAA

121501    AGAGTTCCTA GAGAAGTTTC TTCCCAATAA AACAGGCAAC GTTATCGATT

121551    GGGATACCAA GGAAATTGTA GGGCAACATC AGGGAGCTCA CTATTATACT

121601    ATAGGGCAGC GGCGAGGACT TGATCTTGGA GGATCCGAGA AACCCTGTTA

121651    TGTTGTGGGA AAAAATATAG AGGAAAATAG CATTTATATT GTGAGGGGGG

121701    AAGACCATCC CCAGCTCTAC CTACGGGAAT TAACAGCTAG AGAGCTCAAT

121751    TGGTTTACCC CTCCTAAATC CGGATGTCAC TGTAGCGCTA AAGTCCGCTA

121801    CCGTTCTCCT GATGAAGCTT GCACGATAGA TTATAGCTCA GGTGACGAGG

121851    TCAAGGTGCG ATTTTCACAA CCCGTCAAGG CGGTAACTCC AGGACAAACA

121901    ATAGCGTTTT ATCAAGGAGA TACCTGCCTT GGTAGTGGAG TTATCGACGT

121951    TCCTATGATT CCAAGTGAGG GCTAGGGAGA GCAGCTTCCT GCTCCTCTTC

122001    TTCCCTTTCA AAGGCAACGC GATTTCAAC CAAGGTTGCT CGTAGCTTGC

122051    GAGCTTCTTG ACGGCAGGAC TCTTTAAGCA AGAGCTCCGC TAGAGGATCT

122101    TCAAGGTACT GCTCAATGAC ACGGCGTAGA GGACGTGCTC CCATTTCTGG

122151    AGAATGCCCC TTCGTTACTA GGAAGGAAAT CACAGAGTCT GGGATGTTCA

122201    AAGCCATTTG GTAGTTTTTC AGTCTCGAGT CCAGTTTGTT GATCTCTAAA

122251    TGGATGATCT CCGATAGAGA TTCTTTCTCG AGGGGACGGA AAATCACACT

122301    TTCATCCAAA CGGTTAATGA ACTCAGGCTT TAAGTGTTTC TTCATAGCAT

122351    GTTCGATTTT CTCTTGGATG ACCTTATAGT CCATATGGGA CTTCAAGCCA

122401    AAACCAATTT CTCCGCTTTT ACGAATGAGA TCAGCTCCCA AATTGGAGGT

122451    CATGATAATA ATGGCATGAC GGAAATCCAC TTTGCGACCA AAAGAATCAG

122501    TAAGACGTCC TTGCTCTAAA ATTTGCAACA TCAGGTCCAT AATGTCTGGG

122551    TGTGCCTTTT CTATCTCATC AAAGAGAACA ACGCAGTAAG GACGGCGACG

122601    TACCTGTTCC GTAAGGTGGC CCCCTTCTTC ATGACCTACA TATCCTGGAG

122651    GTGATCCCAT CATCTTGGTA GCAGCAAATT TCTCCATGTA CTCTGACATG

122701    TCTACCTGAA TCAGAGCGTC TTCACCACCG AACATCTCTA TAGCAATTTG

122751    TTGGGCGAGC AGGCTTTTCC CTACACCGGT AGGCCCAAGG AATAGGAAGG
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122801  AGCCCGTAGG  TCGGTTAGGA  TCTTTGATCC  CTGTTCGAGA  ACGTCGGATG

122851  GCACGGCAAA  TGCTGGTAAC  GGCATCATTT  TGACCAATGA  CTTTTCTTCT

122901  TAACGTGTCT  TCTAACTTCA  GAAGCTTCTC  ACTTTCAGCT  TCTGTGAGCC

122951  TTGCTGAGGG  AATTCCTGTT  TGTAGAGAAA  CTACCTGAGC  GACTGCTTCT

123001  TCATCTACAG  GAACTTGGTG  CTCTTCTTTA  TGATTTCCC   ATTCCTGTTT

123051  CATACTTTGC  AGACGTTCGC  GAAGTTTTT   CTCTTCATCA  CGTAAACCTG

123101  CAGCTTTTTC  GTATTCTTGA  GTTCCAATGG  CCTGCTCTTT  GGCCAATTTT

123151  GTATTTTCGA  TTTCAGCCTC  TAGCTTCATT  AAATCTGTAG  GCTGACCCAT

123201  TGTATTCACA  CGGACACGAG  CCCCAGCTTC  ATCTAAAAGA  TCTATTGCTT

123251  TATCAGGGAG  GAAACGTCCA  TGAACATATT  GATCAGAAAG  AGTCGCAGCT

123301  GCTTTTAAAG  CTTCTTCAGT  AATGAAGACA  TTGTGATGTT  CTTCATACTT

123351  TTTCTTGAGG  CCACGTAAAA  TCTCAATAGT  CTCATCTACA  CTAGGAGGGT

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123551  CTGCTCCTGC  TCCTACAATC  GTGTGGAGCT  CGTCAATGAA  GAGCAAGATG

123601  TTTCCATGCT  TGCGAACTTC  ATCCATGACA  GCTTTGATCC  GTTCCTCAAA

123651  TTGCCCTCGA  TATTTTGTTC  CAGCAATCAT  TAATGCTAGA  TCTAGAGTAA

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123801  AAGTACAGGA  TTGTTTTTTC  TTCTTCGGCA  AAGAATCAAA  ATCAACCGTT

123851  CGACTTCTGA  AGAACGACCA  ATGACAGGAT  CGAGCTTAGA  CTCTCGGACC

123901  ATCTCCGTTA  AATCATAACC  ATATGCTTTC  AGAGCAGAAA  GCTTTTCGTT

123951  TTTGTCAGAA  CCTAAGCTAT  GACCTAAAGG  AGATTTTGAA  GATGAAGGGT

124001  TGCTTCGAGA  GGATGAGGAA  GAAGACGACG  ACGAAGGAGG  AAGTTGTAGA

124051  TTGAAGGTCT  CTAATTCTCT  AAGAATTTCC  TTACGAACCT  CTCTTGGATC

124101  GATATGTAAG  TTTTCTAATA  CCTGAAGAGC  GACACTATCT  GATTGATGTA
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92

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124201  CTGGCCTCTT CATTTGCTGA TTCAAAGAT TTTTTTACTC TTCCTGTAAG

124251  GGCAGGGTCT CCGTAGACTT GAATTCTGG ACCATAACCA ATCAGGCGTT

124301  CCACCTCTTG CCGTGCCGTA TCAAAATCTA TACCGAGGTT GCGTAATACA

124351  TTAACAGCTA CCCCTTGACC AAGTTTGAGA AGACCAAGCA GGATGTGCTC

124401  AGTACCCAGG TAGTTATGAT TTAAACGCTG AGCCTCCTTT TTCGCCAGTT

124451  TAATGACTTG TTTTGCTCTA TTAGTGAACT TCTCAAACAT AAAAACCTAA

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124551  TGCAACTCTT CGCTCTAAAC CAGCAAATTT GGTAAAATTC CTCTGAGTTT

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124651  CTTTTGAAAC AGTCTTAATT AGTTTATGT TTGTTATATG AAAGTTCGTA

124701  TCGTAGATTC AGGAAAATCT TCAGCGGCCT CCCACATGGC TAAGGACAGA

124751  GATTTATTAG AATCTCTGCA AGATGGGGAG CTCATTTTAC ACCTTTATGA

124801  GTGGGAGAAT CCTTGTTCTC TGACGTACGG TCACTTTATG CGTCCAGAAA

124851  AATTTTTACT TTCCAACTAT GCGGATCTAG GATTGGACGC CGCAGTGCGG

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124951  TCTTATGTCT GCGACACATC CTTCCTATTC TTCTTCGGTA CTTGAGAACT

125001  ACCATACTGT AAACTCTTTT GTAGCGAAGG TTCTAGAGAA AGTATTTCGG

125051  ATCCAGGGAA TGTTAGCTCC AGAAGACGAA AACTCTTCTT CCAGAGATTC

125101  AGGAAATTTT TGTATGGCAA AAACTTCGAA GTATGACGTT CTTTTTGGGG

125151  ACAAGAAGAT AGGGGGCGCT GCCCAACGCA AGGTGCAACA GGGATTTTTA

125201  CATCAAGGAT CCTTATTCTT ATCGGGAAGT TCTTCTGAGT TTTACCAGAG

125251  ATTTTTAAAA CCCGAGGTTC TTGAAGAAAT TATTGAACAA ATCCAGATTC

125301  ACGCGTTTTT CCCTTTAGGT TTGGAAGCTG CTGATGAAGT GCTGCAGGAG

125351  GCGCGTCAGC AAGTCAAAGA GGCGTTATT AAATTGTTTT GTGGTGAGGG

125401  GTTATGATGA GTCGGTTGCG TTTTCGCTTG GCAGCTCTTG GAATATTTTT

125451  TATTTTGCTG GTTCCTAATT CTGTTTCAGC AAAGACAATC GTAGCTTCAG
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125501   ACAAGGAGAA  GGTTGGAGTT  CTTGTTTATG  ACAATAGTGT  AGAGGCCTTT

125551   CAACAGATAT  TGGATTGCAT  AGATCATGCA  AATTTTTATG  TAGAACTGTG

125601   TCCCTGCATG  ACAGGAGGCC  GAACGCTTAA  AGAGATGGTA  GATCACCTCG

125651   AGGCTCGTAT  GGATCTGGTT  CCAGAGCTCT  GTAGCTATAT  CATTATCCAA

125701   CCCACGTTTA  CCGATGCTGA  AGACCAAAAA  TTACTCAAAG  CTCTCAAAGA

125751   ACGTCATCCC  AACCGGTTTT  TCTACGTTTT  TACAGGGTGC  CCACCCTCAA

125801   CAAGCATCCT  CGCTCCTAAT  GTCATTGAAA  TGCATATCAA  ACTTTCTATC

125851   ATCGATGGGA  AATATTGTAT  TTTAGGTGGT  ACCAATTTTG  AAGAGTTTAT

125901   GTGCACTCCA  GGGGATGAGG  TTCCTGAGAA  AGTGGATAAC  CCACGTTTAT

125951   TTGTCAGTGG  AGTGCGTCGG  CCCCTAGCAT  TTCGTGATCA  GGATATCATG

126001   TTGCGTTCTA  CAGCATTCGG  TTTGCAGCTC  AGAGAAGAAT  ATCATAAGCA

126051   ATTTGCTATG  TGGGACTACT  ATGCACATCA  TATGTGGTTC  ATTGATAATC

126101   CTGAACAGTT  TGCAGGCGCC  TGTCCTCCAC  TGACTTTAGA  ACAAGCCGAG

126151   GAGACAGTAT  TTCCTGGATT  TGACAAACAT  GAAGATCTTG  TTCTTGTCGA

126201   CTCTTCCAAG  ATCAGGATAG  TTTTAGGTGG  TCCCCACGAT  AAGCAACCCA

126251   ATCCTGTGAC  TCAAGAATAT  TTGAAACTTA  TCCAGGGAGC  TAGATCTTCT

126301   GTGAAGCTTG  CTCACATGTA  TTTCATCCCT  AAGGACGAGC  TTTTAAATGC

126351   TCTTGTCGAC  GTTTCTCATA  ATCACGGTGT  TCATCTGAGT  TTAATTACGA

126401   ACGGCTGTCA  TGAATTAAGT  CCTGCAATTA  CAGGACCCTA  TGCTTGGGGA

126451   AACCGTATTA  ACTATTTCGC  CTTGCTCTAT  GGGAAACGGT  ATCCTCTTTG

126501   GAAAAAATGG  TTTTGCGAAA  AGCTAAAACC  TTATGAGCGG  GTTTCTATTT

126551   ATGAGTTTGC  TATTTGGGAA  ACGCAGTTGC  ACAAGAAGTG  TATGATTATC

126601   GATGATGAAA  TTTTTGTGAT  CGGAAGTTAT  AATTTTGGAA  AGAAAAGTGA

126651   TGCCTTTGAT  TACGAAAGTA  TTGTAGTTAT  CGAATCTCCA  GAAGTCGCTG

126701   CAAAAGCTAA  CAAAGTCTTC  AATAAAGATA  TCGGATTGTC  GATTCCTGTA

126751   AGTCATGGCG  ACATTTTCTC  TTGGTATTTC  CATTCCGTAC  ACCACACTTT

126801   GGGACATTTG  CAGCTGACCT  ATATGCCAGC  CTAGCGTCCC  TGGGTGCGAA
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126851   TCTACCAACA GGATCTCTTC TGCAGGCTCT GCAGGGATCC TGCCTGGTTT

126901   TTTTCTCTGC TATCGTTTAC ACTACGCTTT TATTGTTTGG GTAGAGGGTG

126951   GACCTTGTTA TCGTTCTTCT ATAAGCATCA AAAAAAATTT ATCGGCATTG

127001   TCATTGCTGT AGTTTGTGTT TCTTGGTATT GGAGTGGGTT GGGGACGATT

127051   CTCTAGAAAA GGTTCTGCAG AGTCCACCTC ACGTCGGACT GTTTTTACTA

127101   CCGCTTCAGG GAAGCGGTAT GTAGAGAAAG ATTTCATGGC TATGAAGAAG

127151   TTCTTTGCTC ACGAAGCGTA TCCATTTACA GGGAACCCTA GAGCTTGGAA

127201   TTTTATCAAT GAGGGGCTAC TTACTGATTA TTTTCTAACG ACAAGGGTGG

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127751   AAGAATAAGG AATTTTCCTT AGGATTTGAA GAATTTGTAA ACTCGTATTT

127801   TCAGTTTTTA GAGATCTCTG AGTCCGAATT TTTCAATATG TATCGAGACA

127851   TATTGTTGTG CAAAAGAGCT CTTCTCCTAT TGCAGGGAGG CGTTTCTTTT

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127951   AGTAGAGTTC TTTAGACTCC CTAAGGAGTA TAGCTTTAAA ACAAAACAAG

128001   AGTTAAAAGC TTTCGAAGTC TATTTAAAGT TAGTGAGTTT ACCTAAATCG

128051   GATAGTTTGG ATGTTCCTAA TGAGATCCTT CCTATAGCGA CCATAAAAGC

128101   TAAAGAGCCT CGGTTAGTAG GCAGACGGTT TTCTATAGAC TATAAGAGAG

128151   TCGCTTTGCA AGACTTAGCA GCTACTGTAC CTATGGTTGA AGTGCTGCAC
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128251 CGTTGAGACG TGTCAGTCGT ATAAAGACTT CCAACATCTT AAGCCTGCGC

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128351 CCTGAGAGAA TTCTGCAATC GCTACAGCAA GTTCCTAAGC AGAGCCAAGA

128401 AGTTCTCTTA TCTGCAGGGA AGAATAGTGC TCTACCAGGA ATATCCGACG

128451 GTCAGCAATT AGCCAAAGTG TTGCTTGAAA ACGAGGTTTT AGATTTATAT

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128651 TCTGCGTTGC GTACACGGTA TCCAGGAGAA GAAGGCGCTA GCCTATGGCA

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129401 CATTTTTTTC AGAAGATAAG AGGTATTTTT TTAAGGCTAA AACATTTAAA

129451 ATTTATGTCT AAGGTTTAAA AAATACATCA GAATTATTCT ATGGATCCAG

129501 CTAGTCCGGT AGCCCCTCAT GTCCTACAAG ATCATGTGCA ACTATCTTCT

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129601   TATAGCCATC ATGGTCCTTT CATTGATAGC GATTTCTTTG GTAGCCTGTG

129651   GCCTATTTTT AACGGGATCG GCACCTCTAC AGCTCTCGAT CTGGATTGCT

129701   GCGAGTTGCA TTACCTTATC TATGTTAGTT TGTGCGTGTT GGCGTTATAA

129751   GATTTCCAAT GCCTTAGAAA AAACTAAGGT AGCGCATGAA AGCTGAGTTG

129801   GACATTTTAT TGATTGAAAA ATCATGACTA CATTACCTAA GTACGTTCCC

129851   CGTTCTCGAC AAAATCCCGA TACTCTGACC TTCCTAAAAC GGTATTCTAG

129901   TGTCCTTCTC CATTCGGAGA ATTCTTTATC TTATCGGATT TTTGCGAAAG

129951   TGCTTGCTAT TCTCCTCACT TCGTTAGCTG TAGCTTTCGC CGTGACTTTG

130001   TTTTCTTGTG AAGGTTCTCA ACTGAGACTC TGCGCTCTCT ATATAGGTAT

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130101   GTAAAATCGC CACAGCTTGC AAAAAGCCGC CTTCCATATC TCGAATTGAA

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130201   AGGAAAGTTC CTAGAGAGAG CGACGCTGCG TTCGTGCTTT AGAAATACTT

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130301   AACTTCAGTC TCTAGAGGAG CTCTTTGAAT CTTTGCTGAA GGTTTAGAAA

130351   TATCAATACC TGTTAAGCTC ATAAAGCCA TAGCAATGAG GCCTGTTGTA

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130451   GAGTTTTTCT TTGATAGTGG CTAAAATAAC AATAGCGAGC CACCACCCAC

130501   ATCCCGCTCC TAAAGAGAAG ATCATCATAG GAATAAAAGG ATAACTACGT

130551   GTGATTCCGA AGAGCACACC CCCTAGGATC GCGCAGTTCA CAGCAATCAA

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130701   ATCAGCTCCA GAAAACCTAG GTTTACAGAA GCTAAAGATG GAGAGATCCA

130751   AGTTAGAGCT TTAGGGCCCG TGATGAAAGC ATGGACAAAC CAGTTGATGC

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130851   GTAGAAACCC TAGTAGAGCA AGCAAGGTAA CTACACATCC CCAAGAAATT
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130951  CATTAAGCCA AGTATACGCA CCTAACCACA TAAACTACCT TTTTCTCTTT

131001  TTAGAGTCTC GAATGTTAAC AAGCCAAATC ATAATACCAA GTAGGAAAAA

131051  AGCCGACGGT GCTAGCACCA TAAGACTTAA ATTTTGGTAT CCATCGGGGT

131101  GGGTTTCGGA AGCATAAACA AATTGAGGGA TGATGCGAAA CCCCATAAGA

131151  GTTCCAAAAC CAAAGAGTTC TCTGATGACT CCAATGACAA GTAAGACCCA

131201  GCCGTATCCT AAGCCAGAGG CAAACCCATC TAAGAACGCT GGAATAGGAG

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131801  CCTTTAACTA CCTCAAGCCC TAGGTCTGTT GTTGCAAAAT TTGTAGTTCC

131851  AGAAGAATCT TGTAGGAAGA TTTTCTTCCC ATAGAATTGC TCTTGCCATT

131901  CGGGATTTGT AATATTTGCT CCTAAACCTG GAGTTTCTCC TTGTTGGTAC

131951  CATGCGGTTC CCAATACAGT GTCACCGTCG TTTTTCACTC CTAGATAGCC

132001  ATGGATGGGG ·CCCCAAAGGC CGAATCCTGA TATAGGGAAG ATCAAAGCTT

132051  GAACTGTAGA AAGGTCTTTC GCAACGTCGG CTCCTGACAT ATTTTCTGTG

132101  CGAGAGGTAT TCTCTAAAAT GACATAAAAG GGGAGGGGGG ATTGCTGACA

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132201  TTTCTTCAAA AGAAAATACC TTGCCTTGGG CATCTGTAAG TAGAGGACGG
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132251   ACAAAGCGCT CGGCATACAG CTCTAATTCA GGATAGGAAA CCTCAGAGAC

132301   TTTTTTTGTA GCAACTTCAA GAAGTTGTGT TTTTTTATCG AAAGTCGCAG

132351   GCACCCACTC TTTTTTTTCC TGAATTTGAA ATCTTCCTTT AAAATCTAAA

132401   ATATGAGCAG CTAAAAGCAT TTGCTTATTG CGATCGAAAG TAGCAGCTTG

132451   TTCCTGTATT GGGGAGAGCA CATAGTAGAT TGTGGATAAC AGCACTCCTG

132501   CAAATAAGCT GAGGCCCAGG ATAAAGGAAA CGATGTACCA GGTTTGGTTT

132551   ATGCGGACGG TATGTTTTGA AGAGCCTTTA GACATATTCT AGACTCCCCT

132601   TTTTCTATAC TTTCTAACAG CAAAATAGTC GATAAGAGGG GCAAATACAT

132651   TGCCCAGAAG GATCGCTAAC ATCACTCCCT CAGGATACGC AGGATTGATA

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133451   CAAACGTCAC CACTCATCTT TGCTGGAAAC GTAAAAAATA AGAATGCCCT

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133551   CTTTACTGAC AACAATACCA AAGGCGATCC CTAAGGCTGC CATCCAGTAA
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133701   TACCCCCGAC AACATAGCTA ATCGTAAGTA GAGGAATAAA GATCTTAAGT

133751   CCTTCCCAAA GGATAGGAAC TATATGGATC TCTTTGTAAA CAAAGGATAA

133801   ATAACTACCA AATCCAGAAA TATGTAAGAA TTGCTCCATC AGCACAGGAT

133851   TGCCTGAGCT ATAAACGATA GATTGAAGTC CTGAATTCCA GATCGCAACA

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134851   AATGATTGCG CCTCCACGGA GTTCGACTTT TCCAGATACT GTGATATTTC

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136151   ATGCGTAGAT TTTTATGATG TTCTCTTACG TAGTGACCTA CGGCATGAAG

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136251   AGGAGCGGCC AGGTTTCCCA GCAATACCTA CAGCTGCAGA CTTCACAAAT
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137351   TTTGATGATC  ATAGATACTT  AAAGGATCTA  AGATCACTAG  AGCTTCAAAA

137401   AAAAGAATCG  CTTTTGAATA  ATGCCCTTGG  CGTAGAAAAG  AATATCCTGA

137451   GATTCTGAGT  TCTTCTAACT  CATCATCTCC  CCAGCCTAAG  ATTGCTTTCC

137501   ATTCATTATC  CAACATACAT  TATCCTTGAA  CAAATTGAAA  GATACGAGAG

137551   ATCACATAGT  CTATCATCAC  ATTTGTAGAC  TTGACTCCAA  GATCTAGAGC

137601   TTTTAAGAGC  ACTTTCCCTT  GTTGTACTCT  AGGATCGTCA  TCGTCTTCTT
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103

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139001  GGCTCCTCAG GGACGGCTTG TCATTATTTC TTTTTGTAGC TCTGAGGATC

139051  GTCCTGTGAA GTGGTTTTTT AAAGAGGCGG AAGCTTCTGG CCTGGGGAAG

139101  GTAATCACAA AGAAAGTGAT CCAACCTACC TACCAAGAAG TACGAAGAAA

139151  TCCTAGATCG AGATCAGCAA AACTACGGTG TTTTGAAAAA GCTTCCCAAT

139201  GAACAAAAGT CGTTTTTTAC GTTTATGCTG CTGTCTATGC TTTTGTGGAA

139251  GTCTCTTTTA TTTCTATATT AATAAGCAGA ACTCGCTGAC GAAATTACGC

139301  CTCGAAATTC CTTGTTTATC TGTACGCTTG CGTCAGCTTG AGCAGCAAAA

139351  TATTTCTTTA CGTTTTTTAA TTGATAAAAT AGAAAGACCT GATCATTTGA

139401  TGGAAATAGC AGCTCTTCCC GAATACCAAT ATTTGGAATA TCCCTCAGAA

139451  GAAAGTATCA GTCTTTTATC CTATGAGCTA CCGTAAACGT TCGACTCTAA

139501  TTGTTCTAGG AGTGTTTGCT CTTTATGCTC TTCTAGTATT GCGTTATTAT

139551  AAAATTCAAA TTTGTGAAGG AGACCACTGG GCCGCAGAAG CTCTCGGGCA

139601  ACACGAATTT TGTGTCCGTG ATCCTTTTCG AAGGGGCACC TTTTTTGCTA

139651  ACACGACAGT ACGTAAGGGA GACAAAGACC TTCAGCAGCC TTTCGCTGTC

139701  GATATTACAA AATTTCACCT TTGTGCAGAT CCTTTAGCTA TTCCCGAATG

139751  TCATCGTGAT GAGATCATCC AAGGGATTCT CCAATTTATT GAGGGGCAGA

139801  CCTACGACGA CCTCTCCCTA AAGTTAGATA AGAAATCTCG GTATTGTAAG

139851  CTGTATCCTT TATTAGATGT TTCTGTCCAT GACCGGCTAT CCCTTTGGTG

139901  GAAAGGATAT GCAACAAAGC ATCGCTTACC AACAAACGCC CTATTTTTTA

139951  TTACGGACTA CCAACGCTCG TATCCTTTTG GGAAGCTCCT TGGACAAGTT

140001  CTCCATACCT TAAGAGAAAT TAAGGATGAG AAAACAGGAA AAGCCTTTCC

140051  CACAGGCGGG ATGGAGGCGT ACTTTAATCA TATTCTGGAA GGGGACGTTG

140101  GAGAGAGAAA GCTGTTGCGT TCTCCTTTGA ACCGTTTAGA TACGAATCGT

140151  GTTATCAAAC TGCCTAAAGA TGGCTCTGAT ATCTACCTTA CGATCAATCC

140201  TGTGATCCAG ACCATTGCAG AGGAAGAACT CGAACGGGGC GTGCTAGAAG

140251  CTAAAGCCCA GGGGGGTAGG CTCATTCTAA TGAACTCCCA AACAGGAGAG

140301  ATTCTTGCAC TGGCTCAATA TCCGTTTTTC GATCCCACAA ATTATAAGGA
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104

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·140351   ATACTTCAAT AACAAAGAGC GCATCGAACA TACGAAGGTA TCTTTTGTGA

 140401   GCGATGTTTT TGAACCCGGG TCGATCATGA AACCTTTGAC TGTGGCGATT

 140451   GCTTTACAAG CTAACGAAGA GGCTAGCTTA AAATCGCAGA AAAAGATTTT

 140501   TGATCCTGAA GAACCTATCG ATGTGACCAG GACACTCTTC CCTGGACGAA

 140551   AAGGATCTCC GCTTAAGGAT ATTTCTAGAA ACTCTCAATT GAATATGTAC

 140601   ATGGCTATCC AGAAATCTTC GAATGTCTAT GTAGCTCAGC TGGCTGACCG

 140651   CATCATACAA TCTTTAGGAG TGGCCTGGTA CCAACAGAAG TTGCTAGCTC

 140701   TGGGATTTGG AAGAAAAACA GGGATCGAGC TTCCCAGTGA GGCCTCTGGT

 140751   TTGGTGCCTT CTCCCCATCG TTTCCATATT AATGGTTCCC TGGAATGGTC

 140801   CTTATCTACT CCATATTCTT· TGGCTATGGG ATATAATATT TTGGCAACAG

 140851   GGATACAAAT GGTTCAAGCC TACGCTATCC TTGCAAACGG AGGTTATGCC

 140901   GTCCGGCCCA CTTTAGTAAA AAAGATCGTC TCTGCTTCAG GAGAGGAATA

 140951   TCATCTTCCT ACTAAAGAGA AGACACGACT CTTTTCAGAA GAAATTACTA

 141001   GAGAAGTTGT TCGTGCCATG CGTTTTACAA CGTTACCCGG AGGTTCGGGA

 141051   TTTCGAGCCT CTCCTAAGCA TCACTCTAGT GCTGGGAAAA CAGGAACTAC

 141101   AGAAAGATG ATTCATGGAA AATATGATAA ACGCCGTCAT ATTGCTTCTT

 141151   TTATAGGTTT TACTCCCGTA GAGAGCTCGG AGGGAAATTT CCCACCTTTA

 141201   GTGATGCTCG TCTCCATAGA TGATCCTGAA TATGGTTTGC GAGCCGACGG

 141251   CACGAAAAAT TATATGGGGG GGCGTTGTGC GGCACCCATT TTTTCTAGGG

 141301   TTGCTGACCG CACACTCCTC TATTTAGGGA TTCTTCCAGA CAAGAAGCTA

 141351   AGAAATTGCG ACGAAGAAGC TGCTGCATTA AAGCGTCTCT ATGAAGAATG

 141401   GAATCGTTCT CCGAAACAAG GGGGAACGAG GTGAGGATCT CTATTTCCAT

 141451   CTTGCTATAG ACTTTTACCG TTGAGCAAAG ACTCTCTATC AGAGAGCCCG

 141501   TCTCCTCTTT ATCCTCTATG AGTAGTTTAT GTTATGGCTA GGGTAGGTCC

 141551   TAAACTATAG AAATAACTTT AGCTTCTTC CCCTAAATAA GAGACCAAAG

 141601   TCTTGATGAG ACGGTCTATT GAAGTTTATG GAAGGGGGAG GTAAGGCTGT

 141651   GTGTTTGGGG ATTTAGATTT GGGATAAAGG AGGCTTCTGT TCGTAGAAAC
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105

141701 AGGAGAGCGA AATTTTATAT TTCAGAGAAG AGTAAGAACT TTATGGACAG

141751 TTTTTTGTGA TTGCTTGTAT ACTATCTTGA TTGAATTTTT TGTCGACCTA

141801 CGAGTAAAGA AATCCTTTAA GCATTTTTA AAAATCAGAG TGAGAGCATG

141851 CCCCTAGAGG GCTTTTTATG AAAAAGTTG TTTTTCAATA GTCCCTGGAG

141901 CGTAAATGGA TTTAAAGAG TTACTCCATG GGGTTCAAGC TAAAATCTAT

141951 GGGAAAGTTC GCCCTCTTGA AGTGCGCAAC TTGACACGTG ATTCCCGTTG

142001 TGTGAGTGTT GGCGACATTT TTATAGCCCA TAAGGGACAG CGCTACGACG

142051 GAAATGATTT TGCTGTCGAT GCTTAGCTA ATGGAGCAAT TGCCATTGCT

142101 TCTTCACTAT ACAATCCGTT TCTTTCCGTT GTTCAGATCA TCACTCCTAA

142151 TCTCGAAGAA TTAGAGGCTG AGCTTTCTGC AAAGTATTAC GAATACCCTT

142201 CAAGTAAGCT CCATACCATT GGGGTGACTG GAACCAATGG GAAAACTACA

142251 GTTACATGTT TGATTAAAGC TTTATTGGAT AGCTATCAAA AACCTTCAGG

142301 GCTTTTAGGA ACCATAGAGC ATATCTTAGG AGAGGGGGTG ATTAAAGATG

142351 GGTTACTAC ACCTACACCC GCTCTTTTAC AGAAGTATTT AGCCACTATG

142401 GTACGTCAAA ATAGAGACGC TGTTGTTATG GAAGTCTCTT CTATAGGACT

142451 TGCCTCTGGA AGAGTAGCCT ATACCAATTT TGATACAGCA GTTCTGACTA

142501 ATATTACCTT AGATCATCTC GATTTTCATG GCACATTTGA AACCTATGTT

142551 GCGGCGAAAG CCAAGCTTTT CTCTCTCGTG CCCCCTTCGG GAATGGTTGT

142601 TATCAACACA GACTCTCCCT ACGCTTCTCA GTGTATTGAG AGTGCAAAGG

142651 CACCGGTCAT CACTTATGGT ATAGAGAGTG CTGCTGACTA CCGAGCCACC

142701 GATATCCAAC TTTCTTCCTC GGGAACAAAG TATACCTTGG TGTACGGGGA

142751 CCAAAAAATT GCGTGCTCTT CCTCATTTAT TGGAAAGTAC AACGTCTATA

142801 ACCTACTTGC TGCGATCTCT ACAGTACATG CAAGTTTGCG TTGCGATCTT

142851 GAAGATTTGC TAGAAAAGAT AGGCTTGTGT CAACCTCCTC CAGGTCGTTT

142901 GGATCCTGTA CTTATGGGTC CCTGCCCTGT ATATATTGAT TATGCACACA

142951 CCCCCGATGC TTTAGACAAT GTCTTAACAG GATTGCATGA GTTACTTCCT

143001 GAGGGGGGAA GACTGATTGT TGTTTTTGGT TGCGGTGGAG ATAGAGATCG

106

143051   CAGTAAACGG AAGTTGATGG CCCAGGTGGT AGAGCGTTAT GGTTTTGCTG

143101   TTGTAACTTC AGATAACCCT AGGAGCGAGC CTCCTGAAGA TATTGTGAAT

143151   GAAATTTGTG ATGGGTTTTA TTCAAAAAAC TATTTCATCG AAATCGACAG

143201   AAAACAAGCA ATTACATATG CTCTGTCTAT TGCCTCAGAT AGAGATATAG

143251   TGTTAATAGC GGGAAAAGGG CATGAAGCTT ACCAAATATT TAAACACCAA

143301   ACAGTTGCGT TCGATGATAA GCAGACTGTT TGTGAGGTAC TCGCTTCCTA

143351   TGTCTAAGCA ACTGTCGTTT TTTGCTTTAT GTGTGTTAGG AAGTCACCCG

143401   ATTTTTGCTC AAACACCGAA TCCTCCTCAG CGTGTACGAC GCAGTGAGGT

143451   TATATTTATA GATCCTGGAC ACGGGGGAAA AGATCAAGGC ACGGCAAGTA

143501   AGGAACTTCA TTATGAAGAG AAGTCCCTGA CCCTGTCTCT TGCTTTGACG

143551   GTTCAAAGTT ACTTAAAGCG GATGGGTTAT AAACCTCAGC TAACCCGATC

143601   TTCTGATGTA TACGTTGACT TAGGGAAACG CGTTGCTTTG TCGAACCGTG

143651   GGCAGGGGGA TGTCTTTATC AGCATCCACT GTAATCATTC TTCAAACGCA

143701   GCAGCCTTTG GCACCGAAGT ATATTTTTAT AATGGTAAGG TCGGATCTCC

143751   GACTAGGAAT CGCATGTCAG AAGTACTGGG AAAAAACATT TTAGCTGCTA

143801   TGGAAAAAAA TGGCATTTTG AAGTCTCGAG GTTTGAAAAC TGCGAACTTT

143851   GTTGTGATTA GAGATACTTC TATGCCTGCA GTTTTGGTGG AAACCGGGTT

143901   TTTATCCAAT AGTCGTGAAC GTGCGGCCCT GCAAGATGCT CGCTATCGTA

143951   TGCATGTAGC GAAAGGCATC GCCGAGGGAG TTCATAATTT TCTTTCTGGA

144001   CCTAGTTTTC AGAAACCAAA ACAGAATATC GCTAAAATAC GTAAACCACA

144051   GATACAAGCA AATTAGTACT TTAGGAGTTA AAGGCAAAAA ATCGTCCTCG

144101   ATGCGATTCG AACGCATGGC CTGCTGCTTA GGAGGCAACC GCTCTATCCT

144151   GCTGAGCTAC GAGGACGCAA AGACCAGCAC TTTACCAAGT TAGATTAAAG

144201   AAGTCACGTG TTAGATGCAC GCTAGCAATT TAGGGGAAGT TTTTCTCAAG

144251   ATGTGGGAAT GATTTTTCTA GGTTCTAGAA ATATAGTTAT TCGCATTAAT

144301   CGATATGGTT TATAGTGATT GCGCATTTTT TAAAAAATGT CTTGAATCCA

144351   AAGGATGAAT AGATATGATG AGCTTAGACT TCAAAAGTTT ATTATTTACG

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144401   GTTACTCAAC GAGCTACTTT AGGGCACTTT AATAGGAGGC ATTGTCTAAT

144451   ATGGCTACCA TGACAAAGAA GAAACTAATC AGCACGATCT CACAAGATCA

144501   CAAAATTCAT CCTAATCACG TACGTACCGT GATTCAGAAT TTTCTAGATA

144551   AAATGACCGA CGCCTTGGTT AAAGGTGACA GGCTTGAGTT TAGAGATTTT

144601   GGTGTGTTGC AAGTAGTAGA AAGAAAACCA AAGGTAGGAC GTAATCCTAA

144651   GAATGCAGCA GTCCCCATTC ATATTCCTGC TAGACGCGCT GTAAAGTTTA

144701   CTCCAGGGAA AAGAATGAAG CGCTTGATAG AAACTCCGAA TAAGCATTCT

144751   TAATTCTTGT AGTCTTCTTT GTCTCAGTTG TTAGAGTCAG ACCGGTTTTT

144801   TACCGGGCTT GACTCTAATT TTTGTTATTA TTATCGTTTG GTGCAATGCT

144851   TTTCTGATCA AATTGTGCGT GATAATGGGG CTGCAATCCA GGTTACAACA

144901   TTGTATAGAA GTGTCCCAGA ATTCGAACTT TGATTCACAA GTAAAACAGT

144951   TTATCTATGC GTGCCAAGAT AAGACATTAA GGCAGTCTGT ACTCAAGATT

145001   TTCCGCTACC ATCCTTTACT AAAAATTCAT GATATTGCTC GGGCCGTCTA

145051   TCTTTTGATG GCCTTAGAAG AAGGCGAGGA TTTAGGCTTA AGCTTTTTAA

145101   ATGTACAGCA GTACCCTTCA GGTGCTGTAG AACTGTTTTC TTGTGGGGGA

145151   TTTCCTTGGA AAGGATTACC TTATCCTGCA GAACATGCGG AATTTGGCCT

145201   ACTCCTGTTA CAGATCGCAG AGTTTTATGA AGAGAGTCAG GCATACGTCT

145251   CTAAAATGAG TCATTTTCAA CAGGCACTCT TTGATCACCA AGGGAGCGTC

145301   TTTCCCTCTC TCTGGAGCCA GGAGAACTCT CGACTCCTAA AAGAAAAGAC

145351   AACTCTTAGC CAATCGTTTC TCTTCCAATT AGGAATGCAA ATTCACCCAG

145401   AATACAGTCT TGAGGATCCT GCACTAGGGT TCTGGATGCA AAGAACGCGT

145451   TCTTCATCCG CTTTTGTAGC CGCTTCAGGA TGTCAAAGTA GCTTGGGAGC

145501   GTATTCCTCA GGGGATGTCG GTGTTATCGC TTATGGACCT TGCTCTGGAG

145551   ACATTAGTGA TTGTTATTAT TTTGGATGTT GTGGAATCGC TAAAGAGTTC

145601   GTGTGCCAAA AATCTCACCA AACTACAGAG ATTTCTTTTC TCACCTCTAC

145651   AGGAAAGCCT CATCCCAGAA ATACGGGATT TTCCTACCTT CGAGATTCCT

145701   ATGTACATCT GCCGATCCGC TGTAAGATCA CTATTTCCGA CAAGCAATAT
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145751  CGCGTGCACG CTGCGTTGGC TGAGGCCACC TCTGCCATGA CGTTTTCTAT

145801  TTTCTGTAAG GGGAAGAATT GTCAGGTTGT TGACGGCCCT CGCTTGCGCT

145851  CCTGTTCCCT AGATTCTTAT AAAGGTCCCG GAAACGACAT TATGATTCTT

145901  GGGGAAAATG ACGCAATCAA CATTGTTTCT GCAAGTCCCT ATATGGAAAT

145951  TTTTGCTTTG CAAGGCAAAG AAAAATTTTG GAATGCAGAC TTTTTGATTA

146001  ATATTCCTTA CAAAGAAGAG GGCGTCATGT TAATTTTTGA AAAAAAAGTG

146051  ACCTCTGAGA AAGGAAGATT CTTTACGAAG ATGAATTAAT TTGGGTCTG

146101  TAATTGTGTT TAAGAATTGT TTGTATTAAA ATGATTCTTT TTATACGAGG

146151  AGAGCACATT CTAATGGAAC TTCTTCCACA CGAAAAACAA GTAGTTGAAT

146201  ATGAAAGGC TATAGCCGAA TTTAAGAAA AAAATAAGAA AAATTCTCTC

146251  TTATCTTCTT CAGAGATTCA GAAATTGGAA AAGCGTTTAG ATAAATTAAA

146301  AGAAAAGATC TATTCGGATT TGACTCCTTG GGAGCGTGTA CAAATATGTC

146351  GCCACCCTTC GCGTCCCCGT ACTGTCAACT ATATTGAAGG GATGTGTGAG

146401  GAGTTTGTCG AGCTTTGTGG AGATCGCACC TTCCGAGATG ATCCCGCAGT

146451  TGTTGGTGGC TTTGTAAAAA TCCAGGGTCA GCGTTTTGTC CTTATTGGCC

146501  AAGAAAAGGG ATGCGATACA GCGTCACGCC TTCATAGGAA CTTCGGTATG

146551  TTATGTCCCG AGGGTTTCAG AAAAGCCCTT CGCTTAGGAA AACTCGCTGA

146601  AAAGTTTGGC TTGCCTGTGG TCTTTCTTGT CGATACCCCA GGAGCATATC

146651  CTGGATTGAC TGCTGAAGAG AGAGGACAAG GATGGGCAAT TGCCAAAAAT

146701  CTTTTTGAGC TCTCAAGACT TGCCACTCCC GTGATTATTG TCGTTATCGG

146751  TGAGGGATGT TCAGGTGGAG CTTTGGGCAT GGCTGTAGGT GATTCTGTAG

146801  CTATGTTAGA GCATTCCTAT TATTCTGTAA TTTCCCCAGA AGGATGCGCC

146851  TCCATTCTTT GGAAAGATCC TAAGAAAAAT AGCGAAGCAG CTTCCATGTT

146901  GAAAATGCAT GGAGAAAACT TAAAACAATT TGGCATTATC GATACTGTTA

146951  TCAAAGAGCC CATTGGGGGA GCTCACCACG ATCCTGCATT GGTATATAGC

147001  AATGTTCGAG AGTTTATCAT CCAAGAGTGG TTACGATTAA AAGATCTAGC

147051  TATAGAAGAG CTGTTGGAGA AACGGTACGA AAAATTTCGC TCTATAGGTC
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109

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147101   TTTATGAAAC TACTTCTGAA AGCGGTCCTG AGGCATAAAA ATCATCTCGT

147151   TATATTAGGC TGTTCTCTAC TCGCAATTTT AGGACTTACC TTTTCATCTC

147201   AGATGGAGAT TTTTTCTTTA GGGATGATTG CTAAACAGG CCCCGACGCC

147251   TTTTTACTTT TTGGACGTAA GGAATCTGGA AAACTTGTAA AGGTTTCAGA

147301   ACTAAGTCAG AAAGATATTT TAGAGAATTG GCAGGCAATT AGTAAGGATT

147351   CAGAGACACT TACAGTCTCT GATGCCACGA CATACATCGC CGAACATGGG

147401   AAAAGCACAG CCTCTCTGAC GAGCAAGCTC TCTAAGTTTG TCCGTAACTA

147451   CATCGATGTG AGCCGCTTTC GAGGACTGGC AATCTTCTTA ATCTGCGTTG

147501   CTATTTTTAA AGCAGTCACC TTATTTTTCC AACGTTTCCT TGGGCAAGTC

147551   GTTGCTATAC GGGTAAGCCG AGACTTACGT CAGGACTACT TTAAGGCCCT

147601   ACAACAACTC CCCATGACCT TCTTCCATGA TCATGATATC GGTAATTTAA

147651   GTAATCGTGT CATGACAGAT TCTGCAAGCA TTGCCTTAGC AGTAAACTCT

147701   TTAATGATTA ACTACATTCA AGCCCCAATT ACCTTCATAT TGACATTGGG

147751   AGTCTGTCTG TCGATTTCAT GGAAGTTTTC AATTCTTATT TGTGTTGCCT

147801   TTCCTATCTT TATCCTTCCC ATTGTCGTGA TCGCTAGAAA GATCAAAAAT

147851   TTAGCAAAAC GTATTCAAAA GAGTCAGGAT TCATTTTCCT CCGTTCTTTA

147901   TGATTTTCTT GCTGGGGTTA TGACAGTAAA AGTCTTTCGT ACAGAAAAAT

147951   TTGCCTTCAC AAAATATTGT GAGCATAACA ATAAGATTTC TGCTTTAGAG

148001   GAGAAAAGTG CTGCTTACGG TTTGCTTCCA CGACCCCTCC TGCATACCAT

148051   AGCTTCTTTA TTTTTTGCTT TTGTCGTCGT TATCGGAATT TATAAATTTG

148101   CTATTCCTCC CGAAGAACTT ATCGTATTTT GTGGTTTGCT CTACCTAATC

148151   TACGACCCTA TTAAGAAGTT CGGGGATGAA AATACCTCCA TCATGAGGGG

148201   ATGTGCTGCT GCGGAGAGAT TTTATGAAGT CTTGAATCAC CCCGATCTTC

148251   ATAGTCAAAA AGAAAGAGAA ATCGAGTTCC TTGGACTTTC TAATACAATC

148301   ACATTCGAGA ATGTTTCCTT CGGCTATCAG GAAGATAAGC ACATCCTCAA

148351   AAATCTAAGC TTTACCTTAC ATAAAGGCGA AGCTCTAGGC ATTGTAGGAC

148401   CTACAGGATC TGGAAAAACA ACACTTGTTA AATTACTTCC TAGGCTCTAC
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148451   GAAGTCTCCC AAGGAAAGAT TCTTATCGAC TCTCTTCCTA TTACGGAATA

148501   TAACAAAGGG TCCTTAAGGA ATCACATCGC CTGTGTATTA CAGAATCCTT

148551   TCTTATTCTA TGATACTGTA TGGAATAACC TTACCTGTGG TAAGGATATG

148601   GAGGAGGAGG CTGTTTTAGA AGCTCTAAAA CGTGCCTACG CTGATGAGTT

148651   TATTTTAAAG CTCCCTAAAG GAGTCCATAG CGTGCTCGAA GAATCTGGGA

148701   AGAATCTCTC AGGAGGACAG CAGCAACGTT TGGCAATAGC ACGTGCTCTG

148751   TTGAAAAACG CCTCCATCTT AATTTTAGAT GAGGCAACGT CAGCTCTAGA

148801   TGCCATTAGT GAAAATTACA TTAAGAATAT CATTGGAGAG CTTAAAGGAC

148851   AGTGCACACA AATCATTATT GCCCACAAGC TGACCACTCT TGAACATGTA

148901   GATCGCGTGC TCTACATAGA AAATGGTCAA AAAATTGCCG AAGGCACAAA

148951   AGAAGAACTC TTACAGACGT GTCCTGAATT TTTAAAAATG TGGGAGCTCT

149001   CAGGGACTAA AGAATATAAC AGGGTCTTTG TTCCTGATCA CAAATTAGTC

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149101   ATGAGCTCAG GCAACAACTC TACAAGTGTC TGAGTTAGCT TTTGTGATAC

149151   CTCCTCCAAT CTGCTGAAGG GACAGTCTCC TGGAACAGTA TAATCAGAAG

149201   TGATCTTGAG AAAAGAACAG GGGATGTGAT GTTCTGCTGC TTGTGAGGCT

149251   ATAGCATAGC CTTCCATATC TAGAAGTTTA AACGTCTTAT GAAACCCATA

149301   ATGGTACAAT ACTGGAGAGG TAACCAGAGA GCTTTTAGGT AGAGAATCCG

149351   GTAGAGCGTC AAAGATATAA GGGGGATCTT CAGAGAGAAC AGGAGGTGTA

149401   TCCGTAGTGA GGTTTGCAAT TTTCTCAATA GTGTAACATT GACCTAAAGG

149451   AATCTCGGGA GAACATGCCC CCACAAAACC TGGATTGATC CACAGATCGT

149501   AATCTGTATA TGCTTGGCAA TAGCTTTGAA GAGCATTTAA AACGGCTGTA

149551   CTTCCCCAAA CATGGACAAT ATAGAGATCT AGATGGTAGT CAGTACAACG

149601   ATAACTATAG AGATGCTCGT TGATCTGTGT AAAATCAAGT TGTTCAATTA

149651   GAGGAGAAAT TTCTCTATAG TCTGCAACAA TGCAAAGGAT TTTTTTAGGT

149701   GTATTGACAG CATTCATTGG CCTTCCAGAG CATATGTAAA GCTTTTTTCC

149751   CAGTTTTAGA TAGTTGAAAG GTTTCTTTGT TGATATAGGT TCCTATGAAT
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111

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149801  CTATGAATCA  CGGTCACGTT  TTTATTTTTA  GAGTATTCTA  CTGCTTTTGC

149851  TCCCGCAGTT  ATAGGATCTT  TCAGGGAGCA  AATTAAAGAC  TTTCTTAATG

149901  CTGCTGTTAG  AGCATCCACT  GTAGCCATAG  GAACATATTT  CGCAATGGCT

149951  AAACATCCTA  AAGGAAGGGG  AAAGATGGTC  TTACGGCGCC  ATAGCTCTCC

150001  AAAGTCTGCC  CGCAATGTCA  ATTGGAGATC  GTAGCTGAAG  CGCTCTTCAT

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150101  TTGTCATAAG  GCATGGGAAT  GAGTTTTGCC  TTGGGATAGT  AAAGTTTACA

150151  GAGAGCATGA  GCGGTTGTCA  TCTCTCCAGG  AGTTGCCAAG  GTATCTAGAG

150201  AACATTCAGG  ATCTAAGGAG  AGGACGATAG  GACCGCTGTT  GTATCCTAAG

150251  GTATTTCCTA  CGTCCATAAG  ATTATAATAA  TCAGAAACTA  GAGGGAAGAG

150301  CGCTGCTGAC  ATTTTCATTA  GGGAGAGCCG  TCGCTGCAGA  GCTAGGGTAT

150351  TCAAAGTTTC  AATATCCGCA  ATTGTTACCT  GGTTAAGAAG  AGGCCTGAAT

150401  TGGGGGTCTT  TTAAGAAAGA  ACGAAAAGG   AAAATATCAT  TCGGGCAAGG

150451  AGAAAAGGCA  GCAGTCAGTA  TCATGTCGGT  TGATGTAATA  GAGCTATAGC

150501  GGCTTTGATG  TCTTTATTTT  CAGGCTTATC  CAAAGCTCCT  TGGTTTTCCA

150551  GCCATTCGAA  GTAAGACTTA  GGAATATCCA  CAAGAGGCTG  CCCTTTGTAT

150601  TTGCCAAAAG  GCATTTGAA   GACTTTCGGG  TGATAGCTCT  GTTGCAGCAA

150651  GTCGAGGACT  TGCTGGGGCG  GTAAATCACC  GATTAAAGAA  GTAAATACCT

150701  TGTGCAATAT  CACTACGTCA  TCTAGAGCTC  GGTGTGCTTG  ATTTTCAGCA

150751  AAACCGTAAA  CTTGTCTTAG  GTATTGTAAA  TTATGTTTTG  GTAGATCGGG

150801  GCGATATTTT  TGTGCCCATT  TTAGAGAGTC  TATTGTACGG  TTTGTCAGAG

150851  GCTCTAAGGA  ATGTCTGCGA  CATTCCTTAC  CGAGTAGGGG  GAAATCAAAA

150901  CCGTCATTAT  TATGAGCCAC  TAAGATGCTG  TCCTCTCCGC  AAAATTTCCT

150951  AAATCCCTCG  TAGGCTTCAG  GAAATTTGGG  AGCAGAAAGT  ACCGCATCCG

151001  TAGTGATTCC  ATGAATTTTG  GATGCCTCAT  CAGGAATGGG  AATTTCCGGA

151051  TTCACATAAG  TAAGAAAGGA  CTCATCTGTG  ACACTATTGT  AGGCAGCAAT

151101  TTCTATAATG  CGATCTCTTT  CTATTTGTGT  TCCTGTGGTC  TCCGTATCAT
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149801   CTATGAATCA CGGTCACGTT TTTATTTTTA GAGTATTCTA CTGCTTTTGC

149851   TCCCGCAGTT ATAGGATCTT TCAGGGAGCA AATTAAAGAC TTTCTTAATG

149901   CTGCTGTTAG AGCATCCACT GTAGCCATAG GAACATATTT CGCAATGGCT

149951   AAACATCCTA AAGGAAGGGG AAAGATGGTC TTACGGCGCC ATAGCTCTCC

150001   AAAGTCTGCC CGCAATGTCA ATTGGAGATC GTAGCTGAAG CGCTCTTCAT

150051   GAATCAGAGC GCCTCCATCG ACTTTCCCTT GCAGTATCGC GGATAGAATT

150101   TTGTCATAAG GCATGGGAAT GAGTTTTGCC TTGGGATAGT AAAGTTTACA

150151   GAGAGCATGA GCGGTTGTCA TCTCTCCAGG AGTTGCCAAG GTATCTAGAG

150201   AACATTCAGG ATCTAAGGAG AGGACGATAG GACCGCTGTT GTATCCTAAG

150251   GTATTTCCTA CGTCCATAAG ATTATAATAA TCAGAAACTA GAGGGAAGAG

150301   CGCTGCTGAC ATTTTCATTA GGGAGAGCCG TCGCTGCAGA GCTAGGGTAT

150351   TCAAAGTTTC AATATCCGCA ATTGTTACCT GGTTAAGAAG AGGCCTGAAT

150401   TGGGGGTCTT TTAAGAAAGA ACGAAAAGG AAAATATCAT TCGGGCAAGG

150451   AGAAAAGGCA GCAGTCAGTA TCATGTCGGT TGATGTAATA GAGCTATAGC

150501   GGCTTTGATG TCTTTATTTT CAGGCTTATC CAAAGCTCCT TGGTTTTCCA

150551   GCCATTCGAA GTAAGACTTA GGAATATCCA CAAGAGGCTG CCCTTTGTAT

150601   TTGCCAAAAG GCATTTTGAA GACTTTCGGG TGATAGCTCT GTTGCAGCAA

150651   GTCGAGGACT TGCTGGGGCG GTAAATCACC GATTAAAGAA GTAAATACCT

150701   TGTGCAATAT CACTACGTCA TCTAGAGCTC GGTGTGCTTG ATTTTCAGCA

150751   AAACCGTAAA CTTGTCTTAG GTATTGTAAA TTATGTTTTG GTAGATCGGG

150801   GCGATATTTT TGTGCCCATT TTAGAGAGTC TATTGTACGG TTTGTCAGAG

150851   GCTCTAAGGA ATGTCTGCGA CATTCCTTAC CGAGTAGGGG GAAATCAAAA

150901   CCGTCATTAT TATGAGCCAC TAAGATGCTG TCCTCTCCGC AAAATTTCCT

150951   AAATCCCTCG TAGGCTTCAG GAAATTTGGG AGCAGAAAGT ACCGCATCCG

151001   TAGTGATTCC ATGAATTTTG GATGCCTCAT CAGGAATGGG AATTTCCGGA

151051   TTCACATAAG TAAGAAAGGA CTCATCTGTG ACACTATTGT AGGCAGCAAT

151101   TTCTATAATG CGATCTCTTT CTATTTGTGT TCCTGTGGTC TCCGTATCAT
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151151   AGAAAATAAG AACATCCATA GTTTGACTAC TCATTACGTT TTTCTTGTTG

151201   CTCTTGAAGA GCCTGACGTC TTAGTTCATC CAAATTCATA TTCCCAGAAG

151251   AGATCAACCC AATAGCATGA GAAAAACTAT CACAGACTAG CTTTATTGTA

151301   TCGATATATA TCCGTAATAG TGTGTCATGA ATTTCTCCGT TTAGGCAGGG

151351   CAACACAAGC CGATAAAATA TCAATCCCTG TTCTTCATCC ATGCCAAAGC

151401   CGGGAATATC AATGTCCCTA TTTAAGAGAT GGAGTAAACG AGCTGTTGAT

151451   GCCTTATGAG ATTCATGCAA TTGGTAGGGA AGGTAACAAA TCAACTGCAG

151501   TATTTCTCCC TCACTGCGGA TTACAAAAAA TAAAGGGAGT TCATTGCCAT

151551   TAGCTTGAAT GTTAATGTAA GTAAGACCGC TTTCTCTTTC TAAGAAAGGT

151601   TCTTCATCCG AACTTTTAAG AAATTTTGTG AGATTATTTT GATTTAATGT

151651   CCATGTCGTC ATTTAGGAAA TACTCCAAGT TGTTCCTAGA GCCTGCATCA

151701   TTGCTGGCTG ATAATACTAG ATCTAATCTT GATTCGTCTG TTGTTTTTTT

151751   TGTATCTTTT GTATTGCTTT ACTGAGGAAA TCAGAGGTTG CAGAGGAAGA

151801   AGACTGCTTA TTATTTTCTT GAAGTAGATG ATTGATATCA GTGTCGGGAG

151851   GAAACTCTGT CAGTAGCGTA ATTTTTTCTG GTGTTTCTGC AATCACAAGA

151901   GTTTTATTCA CAACTCGAAT GAGGTAAATA GAAGTTTTCG GCGTTAGGGA

151951   ACGTCGTTCT AGGATTTTGA TTTGAGACGA GCCTCCAAAA CCGTGACTTC

152001   TTGATCTCAC AAACTTTTTA AACGCCCAAA CTCCAAAGCC AAAAATTGTT

152051   AAAAGTAGAA TCAAAGATCC TAGCATTTTA AACATTTCTA ATTTCATGCT

152101   TCCTGGGAAC ATTTCATGTA CAGAAATGGG CTCTTGGATC GTTTCTGCAA

152151   GAGCAAGCTC ATCAGAAAGC TTAAAAACTA AAGAAAAAAG ATTAAAAAAC

152201   ATGTGTAAGA CCCGCGATCA TCTCTATAAA ATTATAGTGG TAGCCCGATT

152251   TGTATCCAAC TACATACAAG TAATAATGAA GTATAGTTTT AGTCGATGCT

152301   ATATAAATTA TAGTACAATG ATTTCCAAGT ACAGATTAAA CCGTAATCAT

152351   GTATATTCCT GCAAGTACCG TCTAGAGAGC TCCCCTAGAT GATTTGGGTA

152401   ATTCACAGAC TCCTTTATAC CCTTCTAGGG TGTGCTCGTT CCACAGAGCC

152451   CAAGCTCTTG TCTTTCATAG ACAAAACGAC AGCAGTCTGT CGGTGGATGC
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152501  AAAGAATTTT TTCAAGTTGC CTGAGAAATT CCTTGGCAGC GCTTAATAAA

152551  ACTATGGTGA TGCTATGGAA AAGTTACTAG TGACTGATAT TGACGGTACA

152601  ATTACCCATC AATCTCATCA TTTAGATAAA AAGGTGTATG AGCGGCTCTA

152651  TGCGCTGCAC CAAGCTGGTT GGAAGTTGTT TTTCTTGACG GGAAGGTATT

152701  ATAAATATGC TGCACGCTTG TTTTCTGATT TTGATGCTCC ATATTTATTA

152751  GGATGCCAAA ACGGCGCTTC TGTATGGTCT TCAACATCAT CAAATCTTCT

152801  CTATTCTAAA AGTTTACCCT CAGATTTATT ATGTATTTTA CAAGATTGTA

152851  TGGAGGGGGC AACGGCTCTT TTTTCCGTGG AATCAGGAGC TCCTTACGGG

152901  GATCACTACT ATCGCTTTTC ACCGACTCCT ATAGCTCAAG ATTTACACGA

152951  ATATGTAGAT CCTAGGTACT TTCCTAATGC TAAGGAAAGA GAGATCCTAT

153001  TTGAAACGCG CTCTTTAAAA GACGACTATG CTTTTCCTAG TTTTGCTGCA

153051  GCAAAAGTCT TTGGACTGCG AGATGAGGTC ATCAGAATTC AAAAGGAGCT

153101  GGAACGCCAA GAAGCACTGA CTTCAGTCGC GACGATGACG TTAATGCGCT

153151  GGCCCTTTGA CTTTCGCTAT GCCATCTTGT TTTTAACAGA TAAAAGCGTC

153201  TCTAAAGGCA AAGCCTTAGA TCGTGTTGTC AATATACTTT ATGATGGAAA

153251  GAAACCCTTT GTCATGGCTT CAGGAGATGA TGCTAATGAT CTCGATCTTA

153301  TTGAGAGAGG AGATTTTAAA ATTGTGATGA GTTCCGCACC TGAAGAGATG

153351  CACGTTCATG CGGACTTTCT AGCTCCCCCA GCAGATAAGA ATGGCATTCT

153401  TTCAGCTTGG GAAGCTGGTG TCCGCTATTA TGACGACCTT ATGAGTCTTT

153451  AGGGAACATC TCAGGACCAA TTCCCATCAC ATTGGCTCCG TGATCTACGT

153501  ATAAGGTCTC ACCAGTAATT GCTGAAGCTA GAGGTGATGC TAAGAAAGCT

153551  GCAACGGCAC CCACCTGCTC GGCATTCATA GCCTCGGGAA TAGGCGCCCA

153601  CTCTTGGTAA TAGTCTACCA TTCTTTCAAT AAAACCAATT GCTTTTCCAG

153651  CTCGGCTTGC TAAAGGTCCT GCAGAGATGG TATTGACACG TATGCCCCAA

153701  CGGCGTCCCG CTTCCCAAGC AAGAGTTTTG GTGTCACTTT CCAAAGCTGC

153751  TTTTGCCGAA CTCATGCCCC CTCCGTATCC AGGAACAGCG CGCATAGAAG

153801  CCAAATAGGT GAGCGATATT GTCGATCCAC CACGGTTCAT GATACTTCCA
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153851  AAGTGAGAGA GAAGGCTAAC AAAAGAATAA CTAGAGGCAC TGAGAGCCGC

153901  TAAGTAACCT TTTCTTGATG TTTCTAATAG AGACTTAGAA ATTTCAGGAC

153951  TATTTGCCAG CGAGTGGACA AGAATGTCAA TATGACCAAA ATCTTTTTT

154001  ACCTGTTCTG CGACTTCTGA TATCGTGAAT CCCGTAATGC CCTTGTAACG

154051  TTTATTTTCA GCAATATCTT CAGGAACATC TTCAGGGCTA TCAAAACTTG

154101  CGTCCATGGG ATAGATCTTA GCAATCTCTA AGAGAGTGCC ATTCGATAAT

154151  TTTCTAGATT CATTGAATTT TCCTAATTCC CAAGACTGAG AGAAAATTTT

154201  GTAAATCGGT ACCCATGTTC CTACAATAAT CGTAGCTCCT GCTTCTGCAA

154251  GAAGTTTAGC AATACCCCAG CCATATCCTT GGTCATCACC AATGCCCGCA

154301  ACAAATGCTA CCTTTCCTGT TAGATCAATC TTTAGCATGA ATCCGCCTTA

154351  TACTTTTGAA GCTTATTGGA AGGAGAGTAA CAAATCTTTC GATTATTAAG

154401  AAAACCTTTT GGTGCCTCAA CAGGGGAGAT CCTGCCTCCA ATGTAAATAG

154451  AAACGTAAAT TCTTTAAATT TTTTTCTTTA CATATTTTAT AGAATATCCA

154501  AACTTCTCAC TCCCGCGTAC TGCTAAAAAA ATTTTCAAAA GAATTTACGA

154551  TCCGAACTTA TCGTAGTTTG GGTTCACTG ATTACTTAGG AGGTTGTTTG

154601  ACGAATCCTT TAGGGAAATT CCCCTCACCA CAGAATCCAC AGGTTGTTAC

154651  GATAGCGCCT TCTTCCACAA CACCACAAGC AGTCTCATCT GCAGTTCAAG

154701  GTTTTCTTCA AACTGGAGGA GCTGCCTCCT CTACAGCGAC AACTACTACC

154751  GCATCCGGAG CCTCTGCATT AGGACTTTCA CCTGATCAAG TGCAAGCGTT

154801  GCTTACTAAT TTATTAAATG TGGACAACC ATCAGTGGGA CAACCATCAA

154851  CTTCAGCAGG AACTTCGGGA GCCTCCTCTT CCAGTGCAAG TATGCAGCAA

154901  CAGCTTTTGC AACTTATCTT AGACAAGACA ACAGGAAGTG GCGGATCGTC

154951  CGTGAGTTCA GAGCAATTAC AGCAACTCCT TAGCTTGGTG AGCCAGATGA

155001  CTACGTCTCA AGGAGGAAGT GGTGGAACTC AGGCAGGACA GGCCGCTTCG

155051  GTACTGTTGA ATTTGTTATC GGCAACAGGA TCTGCAGCAG CAAATCCTTT

155101  AGGGACAGCT GCATCGTTGG CACAGATCAT TTATGCAGCA GTAACAAGTC

155151  CTGGAGCAAA GAAAACTAGC GAATTTTGTT ATAATTATTG TGGAGAGACC
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155201   TGCCAAGGCA ACTGCGGTTG TCCTACCTGT GGCTGTCCAG ACGGACAGTG

155251   CGGTTGTGGA GGATTTGGCC GTTTTTTCTG TGGTGTATGG AAAAATTGTT

155301   GCGGGATAGG AGAGGGATCC CAAGAACCCG CAATCCCTTT ATAAGAACTC

155351   GAGGCTTTAG AACAGAAATA TGGCAAGGCT GTTCTTTTAA TTGCGTTAAG

155401   TGAGCTTGGC ATTGATACCA TGAGCTTATT ATCAGGACAT CGACTCGAGG

155451   GATTTCCTCC AATCGCGGAG GTCATGGCTG CATGTGACCG GTGTTCTATG

155501   GACTTTTGTG AGATCTTGAA GTCTCAAAGC ATGGATCTGT GGGCGGATGC

155551   GGCGAGTTGT GTGGATGGTT TATTACAGGA TCCTTTTTGG AGTACAGCAA

155601   TTGCCTCAGG GATTGCTAAG TCTTCTCTTC AGGAAACGGA ATTCGAGTGT

155651   GAAAGCAAAG TGATGGTTCT TTCTTCATGG GGAGAGCAAG GAGCACAGGT

155701   TTGTAGCCCT TTTAACCTAG AGAGGATATG TATGTCTTTC CCATCACTTA

155751   AGGTCTTCTC CCTTAAAAAG AACGGGTGCG AGAACATGGG AATCCAGTTG

155801   TCTGCATCCT GCATGAATCT ATTAATGTCT ATTTTCTTTG TAGCTACCAA

155851   TGGAGGAAGC ACTCCGATTT GGATCACCAA AGAAAATCTG ATGGCGTTAG

155901   TTGCTTTGGT TTTATCTCAC TATCAATGTT ATTTTGTCCC AGCCACAGGA

155951   GATCCCCAAC GTGGCAACAT TTTAGGTAAT CCAGAAGTCA ATGCTATTTT

156001   GGCTCGGGGG ATGGGCATGC GTGTCGATCT GGAAAGGAAG CGAGGGGGAG

156051   AATCTTCCTC GTCACGCTAT TTAGAATTAG CTGCACGATG TTTTGAGAAT

156101   TCTCTTACGA AAACAAGTTT GTTAAGCGAT GCTAACAATG TTCAAGAAAG

156151   AGATAAGTGC CTACTACAGA TGTCAACTTC ATTGATGCAT ACGGCGGGAC

156201   TAAATTTACA ACGCCCCCCT GTACCCACAC CTTCTGGAGT CACGGCACAT

156251   CCGCAACCTC AACCAGATCC TGTGGTTACG TCTCAACCTT CTTTATTAGG

156301   TGCTAGAGAG CGTTCCCCTG TGTCTTCTAG AGGGCGTTTT CCTGTAGTTT

156351   TACCTTTAAG TGTGATTTCT CCTAGGTCGC ACCCCGGAAG GGTAGAAAGG

156401   CGGGATTTAG AAGATGAAGA AGAGGAGGTT ATGTTTTGAA GCAGTGTAAA

156451   CGACTCCAAT TACAGTTTTA TGAATCTCTA ATTGTAAAGT CTAGGGGTT

156501   TTTCTTGAAG TAAGTGCCGA GCACATTCTC TAGGATCTTC GGTTGATGAC

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156551   GCACAAATTT TTAGGGGAAG ATTTGTGAAT GGGGAGATAA ATTCTAGGGA

156601   GTGAGCATGG AGGAGAGGGC GGAAGATCTG GGGAGGCTGT TCTTTAGGTC

156651   CGTAGTCGAC ATCTCCGACA ATAGGATGAC CCAGCAATCC CATTTGTAAG

156701   CGGATTTGAT GGGTTCTCCC TGTGATGGGC CTGCGGCTCC AAAAATCACA

156751   GCTCCACACC TCCGGTATAC GGGGGCCGTA TAAGATTTTA CGGTTCCAAA

156801   TTTTTTTTTA GGATGACCAA AAACGAAAGC TATGTATTGT TTATGGATTT

156851   TTCTTTGCTT GAACAATTTC ATGAGCTCAG TAGCCGCTTG TTTAGACTTT

156901   CCCATGAGAA GACACCCAGA GGTGCCTTTG TCTAACCTAT GCACAGTAAA

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157051   GTTGAGGGGA TCAGAGATAG GGAAACACGG TCGCCAGGTT GTACCTTGTA

157101   GGATTCAAAT CTTTCTATGA ACCCGTTCAC TCGACATCGA TGTTGGCGAA

157151   TAGACGCCAA GATTCTTGC TTGCTATGAT TAGGCAGTTG AGATCTAAGA

157201   AAAGAAGATA ATCTTGAGAC TTGTGTGGCA AGCCAGGAAA AATTTTCCAT

157251   AAAATATTGT AAAGCAGCCC TTTTATCATT TGATAATTGC ATAAAATTTT

157301   AAGAGATTTT GTATGACAAA GATAGCTTTT TCTGAAAAGG CAAAGAATTT

157351   TCCTGTAGAG GCATTAAAAA AATGGTTTGA AAAAAATAAA CGATCTCTTC

157401   CTTGGAGAGA TAACCCGACT CCCTATAGTG TGTGGGTTTC CGAAGTTATG

157451   CTACAGCAAA CGCGAGCTGA AGTTGTTATA GATTATTTTA ATCAGTGGAT

157501   GGAGAGATTT CCTACCATAG AGTCTTTAGC TGCAGCAAAA GAAGAAGATG

157551   TCATTAAGTT ATGGGAGGGA TTGGGTTATT ATTCTCGAGC GCGCCATCTT

157601   TTAGAGGGAG CTCGCATGGT TATGGAGGAG TTTCATGGAA AGATCCCTGA

157651   TGATGCCATT TCCTTAGCTC AAATTCGTGG AGTTGGTCCT TATACGGTTC

157701   ATGCTATTCT AGCCTTTGCT TTTAAGAGGC GTGCTGCTGC TGTGGATGGC

157751   AATGTCTTGC GTGTTCTTAG CCGGATATTT TTGATAGAAA CTTCTATAGA

157801   CTTAGAATCA ACTCGTACTT GGGTTTCTAG GATTGCTCAA GCGCTTCTTC

157851   CTCATAAGAG TCCCGAGGTT ATAGCTGAGG CTCTGATAGA GTTGGGAGCT
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157901   TGTATCTGTA AAAAAGTTCC TCAATGTCAT CGTTGTCCTG TCCGTCAAGC

157951   ATGTGGAGCT TGGAGGGAGA ACAAACAGTT CGTATTGCCG GTACGTCATG

158001   CCAGAAAAAA GGTCATCTTT TTGCATCGTT TGGTAGCGAT TGTATTGTAC

158051   GATGGCTCTT TGGTTGTCGA GAAGAGACGT CCTAAAGAAA TGATGGCAGG

158101   CTTATATGAA TTTCCTTATA TTGAAGTTGA ACCAGAGGAA GGTCTTCAAG

158151   ATATAGAAGG ATTTACTAAG AAGATGGAGC TTTCTTTAGA AAGCCCTTTG

158201   GAATTCTTAG GTAACCTTAA AGAACAGCGG CATGCGTTTA CTAATCATAA

158251   GGTTCATTTG TGTCCTATAA TTTTTAAAGC CACTTCTCTG CCTCAGTTCG

158301   GGGAATTGCA TCTTTTGAGT GATATAGATC ACTTAGCTTT TTCTTCAGGA

158351   CACAAAAAGA TTAAAGATGC TTTGCTAATC TACCTCGGGG ATGTCAGGTC

158401   TAGAGAATCA ATAGGAGTAT AGATGCGAGA TCACGCTTTT TCTAAATTGA

158451   TAGGGACTGT CCGTGCCATG GTAGTTGAAG GACGTTGTCC TTGGTCACTT

158501   CAGCAATCCC TAGTCTCTAT GGTAGAGCAT ATTCTTGGAG AGTGTCAGGA

158551   ATTTCACGAG GCCGTCTTAC AAGGTAAGAC GGTACAAGAG GTTGGTTCCG

158601   AAGCCGGGGA TGTCTTAACT TTAGTTCTAA TTTTATGTTT TCTGTTAGAA

158651   CGAGAGGGCG TACTTGCTTC CGAAGACGTT GCCAATGAGG CTATGGAAAA

158701   ATTGCGTCGC CGTGCTCCTT ATATATTCGC TGAAGATTAC AAGCCGGTCT

158751   CGATTGAAGA GGCCGATCGC CTTTGGGAGC TTGCTAAGCA CCGAGAGAAA

158801   AATGAATCTA CATAGTTGAA GTTTTGGTCT ATTTTTAAGC ATATGGTGCT

158851   TTTGAAAAAA CAGAATATAT GCTATCAAAG AAGGGTAAGT TGGGGGCCTT

158901   TTAAGAGAAG GAACCTGCGA ATCGGGTCAG GACTGGAAGG TAGCAGCCCT

158951   AAGGAGAGTT TTCTTTTGCT AAAAGAATGT TCTCCAACTT ACTCTTTTTA

159001   CTTTATTCCC AAAAATAGCA ATGAGGTGAG GTTAAACAAC CCGTGCAGTG

159051   CAATGGGAGA AAGAATGTGC CGATCTTTTT CATATAGAAA CCCTGCAGAT

159101   AAGGAAAAAA CAAAGAGCAC GGGGACAAAG ACCCAACTTC CTAAAGAGTG

159151   TTCAATGTGA ATGAAAGAGA AAATAATAGA AGAGCATAGT ACCGCAGCTA

159201   TGCGCGTCAT TTTGTTTTTC AAGAATGTCT GTAGAATTCC TCTAAAAAAT
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159251   ACCTCTTCTC CAAATGGAGT GAGGACGCCT AAATTTAGAA TCATGCTAAT

159301   GTAGTGTCCT GTTATAGGCA GAGAGTTCTG AACTTCTTGA GTGACTTCTT

159351   GTGTGTGAAT CTCTTGCGTA GGAAGAACCA AAGTTAAAAA TTTACTCATC

159401   ATAATCCCAA TCAGTTGTGT TACTGGGATG ATGATGATCC ACATTCTGAT

159451   GGCAGATCCT AGAGCACGCC ATGAAGTTTT AACCGGTCTT CTCCAGAGA

159501   AAAGTATAGC ACGTGTGATA TCCTTGGGGA GAAAAGCAG GTAGAACAGA

159551   AATGCAAAGG CAAGGCTAAT TCCTGTCATG GTGGAAAGTA ATTCCGCAGT

159601   TTGTGAGCTC ACGCTAAGAG CTACAAGGGA AGAAAAAACA AGAAGAGCAC

159651   CACCAAATAA AACTTGGCGG AGCTTTAAAG GTGTTTTCCC AGAGGGTGCT

159701   GGCCAGATAA AGAAGTTTTT GGAAGCTAGA GCAGCGACGC CAAGGGACAA

159751   GAGAAGAATA AACTTGGACA TTTCCTTAGA CTACGAGTAG TTAGCACAAA

159801   CATAGCCCTC AACTCTGGCA ACAACTTCGC GGAAAAGACG GCTATGCATT

159851   AAGCCCATGG GCGTTGAATC AAAATGTTTT GAGTTCCAGC CATAGCGATG

159901   ATAATCATTG ACTAGGGTAG TTAAAGGCTG GCTGCATTCG ATAATCTCTT

159951   GATAAATGAG AGCTATTTTA TGATGACGGA TATCAAAAAC GCGAACACGT

160001   ACAGACGCTG TTACAGAATC GACACCTGCT TCTTTCCCTG TCTTTTGTTC

160051   TAACAGTTCT GTAGCAACAA TGAATTCTGC AGGAAGAAAT TGCTCAATAA

160101   TTGTTTCGGG TAGACGATTC GCAATCGGAG CATAGAACTG AGAGACTGTC

160151   TGAGGTGAAG CATTGTGCTT GATCAGGAAG ACCTTTTCCG AAGCATAAAA

160201   CCTTTTGCTG ATCTCTTCAG TAAATTCTCC TTGGAGGTTC CAAGGTAAAG

160251   GTTCAAGACT CTTTCCTGGG CGATGAAATA CAGGAAGCAT CGCAATCACA

160301   CCTTTAGTTT TGCTCCCTGA AGTGTATAGC TTAGGATGAT AACTTCCTGA

160351   AGAGCCTAAG TGAGTGCAGC TGGATAGGGT TGGGGATAGA AGTCCTAAAG

160401   ATGCCAATAA TACCAACATT TTTCGCATAG TCACTGTCCT TAAATTGCTT

160451   ATTTTGCAAA AGATTCTAGC CCTGGGAAAG TTTTTACTTT TAAGATCAAT

160501   ACTTTCGCAA TTGAGAGATT TTCCATTTAA AACTCTCATT AGCTTATATC

160551   AAAGAAAAAA ATAAAAACAA GCAAAGAGAC CGTCTCAGTT TTAGTTTAGA
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119

160601 AACTCAAGGT TGAGAAAGGG ATTCTGACCA AAGTTGTGAG GGAACTTTGG

160651 TAACTTTTTC TTTAGGAATC AATGTGCACC CTGGGAGGAA TACAACTGGA

160701 GCTGAGATCA CAGAAAAAAT AAACCACTTC ATGACTACCT CTGCAAAAG

160751 AATACTACTA TTTTCTATTT GCATAGGCAG TTCTTCGATT TATAGCAATT

160801 TTTACTTTAT CATCATAAAA ACTATGATGA AAAGGTTCTT AGTGAACTTC

160851 TAAGGAACAC CATGAGTTTG TGATTAAAAC TCATGGTGCG TAGTTGAACC

160901 CTTATTGAGG AGGGACGCAA CCACTAAGAG CTAACAATAC TAAACAAGAT

160951 AATAGTAAAG AGAATGCTTT TTTCATTATT CATCCTTAGG TTAATTGACC

161001 TTTCCAGCCT AGCTCTAGGG CGATTATTTA TCAAATTTTT CTTTGTAATT

161051 AATGATCATG CGACCATTAA TTTAGCGATA AATTATGATT CGTCAGGAA

161101 AATTCAATTC TTTATAATAA TGATATGAAA TTAGAGAATG TCTATAGGGG

161151 CGGACTCTAT TTGTGATCCA GGATCTCTTT AGGAGCACTT TGTGGATTTT

161201 GATTATTTTG GTCTGAGTGA TATTGGTAGG GTGCGCGCTA GAAATGAAGA

161251 TTTTTGGCAG GTAAACCTCA TGTCTCAAGT GGTTGCTATT GCTGACGGTG

161301 TTGGGGGGCG TCTTGGTGGA GACATTGCTT CTCAAGAGGC AGTGACTAGC

161351 CTTATGGAGC TGATTGATGA GCAACAGTCA AAATTGATGG GGTATGGGGA

161401 TGACCAGTAT AAGGAGACTT TAAAAAAGAT CCTTTTAGAG GTCAATGGTG

161451 TGGTCTATGA ACACGGCCAA ATGGAAGAGC ATCTCCAGGG TATGGGAACC

161501 ACTCTTAGCT TCATCCAATT CCGGAAGGAT AGGGCATGGC TATTTCATGT

161551 GGGAGATAGT CGAATTTATC GTATTCGTGA GGGAGAACTG CGCCGCCTTA

161601 CCGAAGACCA TTCTTTAGAA AATCAATTAA AAAATCGTTA TGGGCTTCCT

161651 AAACAATCAG ATAAGGTGTA TTCTTATCGC CATATTCTGA CTAATGTTTT

161701 GGGAAGTCGT CCCTATGTCA TGCCTGACAT TCGGAATCTT CCTTGTGAAA

161751 AGGAAGATTT GTACTGCCTC TGTTCGGATG GATTGACAAA CATGGTTCCA

161801 GATATCGATA TTCGTGATAT CTTGAACCAG CCCGCCACCC TAGAAGAACG

161851 GGGGAATGCA TTAATTTCTC TAGCCAATAC TCGTGGAGGC GATGACAACG

161901 CTACTGTCGT ATTAGTCCGA ATACAATAGT TCCTTTGCTA AGGATAGTAT

120

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162001  TTTGGAATTT CTCCAAAAAA CCTTCCTTAT AGAAGGGACG TACGCGAATC

162051  CTTCGAGCGT CCATCAATTA GGTAAAAAAT CTCGTCAACT GGTTCTAGAA

162101  GCTTCACACT GGATGCAAAA GGTCCTTTCG TTTCAGGGCC GTGTCCTCTA

162151  TACCTCAGGG GCTACTGAGA GTTTAAATTT AGCAATAGCA AGCCTCCCTA

162201  AAGACAGTCA TGTTATCACC TCAGGTAGCG AACACCCCGC CATCTTAGAG

162251  CCTTTAAAAC ATTCCTCGCT TTCCGTTTCT TATTTAAATC CCGAAGAAGG

162301  GAGATGTGTT CTTACTATAG AGCAGATTGA AAGAGCTGTG ACTCCTAAAA

162351  CTTCAGCAAT CATCTTAGGT TGGGTCAATA GTGAGACTGG TGCCAAAGCT

162401  GATATAGCTG CTATAGCCCA CTTCGCGCAA GAACGACAAT TGCAATTTAT

162451  TGTGGATGCG ACTGCAAATG TAGGTAAGGA GAGGATAGTT CTTCCCTCTG

162501  GTGTCACTAT GGCAGCATTC AGTGGACATA AATTTCATGC ACTCTCTGGA

162551  ATCGGAGCTC TTCTGGTCTC TCCAGGAGTC AAACTACATC CTCAGCTGTG

162601  GGGAGGAGGT CAGCAAGGAG GGCTGCGCGC AGGCACAGAA AATCTTTGGG

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162701  CGTATCTCTC AGGAAATTCT TACCCATAGA AATGGTTTTG AAAAGGCAAT

162751  CAAAGCACGC ATTCCTGATG TCCATATTCA TTGTGCGGAT CAACCACGGG

162801  CAAACAACGT CTCAGCAATT GCTTTCCCTC CGTTGGAAGG TGAGGTATTG

162851  CAAATCGCCT TAGATATAGA AGGAGTGGCT TGTGGTTATG GATCCGCATG

162901  CTCTTCAGGT GCTACCGCAC CCTTTAAATC TCTTGTCAGC ATGGGTGTTG

162951  ATGAAGAGTT GACCCTGGCA ACACTCAGGT TTTCTTTTAG CCATCTTCTC

163001  TTGCAAGAAG ATGTTGAAAG AGCCGTTGGA ATTATAGAAA AAGTCGTAGA

163051  ACGTTTGAAA AATTCCTAAG TCTTAAAAGA GAACATGTTT CTAAGCTGAA

163101  AGAACACTCC TGACTCTTAT TGCAGAATCT ATGAGAGTAA GTTTTTAATC

163151  GATACGGTTT TTATCCCAGA TAAAGACATC TCTTTAACTT CTAAAAGCAA

163201  GTTGTTGATA ATTACAGAAG TTCCTACTTC TGCAGGACTG TCTAGCAGTT

163251  GCAATACCAA TTGGGCTAGG GTTTCTACAG GATATTGCGG AAATTGAATA
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163301  TCGAGTTCTT  TTTGCAGATC  TTTTATGCGA  GAGTTGCCAG  GAAACGTTCT

163351  TTCAATAACA  GAGATGGTCT  TGGGTTTTAA  ATGAGCAATG  TTTGTAGTGT

163401  TGAATAAGAT  TTTGAAAATT  GCATTAAAC   TAAGAATACC  TATAGGTTCA

163451  CCAGAAGCAT  TGAGGACAAC  AGCAACACTC  GAACGGTTGT  CTCGAAACTC

163501  TTTGAGGATA  CGAATAAGTT  TTGATTTTGC  AGTGATAAAC  CAAGGCGAGT

163551  GTAGATTATT  GATTAGGGGT  TCATCAAGAG  CTTTATTGAC  AAAGTCTTTA

163601  GGATGGGCAA  TCCCAATAAC  GTTTTTTCGG  GCCTTGTGAT  AGACAGGAAT

163651  AAAGTTGATA  TCTGTATTTT  TTATAGTCCG  GCAAAAATCT  TTAACATTTG

163701  CAGAAGAAGG  AAGCATGGTA  ACCTGTTCTA  AAGGTTGGCA  TACCTGATCT

163751  GCACAAGTCG  CACTTAAAGA  GAAAATATTT  GTAGCAATTG  TATTGAAATC

163801  TTGTTCTTCA  TGGTGAGTCT  CTAAAGCTTT  TTGGAACTCG  TCTCTACTTA

163851  ATGTAGAGTT  CAATTTTTCT  TTCCTAATAT  TTAGAAGATA  GTAAAGACCC

163901  TCAGTGAGAC  TTCCTATGAG  CTGAATCAGA  GGATAGAAAA  TATAGTGGGA

163951  ATAATAGAGA  ATCGGTGCTC  CCCAAAGTGC  TAATTTTTCA  GGAATCTTCC

164001  GTGATATTGT  TAGAGGTAGA  AGTTCTGCAA  AAATCACAAC  TATAAAAATT

164051  TGAGTGAAAG  GAGCGTAATC  TGGAGTGATT  CCTAAAGCTC  GATAGCAATT

164101  TCTTGAGGAC  TCAGACCCGA  CTTGTAGAGC  GATATTCACT  CCTAACATCA

164151  CCGTTCCAAA  TAAACGATAG  GGGCGGCGAA  TCAGGAAATT  AATGTAGCGA

164201  GCTTTCTTAT  GATCTTTAGT  CAGATAGTAT  TGCAATCGTA  CACGGTTAAA

164251  TGACACGCAG  GCCATTTCCA  TCATCGAATA  GAATCCTTGT  AAGACAATAC

164301  AGATAATGTT  GACTCCTATC  CAAAAGAGAG  CAGAATTAGT  CATACAATTT

164351  CCTTATATAC  ACACGGCGAA  TGCGATTCGG  AGCAGCGTCT  AATACCTGGA

164401  AAAGCAAGTT  ATTCCAAGAG  AGTTTCATTC  CTGTTGTCGG  AATCGTTCCG

164451  ATTTGCTCTA  TTAACCAGCC  TCCTATAGTC  GCAATATTAT  TGTTCGTCGG

164501  TAGGTTGATA  TCGAAGATCT  CACTAAACTC  ACGGAGTTCT  AAAGTTCCTG

164551  AGGCAATAAT  AACATCAGCT  CCTGAGGTGG  TATAGAGTAT  TTTATTATCT

164601  CTCTGGTCTA  CAATTTCTCC  AGCAACAATT  TCAAAGAGGT  CTTCTTGAGT
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164651   GATCAATCCT TCAATAGATC CGTATTCATC AATGATCATC CCTAGGGTTT

164701   CGTCTTCAGC TGCCATCTGA CATAAAGCCA TTTTTGCAGA GATGGTTTCT

164751   GGCATATAAT ACGGTTTTTT CAGCAAGGGG AGGAGATCAT CCGAAGATTG

164801   CAGTGGCTTG TCATGTAAAA GAAGAGAGCG CGCTGTGCAA ATGCCCAGAA

164851   GGTTTTGGAG GTTATCGTTA CATATAGGAA CTCGTGAGCA ATGCTGTTTA

164901   GAAAATAAAA GATAGAGGTT CTCTAAAGGG GTTTGGATAT CATAAAATAA

164951   AATATCCTGG CGTGGCTGCA TACGCTCTTT AACACTACAA TCACTAAGAG

165001   AAAGATAACC ATAGAGTAAA CGGCTTTCTT CTTGATTGAC TACGCCGAAA

165051   TCCTTACAAC TTTGCAATAC TTCCTTCAGC TCTTGGGGTT GGATGATATC

165101   AATCTGTTGC TTCGATAAAA TCCATTGGAC CACATAATTA ATTCCTACGA

165151   TACCCCAGTG GAGTAGGGGT TTGAAGATTT TAGTAACACA AAGAATAAGA

165201   GGGGCTACGG AACTAGCAAT CTGTGTATTA AAAGGAAGAG CTACTGCTTT

165251   AGGGAGAATC TCACCTAAGA TCAAAGTAAT TGCTAAAGGA AGACCTACAG

165301   TAAACCACCA CGAAGCTGCA TCTCCAAATA GAATGGCAAA ACAGTTTTGA

165351   ATAGCAATAT TCAGTCCGAT ATCACAAAAA ATTAAGGTGA TGAGCAGGTG

165401   GTGGGGATGT AGAAGAAGGG TAGCTACTCG CTGCTGTTTC TTAGATTTAG

165451   AGCGCTTATA GTGCGAGATC AAACTCGTAG GCAAAGAAAA CAAAGCAATT

165501   TGAGATAACG AAATGAATCC CGAGCATAAA GTAAAACAGA TAATGAAGAA

165551   CATTAACATG GTAGGAATCA TGGTCTCTTT TCAGTCCTTA TTTTCTGATT

165601   GTTGCTTTGG GGAGACACAG AGTTCTTAT AGCCTTTAGG AATGAGACCC

165651   AGACGCTGGA TTAAAGCAGC TTCTATAGCA GCGGAGTCTT GCCAGTGTTG

165701   CAGATGTAAT TGGAGTTGAC GCTGCTTTTC TTGAGCAGAA AGAATGTCTT

165751   GGCATAAAGA AGAGACCTTG CTTTGTAAGC GTAGCTCTTC TGTACGTAAC

165801   TCCTGGATAG CACGATCATA AACAAAGCCT CCAATTAAGA TGCTAAAGAT

165851   CACCCACCAG GATTTGATCA TCACTTCTTC TAGTAATCTA AAACCCCAGT

165901   TTTTTTTTCT TACTGAAACT TTAGACACAA GGTACGGTGA TGCCTTGTTG

165951   CTTTTGATAC TTTCCTTTTC TGTCTGCATA AGAAACCTCG CAGGTCGTAC
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166001   TAGACTCAAA GAATAAGACC TGGGCAATCC CTTCATTAGC GTAAATTTTC

166051   GCTGGCAATG GCGTAGTGTT AGAAATTTCT ATAGTCACAT GCCCTTCCCA

166101   TTCAGGCTCA AAAGGTGTGA CATTTACGAT AATTCCACAG CGTGCATATG

166151   TAGACTTTCC TATACACATT GTTAAGACAT TTCTAGGAAT TCGGAAATAC

166201   TCAACGCTAC GAGCTAGAGC AAAAGAATTT GGAGGAACAA TACAGACGTC

166251   ATCAGTAATA GAGATGAAGA TATCCTCAGT AAAGCATTTT GGATCAACAA

166301   CAGAGTTATA GACATTGGTG AACACTTTGA ATTCTCGAGA TAGGCGGAGG

166351   TCGTAACCAT AACTCGATAG GCCGTAACTT ATAAGTTTTT CGCCTGTCTC

166401   CTCATTTACG TTCACTTGGC CATTAACAAA GGGATGGATC ATATCGGCAT

166451   TTAGGGCCAT CTCTCGTATC CACTTATCTT CTTTTATGCT CATTTAGAAA

166501   CCTTAACAGT TTGAAATTGC TTTCTTAATG ATATTCTGTT TTTCAATTTA

166551   CTGGTTTTTG GGGGGAACTT TTCTAAGTAT AAGATAGACT TTGATTATCT

166601   CTTGAAAAGA CCAGTTGTAT AAACAAGAAA AGCCTATCCC AAAGGCTACA

166651   ATTTTATCAC GAAACCTAGA GGTAATGTTA GATAATCCTA AGGGAAAAAG

166701   GCAAACCTTA TTTTTAGGGA GAACTTCAGG TAGGTCTGCT CTTTACTCTT

166751   ATAGTAGAAG AATCTTGGTT CTCTTGAATG CATTCATGCG AGGACCTTGA

166801   TAAGAACTTC TTGGATTCAT AAAAAGATTA ACATCTCCTT ATTGATAAGC

166851   TAGAGAATTT TTACTACCAA CTTCTCAGTG GAAAATGTTT TTAAAAATAG

166901   TTCGCCATCT TTAATTTATC TGTTTTAAGA CAAAAGAAAT CTAGATCACC

166951   ACAGGAAGTT TAAATCATAA AATGAAAATG ATGGAGAGGT TCTAGTGCTC

167001   GTACTTTGGC CCTGCTCTCC TTGATAGAAA GAAGAGGTCC ATAGTGTACT

167051   TCTATATAGT ATCTCGTGTA CTATGCCGAG TATAACCGAT CGGCGTTATC

167101   GATGAGAGTT TCAAAAAAAT ATAAATCCA CCTAAAGAAA AAGCGATAGA

167151   GAAGGTTCGT ACATGACGCA TCAAGTAGCT GTCTTGCATC AGGATAAAAA

167201   ATTTGATGTT TCGTTAAGAC CTAAAGGGTT AGAAGAATTT TATGGACAGC

167251   ATCATTTAAA AGAACGCCTA GATCTATTTC TTTGCGCAGC ATTGCAACGA

167301   GGAGAAGTTC CAGGACATTG CTTGTTTTTT GGACCCCCAG GCTTAGGGAA
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167351   AACCTCACTT GCTCACATCG TTGCCTACAC CGTGGGGAAA GGGCTGGTCT

167401   TGGCATCAGG GCCTCAGTTA ATCAAACCCT CGGACCTGTT AGGACTTTTA

167451   ACTAGTTTGC AAGAAGGGGA CGTGTTTTTC ATCGATGAGA TCCATCGTAT

167501   GGGGAAAGTT GCTGAGGAAT ACCTGTATTC TGCAATGGAA GATTTCAAAG

167551   TCGATATTAC TATAGATTCA GGACCCGGAG CTCGCTCGGT CCGTGTCGAT

167601   CTTGCTCCTT TCACTTTAGT GGGGGCAACG ACTCGATCAG GAATGCTAAG

167651   CGAACCTTTA AGAGCACGCT TTGCTTTTAG TGCGAGACTT CCTATTACT

167701   CGGATCAAGA TCTAAAGAG ATTTTAGTCC GCTCCTCACA TTTACTCGGA

167751   ATCGAAGCTG ACAGCTCCGC ATTACTAGAA ATTGCTAAGA GATCCCGAGG

167801   GACGCCACGA CTGGCAAATC ATCTTCTACG TTGGGTCAGA GATTTTGCTC

167851   AGATCCGAGA AGGAAACTGT ATCAATGGGG ACGTAGCAGA AAAAGCTTTG

167901   GCTATGCTAT TAATAGATGA TTGGGGATTG AATGAAATTG ATATCAAACT

167951   TCTCACTACA ATCATCGACT ACTACCAAGG TGGTCCCGTT GGAATTAAAA

168001   CCTTATCGGT AGCTGTGGGA GAAGATATCA AAACTCTTGA AGATGTTTAT

168051   GAACCGTTTT TAATTTTAAA AGGTTTTATC AAAAAGACTC CCAGAGGCAG

168101   AATGGTAACA CAACTTGCTT ACGACCATTT AAAAAGACAT GCAAAGAACT

168151   TATTGAGTTT AGGAGAAGGA CAGTGAAACT ATTGAAAAAC GTACTTTTAG

168201   GTCTTTTCTT CAGTATGAGT ATCTCAGGAT TCTCAGAAGT AAAGGTATCC

168251   GATACTTTTG TGAAGCAGGA TACTGTCGTT GAACCTAAAA TTCGTGTCCT

168301   TTTATCTAAT GAAAGCACCA CAGCTCTCAT AGAAGCCAAA GGTCCTTATC

168351   GCATTTATGG AGATAATGTC TTATTAGACA CAGCGATTCA AGGCCAGCGT

168401   TGCGTGGTCC ACGCTCTATA CGAAGGGATC CGTTGGGGAG AATTTTATCC

168451   CGGACTCCAG TGTTTAAAGA TCGAGCCTGT AGATGACACT GCTTCTCTTT

168501   TTTTTAACGG GATTCAGTAT CAAGGTTCCC TATACGTTCA TCGTAAAGAC

168551   AACCATTGCA TCATGGTTTC TAACGAAGTT ACAATCGAAG ATTATCTGAA

168601   ATCTGTACTT TCTATAAAGT ACCTTGAAGA GCTAGATAAA GAAGCTCTAT

168651   CTGCTTGCAT CATTCTAGAA AGAACCGCTC TATACGAAAA GCTCCTTGCA
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168701  AGAAATCCTC  AAAACTTTTG  GCATGTTAAA  GCTGAAGAAG  AAGGGTATGC

168751  AGGATTTGGT  GTGACCAAGC  AGTTCTATGG  TGTAGAAGAG  GCTATAGACT

168801  GGACAGCTCG  TTTAGTTGTG  GATAGCCCTC  AAGGATTAAT  TATAGATGCA

168851  CAAGGGCTCT  TGCAGTCCAA  CGTAGATCGT  CTTGCTATAG  AAGGATTCAA

168901  TGCACGTCAG  ATTCTTGAGA  AGTTCTACAA  GGATGTGGAT  TTTGTAGTTA

168951  TAGAATCCTG  GAATGAAGAA  CTGGACGGAG  AGATCAGGTA  ACCTCTTTCG

169001  CATGGCTGAT  CGCAATTAGC  GTGGTATGGG  GCTGTAGCGA  CACTGTCGGC

169051  GTTGCTACAT  TTTGAGGGAC  AAACCCTTGC  TGACTCTCGG  CAACTATTTG

169101  ATAAGGAAGA  AAGTTGCTGG  AGGCTTTAGG  TAAGGTCGCA  AGTTGGTCTT

169151  GAGCTCCCAC  GTGAAAAGCA  ACATATACAT  GCGCTTTTGG  CGATTTTATT

169201  TTAAATGCTA  AGAAATTTCC  AGGGCGCCAT  GTCATGGGAT  TTCCCATAGC

169251  ATCTACCCAA  CTGATTTCCT  TATTGGAAAG  AAAGCCTCGA  TTAAAAAGTG

169301  TTTTATATTT  TTTTCGAAAC  GCAATGAGAT  CACAGAGAAA  GTGCATCAGT

169351  GTAGGCTTTG  CGGTAAGCTG  ATCCCAAAGG  AAGTAATTCG  CATTCGAATC

169401  CAAAGCCCAA  CGGTTGTTAT  TGCCTTCCGC  GGTATGGGCA  TACTCATCTC

169451  CTGATTGAAT  CATCGGAATG  CCTTGCGAGA  CCATCAAAGT  AAGGAAAAAA

169501  TTTCGTAACT  GTCTTTCACG  AACTTCAAGA  ATGCCAGGGT  CTTCTGTTTT

169551  CCCTTCCGTT  CCGAAATTGT  AGCTGTAGTT  CGCATCTGTG  CCGTCACGAT

169601  TATCCTCTCC  GTTAGCCTCA  TTATGTTTGT  GGTTATAAGT  CACAGTGTCA

169651  CATAACGTAA  AACCATCATG  GCAACTGACA  TAGTTAATCG  AATTTGTAGG

169701  CGAGCCGTGA  GGATAGATGT  CTTGAGATCC  TGAAATTCTA  GAAGCAAAGG

169751  TTCCTATGAG  ATTTTGATCC  CCATTAAGAA  ATGCTTTCAC  GTTATCACGA

169801  TACGGGCCGT  TCCATTCACT  CCATCTTGGA  GACAGTGTGG  GGAAATAGCC

169851  CACCTGATAC  AAACCGCCAG  CATCCCAAGG  CTCAGCTATA  ATCTTTGTGC

169901  TCGCAAGTAA  AGGATCAAAA  GAAATCGCCT  CTAAAACAGG  AGCGAATTGT

169951  AGGGGAGATC  CCGAAGGACC  ACGAGAAAAG  ACAGAAGCAA  GATCAAATCG

170001  GAACCCATCG  ACATGCATTT  CTTCTACCCA  ATAACGTAAG  ATGTCGAGAA
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170051   TCCATTGGGT CGTGGGGGCG CGGTTTGTAT TGAGAGTGTT TCCACAGCCT

170101   GAATAATTTG TAAAGTGACC TTGTGCATCT AAAATATAAT AGCTCGGAGT

170151   GTCTATCCAA GGCAAAGAGC AGGTCGTCCC TTGCAAGCCC GTATGATTAA

170201   AAACAACATC AAGAATGACC TCAATACCTT CTTGATGCAA GGTCTTTACT

170251   AAAGTTTTAA ACTCTCTACT TGGAGCGCAA GGATCAGAGG CATAAGCATA

170301   ACGTCGGCAA GGAGAAAAGA AATTTAGGGG AGCATAACCC CAATAATTGC

170351   ACAGATAAGG GAATTTCGAA TTTCTAAAAG GATGCGCAGT CTCATCGAAC

170401   TCAAAGATAG GTAAGAGTTC AACAGCGTTG ATTCCCAGCT TATGCAGATG

170451   GTCGATCTTT TCAATGATTC CTAGGAAGGT TCCCGGAGCA TGAACCCTAG

170501   ATGAAGAAGA TTGCGTGAAG GAACGTACAT GCATCTCATA GATGATCATC

170551   TCTTCTTTCG GCAAATGCAG AGGCTGATCA CCATCCCAAG GAAATGGTTC

170601   TTCCTTTAAA TAACAAAATG CATAATCCCC CTGTTTCTTT CGCGAACCAA

170651   AACTCTGTGG GGAATGAATA TTCTTCGCAT AGGGATCTGC AAGATATTCT

170701   TTAAAGAGT ATTGCATTCC ATGCTTTTTA GGCCCATGAA CACGAAATGC

170751   ATAAGACGAT TGATCAGAAA TACCCTCGAT CTCTATATGC CAAATCGCAC

170801   CCGTGCGGTG TGTATCGGGG TAAAGAGGGA CTTCTATGAC TTCTGAATTT

170851   TCGTCTGTTA AAGCAAGGAT GACTTCGGTA GCTTGTGAAG CATATAAAGC

170901   AAATCGATAG CGGTTTGGGG AAATTTTAGA AGCCCCAAGA GGTAAAGGAA

170951   CTGAGGGATA AGAAGAAACT TTTTCCATCG TCGATCAGAT ATCATAACGG

171001   CGCCAGAAAT ACAAGGGAGT TTTTGATTTT AAGCCTCTGA AATCGTTTAC

171051   TAACAAATCA CTCTTATGGT AACTTGAAAC AACAACAATC TATTACAAGG

171101   AGATTCCCTC ATGTCCAGGC AAAATGCTGA GGAAATCTA AAAAATTTTG

171151   CTAAAGAATT AAAACTGCCG GATGTAGCTT TTGATCAGAA TAACACGTGC

171201   ATTTTATTTG TTGATGGTGA GTTCTCTCTT CACCTTACTT ATGAAGAACA

171251   TTCTGATCGT CTTTATGTCT ACGCTCCTCT GTTAGATGGA CTCCCTGATA

171301   ATACTCAGAG GAAATTGGCC TTATATGAGA AATTATTAGA AGGATCTATG

171351   CTTGGCGGTC AGATGGCTGG AGGTGGAGTA GGTGTTGCTA CTAAGGAACA
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127

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171401   GCTCATTCTC ATGCACTGCG TTTTGGATAT GAAATATGCT GAAACGAATT

171451   TACTAAAAGC ATTTGCTCAA TTGTTTATTG AAACTGTTGT TAAGTGGCGT

171501   ACCGTGTGTG CTGATATTTG TGCTGGTAGA GAACCTTCTG TAGATACAAT

171551   GCCACAAATG CCTCAAGGCG GTGGTGGAAT GCAACCTCCT CCTACAGGTA

171601   TTCGTGCTTA ATTAAGCATA TAAGTACTAC ATCTTTTTTC TAAATTTAAA

171651   AGATTGATAA AGCTCTTCTT AGAGAAGAAA TGACTTTATT GACTTCTCGT

171701   TTTTGTCCTG AATCTGTTTT GAGAAGTTCT TAAGATGTAT TAATTAAAGA

171751   AGTATTAAAA ATAGAAATCT AAAGGCTATC TTATGATGTT TGGGCATTTT

171801   GCTGGTTACC TTGGAGCAGA TCCTGAAGAG CGAATGACTT CCAAAGGAAA

171851   ACGTGTGATC ACTCTGAGAC TGGGAGTGAA GACTCGAGTT GGAATGAAAG

171901   ATGAAACTGT TTGGTGCAAA TGCAATATTT GGCACAATCG CTATGATAAG

171951   ATGCTTCCTT ACTTGAAGAA AGGCTCAGGA GTCATTGTTG CTGGCGATAT

172001   CTCTGTAGAG AGTTACATGA GCAAAGATGG TTCACCGCAA TCTTCTTTAG

172051   TGATTAGTGT AGATTCTTTG AAATTCAGTC CTTTCGGTCG CAATGAAGGC

172101   AGCCGTTCTC CATCTTTAGA AGACAATCAT CAGCAAGTGG GATATGAATC

172151   TGTATCCGTA GGGTTTGAAG GTGAAGCACT GGACGCAGAA GCTATTAAAG

172201   ATAAAGATAT GTATGCTGGT TATGGTCAAG AACAGCAGTA TGTCTGTGAA

172251   GATGTTCCTT TTTAATTCCT AGTCATTAAA GGAGAGTTTG TGGTTTTATT

172301   TCATGCTCAA GCCTCTGGGC GTAATCGTGT TAAGGCAGAT GCTATAGTCC

172351   TGCCCTTTTG GCATTTTAAG GATGCAAAAA ATGCAGCTTC TTTTGAAGCC

172401   GAGTTTGAAC CCTCGTATCT CCCCGCTTTA GAAAACTTTC AAGGAAAAAC

172451   CGGGGAGATT GAACTCCTTT ATAGTAGTCC TAAAGCTAAG GAAAAACGCA

172501   TTGTCCTCTT AGGCTTAGGG AAAAATGAAG AGCTCACCTC TGATGTTGTT

172551   TTCCAAACCT ATGCGACACT AACTCGTGTC TTACGTAAAG CAAAGTGTTC

172601   CACAGTCAAT ATCATCTTAC CTACAATTTC TGAATTGCGG CTTTCTGCCG

172651   AAGAATTCTT AGTGGGGTTG TCCTCAGGAA TTTTGTCATT AAACTATGAC

172701   TACCCACGTT ATAATAAGGT AGATCGTAAT CTTGAAACTC CTCTTTCTAA
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172751 AGTCACGGTT ATCGGTATCG TTCCCAAAAT GGCGGATGCT ATCTTTAGGA

172801 AAGAAGCAGC CATTTTCGAA GGCGTATATC TCACTCGAGA TCTTGTGAAC

172851 AGGAATGCTG ATGAAATTAC CCCTAAGAAA TTGGCAGAGG TTGCTCTGAA

172901 TCTGGGAAAA GAGTTCCCTA GTATTGATAC TAAGGTCTTG GGAAAAGATG

172951 CCATCGCCAA AGAGAAAATG GGACTCCTAT TGGCTGTTTC CAAGGGTTCT

173001 TGTGTGGATC CACACTTTAT CGTTGTCCGT TATCAAGGAC GTCCTAAGTC

173051 TAAAGATCAC ACCGTCTTGA TAGGGAAAGG GGTCACTTTT GACTCTGGAG

173101 GTTTAGACCT CAAGCCTGGA AAATCCATGC TTACTATGAA AGAAGACATG

173151 GCAGGTGGGG CTACAGTCCT CGGGATTCTC TCGGCGTTAG CAGTTTTAGA

173201 GCTTCCTATA AATGTCACGG GGATCATTCC TGCTACAGAG AATGCTATCG

173251 ATGGCGCCTC CTATAAAATG GGAGATGTCT ATGTAGGAAT GTCGGGGCTT

173301 TCTGTTGAGA TTTGTAGTAC CGATGCTGAG GGACGTCTTA TCCTCGCTGA

173351 TGCGATTACA TATGCTTTAA AATATTGTAA ACCGACACGT ATTATAGATT

173401 TTGCAACTCT AACAGGAGCT ATGGTAGTCT CTCTAGGAGA AGAGGTTGCA

173451 GGTTTCTTTT CCAATAACGA TGTTTTAGCT GAAGATCTTT TAGAGGCGTC

173501 AGCCGAAACC TCCGAGCCGT TATGGAGACT TCCTCTAGTT AAGAAGTATG

173551 ATAAAACATT GCATTCTGAT ATTGCTGATA TGAAAAATCT AGGCAGTAAC

173601 CGTGCAGGGG CTATTACAGC AGCATTATTC TTGCAGAGAT TTTTGGAAGA

173651 ATCTTCGGTA GCTTGGGCAC ATCTTGATAT TGCAGGTACT GCATATCATG

173701 AAAAAGAAGA AGACCGTTAT CCAAAATATG CTTCAGGTTT TGGTGTTCGT

173751 TCTATTCTTT ATTACTTAGA AAATAGTCTT TCTAAGTAGT TGCTTTCTAT

173801 TTATTTATGT TTTAGTAATG ACTTTATTTT TAGTTTTTTT AAAATAAAAG

173851 TCATTTTTTT TATTAAAGTT TTCAATCGTC CCTGCCGATA GATCAGGTAA

173901 GTAATTACCT GTCTAATTAG GGGAATAAAG ATGATTGGAG CGCAAAAAAA

173951 GCAAAGCGGT AAAAAGACAG CTTCAAGAGC TGTACGGAAG CCTGCTAAAA

174001 AAGTTGCGGC TAAACGTACG GTTAAAAAAG CTACTGTTCG CAAAACCGCT

174051 GTAAAAAAAC CTGCAGTTCG TAAGACGGCT GCTAAAAAGA CAGTAGCAAA

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174101   GAAGACTACA GCTAAGAGAA CAGTTCGTAA GACTGTTGCT AAGAAGCCTG

174151   CAGTTAAGAA AGTTGCTGCT AAACGTGTAG TAAAAAAGAC AGTAGCAAAG

174201   AAGACTACAG CTAAGAGAGC GGTTCGCAAG ACTGTTGCTA AGAAGCCTGT

174251   AGCTAGAAAA ACTACAGTGG CTAAAGGTTC TCCTAAGAAA GCTGCAGCCT

174301   GTGCTTTAGC ATGCCACAAA AACCATAAGC ATACATCTAG TTGTAAACGT

174351   GTCTGTTCTT CAACAGCTAC GAGAAAGCAT GGCTCTAAAA GCCGTGTTCG

174401   TACAGCTCAT GGCTGGCGTC ACCAACTGAT CAAAATGATG TCTCGATAAT

174451   TTGTGATTTT CGCATTATTG CTCATGTTAA CGGGAAAGGG AAACATTGGG

174501   TTTCCTTCCC GTTTTTCTTT TTAAGGTTAA AAAGCTTTAT AGAGCGAGAT

174551   CTTCAGGCTT CATGCTGTAC AGTTGGTAGG AAAATACGTA TAGTAGGTTC

174601   AGGATACTAC TTTTTTGACT CTACCTATGC AAAAATCCTT AACGAGTTTT

174651   GATGACTTTT CCCAGGCGTA TGCAGAGAAA GTGCCCGCTA TAGCTCTTAT

174701   AGGGAGTGCT TTGGAAGACG ATAAAGATGC GCTGATTGAA TTATTAGTCT

174751   CTGAGAGCTT CAAAGAGCTC GGTGGTCAGG GACTCATGCC AGCAACCCTC

174801   ATGTCTTGGA CCGAGACGTT TGCACTCTTT CAAGAGCATG AAACTTTGGG

174851   GATTATTCAT GCAGAGAAAT TCCCTCTAGC AACTAAGGAA TTTCTAAGCC

174901   GCTATGCTCG GAATCCTCAA CCTCACCTTA CGATTTTGAT CTTCACCACA

174951   AAACAAGAAT GCTTTCGAGA ACTGTCAAAA GCCTTGCCAT CGGCTCTTTC

175001   TTTGAGTTTA TTTGGTGAGT GGCCCGCAGA TCGTCAGAAA AGGATCATAC

175051   GCCTCCTGTT GCAAAGAGCT GAGCGTGTGG GGATTTCTTG CTCTCAATCA

175101   TTGGCATCTT TGTTTTTGCG TGCACTTGCT TCAACCTCTC TTCCTGATAT

175151   TCTCAGTGAA TTCGATAAGC TACTGTGCTC TGTTGGCAAG AAAACGTCCT

175201   TGGATCACTC TGATATTAAA GAGCTCGTTG TCAAAAAAGA AAAGGCTTCC

175251   CTATGGAAAT TTCGAGACTC TCTATTGAAG AGGGATCCGG TAGAAGGTCA

175301   CCAGCAGTTG CATTTTCTAC TCGAGGATGG TGAAGATCCC TTGGGGATTA

175351   TTACTTTCCT TCGTACCCAA TGTCTCTATG GTTTACGTAG TATTGAAGAG

175401   GGATCGAAAG AAAATAAACA CCGAATGTTC GTCCTTTATG GAAAGGAGAG
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175451  ACTACACCAA  GCCTTAAATT  CTTTATTTTA  TGCAGAAACC  TTAATTAAAA

175501  ATAATGTCCA  AGATCCTATA  GTAGCTGTGG  AAACTTTAGT  GATTAGAATG

175551  GTTAACCTGT  GACTTTATAT  CTTCTTCCCA  ATACTCTCGG  TACCCGTGCT

175601  GTAGAGACTC  TCCCCTCCGT  TATAGGAGAA  TTAGTTCATA  GACTAGATGG

175651  GCTGATTGTA  GAAAGTGATC  GTGGGGGTAG  GGCATTTCTA  AGTTTATGGA

175701  AAATTCCCGA  AGTTCATAAA  TTTCCTCTTG  CTATTCTTAG  TAAACATGCG

175751  CGCCTCCCTA  AGGCTTGGGA  TTTTTATCTA  GAGCCTATCG  TAAAACACGG

175801  GGAGAATTGG  GGACTGATCT  CTGATGCGGG  TCTTCCCTGT  ATTGCAGATC

175851  CTGGAGCGAG  TTTAGTGCGT  CGTGCACGTG  CTTTGGGGAT  TCCTGTGCAG

175901  GCTTTTTCAG  GTCCCTGTTC  GATAACGTTA  GCGCTCATGC  TTTCAGGCTT

175951  GCCTTCCCAG  AGCTTTACGT  TTTTGGGATA  CCTCCCGCAA  AGTCCTAAGG

176001  AACGTGTAAA  GTCGATAAAA  AAGGCAGCGA  CCTCCAAAGA  GGTATCTACT

176051  TCAGTATGTA  TAGAAACTTC  TTATCGTAAC  GTCTATACTT  TTGAGTCTCT

176101  TCTAGATACT  TTACCTTCCT  ATGCGGAGCT  TTGTGTTGCC  TCTGACCTTT

176151  CGGGCCCGAG  TGAACTTGTT  CTCACACGCC  AAGTGCAATC  ATGGAGAACT

176201  ACTGAGGACT  TAGGTTCTGT  GAAGCAAAGT  ATAACCAAAG  TCCCAACAAT

176251  ATTTCTTTTC  CACATCCCGA  ATTAATTTTT  CTTAGCTTG   TTTTATCCCC

176301  GGTATCATTG  TCAGGAGTTT  CTTAGCATGT  AAGCTCTTCG  GGGATATTTT

176351  TCTTGTGATC  ATAAGCAAAA  ATTAAAGGTT  GCATGATTCT  AAATAGCGCA

176401  TAATCATAGG  TTTGCGTCTT  TTTAAAATAA  TCGTAATCCT  CTATTGCGTG

176451  TTATCAATAC  TTATTTTATA  ATCTTTGCCA  AATAAGTTTA  GAGCGTTGAT

176501  GACAGCACCC  ACAGAATCTC  GATCTTCACC  ACCAACACTA  CTCGAAGAAA

176551  CGGAACCTCT  ATCCCCAAAT  CCTATTCCCG  CCGATATCCA  AATCCCGAGA

176601  ATTACAATAT  CTCCTCCTTC  TCTAGACGTA  TCAACAGTTG  CATCTTCGGC

176651  TGAAGATATC  TCGGTCTTCA  TTGCAGGAGG  CCCTAGAAGT  TCTTCATCTG

176701  CTTCTGTGGC  TTCGGATGTG  TATGAGTTGG  TTTGCCTTTG  TGGCGGTGAT

176751  GAGGATCCTG  AGCCCCCAGA  TTCTGAGGTA  CGTACTCTCT  ATGTAAATGG
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176801  AAGTTGGCAA  ACGCATCAAG  AAGCTGTACA  GGAATTGCTG  TATATTAGTG

176851  AAGTACGGGG  AGAGGCCGTT  CGTCTTCTCT  ATAACGATGG  AAGCGGCATG

176901  TCTCCTTGGC  CCATCAGTCC  TTGTCGTACT  CTTCCTACTC  TCGATCATCC

176951  TTTATGTCAG  GCCCTTTTGA  CGGTTTGGGA  ACAGTTTTTC  TCTGCTCCTG

177001  AAAATCAGAA  TCGTGAGTTT  CTAGTGATTT  TCTATGGGGA  TGCATCGCCT

177051  TATATACAAC  AGGCGTTAAC  GCAATCTAGG  CATAGTCCAC  GTATTGTTGT

177101  TGTAGGGATT  TCCCCGACGG  TCTTTATTCA  AGGAGACTTT  AGGGTCCATA

177151  ATTACCGTGT  TTCTGGAGAC  TTCTTTAGTT  CTCTGGATTG  TCGGGGAACT

177201  AGGGCGGAGA  ACACCACGAT  ACTGCCGTAT  TCTTCGGGTC  TTGAGGGTGT

177251  TTTTCTGCCT  TCTATCCGTT  GTCCTTCTTT  TACTTGGGCG  GTGCGTTTTG

177301  GAGAGCAATG  CTTGGTTGCG  AATAGGGGTG  AGGATGTAGA  AGATAGGGGA

177351  GGTCTTTCTC  AAGATGCCGA  AAGATCACAG  TTACCACACA  GTGAAAGAGA

177401  TCTAGCTGTT  GTCATTGATT  CTACGGATCC  TAGTTCTATG  AGTAGGCTTG

177451  TAGAATGGTT  GAATCAAGGA  TCGCCTTCAT  CAGATATGGA  AATCAATCCC

177501  TATCCCCAAC  GGTGTCCTGA  TGTAGCTCTT  TCTGCGCTTT  ATGCAATTTC

177551  TAGAGTTTCA  GGACTTGCGC  AGGAATGGAT  CCTAGCCTCT  GTTCATGAGG

177601  GCTTAGACTT  GCAGATCTGT  TACTCTTTAA  TTTTGATGCA  CACGACGTTT

177651  GCGGTCCGGT  ATTTTTTCTT  ACTCTTTACA  AATTATCCTC  AGTCTAGAGA

177701  GAGATTCCGT  ACTGCACGAA  TCGTAGCACA  ATCTCTATAT  TTACCAAGCA

177751  TCCTTGTTCT  TGTTTTTGAT  TGTGGCAACG  TCCTGCGTAA  ACTATGGATG

177801  CCTCAGGAAA  TCTTACGAGC  AATTTTTATT  TCTGCGTCTA  CAATTTCAGG

177851  GAGTATTGTC  TTTGTAGAGT  GCACTCGCTG  GATGGGGCGA  GGTCTTAGAC

177901  ATCGTGTACA  ACAATTTGTG  CAGCAACGAG  TTATAGGAAG  TGGCCTGCCT

177951  GTAGGAACAG  TACGAGCTTC  TTATCGCGAT  CGTGCAGGCT  TTATCATAGG

178001  CTTTTTACAA  ACTGTACATG  GAGGACTTTA  TTTGCCGGTA  TCCATTATGG

178051  TGCTTAACCA  GATTGCAATA  CAAGTTCCAC  GTATCTTAGT  ACGTCCAAAT

178101  AACACTGCTG  TTTATGATCT  ACATAATAAA  AGTGCTGAAG  AAAATTGGAG
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178151  CAGTGGTGAT GTATTAGCTG TTGGCCAAAC ATTAAACTTC ATCTTATGTG

178201  CTTTCGTCTT GTTCGTAAAT CTATGGTTCT TTGTGAAGTC CGTATTACGC

178251  CATTCTAGGC GTCGTCGTCG CTAATGTATC TTTGGAGACA TCTTGGTATT

178301  TTTAACATAA GAGCACGGCA AAAAAAGAA AGACCGAGAA AGAAGCTTTA

178351  CCTTTAAGAG TTCTCTGATG TTTCCCGGAG CATCAGGAGT CCGAAGGGCA

178401  GAGTCTAGGT TTTAGCCTTC CGCAGGGATT AGAAGGAATA TCCCATAATC

178451  TCTTCCGCTA TTGTATCGTG GAAGAGACGG CCCTGTCTAT TTAGGGCAAG

178501  ACATTGTCCA TGCACACTGA ATAGGTTTTG TAATTTTACA TCTTGCGTAA

178551  GCATGGAGAT AAGTGTGGAG GGGAACTCCG CGAGGTCTGC TCCTTCAAGG

178601  AGTCGGAGTC GCAGGGCTAA GGCTTCTTTG ATTCGTTCTT TTTTTGGGAG

178651  AATTTCTGAG GTCTCTTGGG TAGGGAGATT CTTACGTACA GCACGTAGAT

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178801  GTTGTGCTTT GCGGGGTAAT CTGGCTTGGC ATATGAAGCA AGTTCATAGC

178851  GTTGGAACCC TTGGGAGAGT AGGAGATTTT CAGCAAGGAG GCTCATCTCA

178901  GCTAGAATTT CTTCTTGGGC AATTGTGGGG ACTAGAATTT TGCGGTGTTT

178951  ATAGAAGGAG GTGTGGGGAT CTATAGTGAG GTTGTATAGA GAAATGTGAG

179001  TGATAGGGAG AGTCAGAGCT TGATGTAGGT CGCTTAGGAA TATCTCCAAA

179051  GACTGTGTGG GCAGTCCGTA GATTAGGTCT ATAGAAAGAT TAGAGAATCC

179101  GTGATTCTGG CATTCTTGCA GTGCTGTGAT TGCCGCAGAT GAAGAATGCG

179151  TTCTTCCGAG GAGCTGTAGG ATAGAGTCGT CGAAGGTTTG TACGCCAACG

179201  CTAATTCTAT TTATTGGAGT CTCTTGTAGT TGACGTAGAT AGCTTACGGT

179251  GAGATTTTCG GGGTTGGCCT CTAAAGTAAT TTCCCGGGCA TGGGGGGCTA

179301  GCTCTTTGAG GATGCGCTTA AGATCAAGAG GAGAAACTAA TGAAGGTGTT

179351  CCCCCTCCAA AAAACACAGT CTCTATGAAA TGCGTCTCTT GGATGGGGGC

179401  TAGCTTTCTT AGCCCCTCTT GAATTACAGC ATTACAATAG AGCGATACAG

179451  ATTCACTTTT GTAGGGGATT GTATAAAAAC TGCAATAGCG ACATTTTTTT
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133

179501   GTGCAGAAGG GAATATGAAT ATAAAGAGCT AGGGGAGCCT TACCATTCAT

179551   TAGCATCGGG ATCAATGATA CCACCGCGTC TCCAGCGATT GCGATCGCTG

179601   AAAGGGTCTT CATCGTCTTC GTGGGAATAG TCGACTTCTA CTGCCCCATC

179651   TTCACGTCCT TCATCGGTGA GTTCCAGTTC TACGGTTTCG CCTGGGTCGA

179701   TATCAATTTC TGTTTCTGTG GGTTCCACAA ATTCAATATC AGACATACTA

179751   GGACCATCAG GGTAGACAGT CTTTGCGGGA CTGCGTCGTG GTGTGACGTA

179801   CTCTTCAATC TCTCCGTTTT CTTTGAGGAG TTGTAGACGT TCTTTTTCTT

179851   CGTAAATTTT ATGTTCTAAG ATTCGGATTT CTTCTTGGTG CCTGCTAATT

179901   TCTTTTTTTG GCACTAAACC CAACTGCATC CATTGCGTAA GGTCATGAAG

179951   TTCTGATTCT AATTTTTTAA GACGTTCGCT TTTCATCCAA GGGTTCCCAT

180001   CCTGTATTCG AGAGCAGGTG CATAGCATTT TTTTGTTTTT TCAACTGCAG

180051   AAAAAAAACA AAGATTTTTT TTTTTTTGAA AAATAAAAAT TTGCTATGAA

180101   GCAGACATTT AGATCGTATT TATTGAGTTT AATTATTTTA TGGATTCCGA

180151   GTTTGTGGGG CAAGTATATT CTTCGGATAT GGATTGGATC GAGTCTATGT

180201   ATCAGAGATT TATGAATCAC GAGACTTTGG ATCCTTCTTG GAAGTATTTT

180251   TTTGAAGGGT ATCAGCTCGG TCAAGCAGCA TCTCCATCAG AAGCTAGTAC

180301   TAAGATTTCT GGGAATGAAA CTATTGCTAT GCTTCAAGAA CAAAAATCTC

180351   AGTTTCTATG TACGATTTAT CGTTATTATG GATATTTGCA AAGTCAAATT

180401   TCAACGCTTG CCCCAACTAC AGATTCTCGA TTCATTCAGG AAAAGATCGC

180451   TAAGATTGAT CTGGATGAGC AGGTGCCTTC TGCGGGTCTA CTTCCTAAAG

180501   CTCAGGTTTC GGTACGAGAG CTGATCGAAG CTTTAAAAAA ATGCTATTGC

180551   GGAAGTCTTA CTTTAGAAAC CCTAACATGT ACTCCTGAGT TGCAGGAGTT

180601   TGTTTGGAAT ·CTTATGGAGA AGCGACAAGT GGAGCGCTTT GCAGAGCAGC

180651   TCCTTCGCTC CTATAAAGAC TTATGTAAAG CAACGTTTTT TGAAGAGTTC

180701   TTACAGATAA AATTTACAGG TCAGAAACGT TTTTCTTTAG AGGGCGGAGA

180751   GACCTTGGTC CCCATGTTGG AGCATCTTGT TCATTATGGA TCGGCATTAG

180801   GAATTTCTAA CTACGTTTTA GGAATGGCCC ATCGAGGTCG TTTGAATGTA

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180851  TTAACGAATG TTTTGGGAAA GCCTTACCGT TATGTCTTTA TGGAGTTTGA

180901  AGACGATCCT GCAGCACGTG GTTTAGAGAG TGTTGGGGAT GTAAAGTACC

180951  ATAAAGGGTA TGTGCTAAAG TCCCATCAGA AAGATAGGGA AACTACCTTT

181001  GTGATGTTGC CAAACGCTAG TCATCTCGAA TCTGTAGATC CTATTGTCGA

181051  GGGGGTCGTG GCTGCCTTGC AACACCAAGG TCACGCAGGT AAAGAGCAAA

181101  GCAGCTTAGC AATTTTAGTT CATGGAGATG CAGCATTTTC TGGTCAGGGA

181151  GTGGTTTATG AAACTCTCCA GCTGAGTCGT GTTCCAGGGT ATTCTACTGA

181201  GGGTACGCTT CACATTGTTG TGAATAATTA CATAGGGTTT ACCGCAGTGC

181251  CACGGGAGTC AAGGTCCACC CCTTATTGTA CGGATATTGC TAAAATGCTA

181301  GGGATTCCTG TATTTCGAGT GAATAGCGAG GACGTCGTTG CCTGTATAGA

181351  AGCTATAGAG TACGCTCTGC AAGTTCGTGA GAGATTTAGT TGTGATGTGA

181401  TCATAGATCT CTGCTGTTAT CGCAAGTATG GACATAATGA AAGTGACGAT

181451  CCCTCAGTAA CAGCTCCCTT ACTCTATGAT CAGATTAAGA GAAAGAAGAG

181501  TATTCGCGAG CTGTTTAGGC AATATCTGTT GGAAGGGCAG TTTGCAGATA

181551  TTTCTGAAGA AACTTTGGCA TCTATTGAAA AAGAGATTCA AGAGAGTCTG

181601  AATCGTGAGT TTCAAGTATT GAAAGGGACG GATCCAGAAC CCTTTCCTAA

181651  AAAAGAATGT CATCACTGCG ATCGCTTAAA TAACGGCGAG CTTATTTTGC

181701  ATGATTGTGA TGTTTCTTTG GATCGCGAGA CTCTTTTTCA TATGAGCTCG

181751  CGTCTTTGTG GTTTCCCTGA CAATTTTCAT CCCCATCCTA AAATTAAGAC

181801  TCTTTTAGAA AAAAGAATGA AAATGGCAGA AGGTGGGGTT GGTTATGATT

181851  GGGCGATGGC CGAAGAATTA GCCTTTGCTT CGCTATTAAT CGAAGGGTAC

181901  AACCTGAGAC TCTCAGGTCA AGATTCTATT CGCGGGACAT TCAGCCAACG

181951  ACATTTGGTA TGGAGTGATA CTGTGACTGG AGATACCTAC TCTCCATTGT

182001  ACCATCTTTC TGCAGAGCAG GGCTCTGTAG AAATGTATAA TTCTCCTCTT

182051  TCCGAATATG CAATTTTAGG GTTTGAGTAT GGCTATGCTC AACAGGCATT

182101  AAAGACTTTA GTGTTATGGG AAGCGCAGTT TGGGGATTTT GCTAATGGTG

182151  CACAAATCAT TTTCGATCAG TATATCTCTT CGGGAATTCA GAAGTGGGAT
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182201  TTACACTCTG ACATTGTTCT GCTTCTTCCC CATGGGTATG AGGGCCAAGG

182251  ACCCGAGCAT TCTTCATCTC GTATAGAACG TTATTTGCAA TTAGCCGCGA

182301  ACTGGAATTT TCAAGTGGTC TTGCCTTCCA CTCCTGTGCA ATATTTTCGG

182351  ATTCTCAGAG AGCATGCTAA GAGAGATCTT TCTTTGCCTT TGGTGATCTT

182401  TACTCCTAAG TTGCTGCTGA GATATCCACA ATGTGTAAGT AGTATCGAGG

182451  AGTTCACAGA ACCTGGGGGA TTCCGTGCTA TTCTCGAAGA TGCCGATCCT

182501  AATTATGATG CTTCTATTTT GGTATTGTGT TCGGGAAAGA TCTATTATGA

182551  TTATGCAGAA ATGCTTCCTC AAGATCGGCG TAAGGACTTT TCTTGCTTGC

182601  GTATAGAGAG CTTGTATCCT TTAGCTCTTG AGGATTTAGT GAGCCTTATC

182651  GATAAGTATT CTCATTTGAA ACATTTGTT TGGCTACAAG AAGAATCCAA

182701  GAATATGGGG GCCTATGACT ATATGTTTAT GGCGTTGCAA GACATTCTTC

182751  CTGAGAAACT GCTATATATA GGACGTCCTC GGAGTAGTTC CACAGCTTCT

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182951  GCTCTGATTC AAGAAAACCA GGGCTTACTA GAAATTGAAA GTGATAAGGT

183001  AAATCAGCTC ATTTATGCCC CAGTATCGGG AAGAATTTTC TGGGAGGTTT

183051  CAGAAGGCGA TGTTGTTCCT GTAGGGGGGG TAGTGGGAAA AATAGAGCCC

183101  GCAGGTGAAG GGAAGAGCT TGGAGATTCT CAGTCTAAAG AGACTATAGA

183151  AGCTGAGATC ATTTGCTTTC CTCAGTCTGG GGTGCGTCAG TCTCCTCCAG

183201  AGAATAAAAC GTTTATTCCT CTTCGTGATC AGATGGACCA AGGATCCCAA

183251  GGTCTTTCTG CAGGAGATCG AGGAGAAACT CGAGAACGCA TGACCTCGAT

183301  TCGTAAGACA ATTTCGCGGC GTCTTTTGTC TGCTTTACAT GAGTCTGCGA

183351  TGCTCACGAC ATTCAATGAG GTCTATATGA CACCTCTTTT TCATTTGCGA

183401  AAGGAAAAAC AAGAAGAGTT TCTATCTCGA TATGGGGTGA AGTTAGGATT

183451  TATGTCTTTC TTTGTGAAAG CTGTCTTAGA GGCTTTGAAG GCATATCCAC

183501  GAGTGAACGC CTATATTGAT GGCGAGGAGA TTGTTTACCG TCACTATTAT
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183551   GACATTTCTA TTGCTGTAGG TATCGATCGA GGACTTGTGG TTCCTGTGAT

183601   ACGCGATTGC GATAAACTTT CTAACGGGGA GATTGAGCAG AAACTCGCAG

183651   ATCTTGCCCT TCGGGCTCGT GAAGGCCTAC TTGCAATAGC GGAGCTTGAG

183701   GGAGGAGGTT TCACAATTAC CAATGGAGGC GTATATGGAT CGCTACTTTC

183751   GACTCCCATT ATCAATCCCC CGCAAGTGGG GATTTTGGGG ATGCATAAGA

183801   TAGAAAAGCG CCCCGTTGTT CTTGATAATG AAATTGTAAT TGCAGATATG

183851   ATGTATGTCG CTTTAAGCTA TGATCATCGT CTTATTGATG GGAAAGAGGC

183901   TGTTGGGTTT TTAGTCAAAG TGAAAGAAGG CCTAGAGAAT CCTGCCTCAT

183951   TACTCGACTT GTAATTTCTC TGATTCTCAT AAAGGCTCTT TTAGAGCCTT

184001   TTCAGATTTT TTAACCTCTT TTCTTATCAT GAAAAGGATT GCACTCATCT

184051   TGAGTAAGGA ACAATGTAAA TTGAGTATCC GCACTTACAT TGGCTTGTAC

184101   CGCAGCCTCA TTCAAGGCGC CTAACAACTT TCCGGGTAAG TACACATTGT

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184201   TCTGCGTGAA TATGTACTGA TGTGAAGCCA TTTTCTAAGA GATCTACAAA

184251   CAGATTTTTC AAGAACTCCT TTGAGTCTTT TTCAGAAAGC GAAGAGCTCA

184301   TCGGATCTTT TCTTTCTAAG ATATCTTGTA CATCCTTGTC GTAATAACCC

184351   CAAGGAGTCC ATGCTAAAAC TAAAGTTGAA CTGACACCAG GAGTTGGAGA

184401   ATTGAAAATT GCCCATTGAC CTGCTTTTTT TCTAGAGTTC ATTTTAGTTT

184451   TCATAGCTTC CCACTGTTCC TCTCCTAAGA GATCTTGCAG TTGCTTTAGG

184501   GGAGCCGAGA CTTCCTTATC CCCTTTCCAA TGCGAAGTTT CTGGTGAAAG

184551   GAGGAATAGC GAAGGTACGC GAGCCCCGTG ATCTCTAATT TCTGTGAGAT

184601   TAGGAGCTTT AGCTGTGACA ACCTTAAATT AAGGACCCTT CTTTAGATGG

184651   TGAATTTCAC AATTCGTAGC TTCTGTAATT TTGATTTCTT TAGTGAGTTT

184701   TTCTTTGGGA GGAAGAGCGT CGTAAGGTAA GGAACAATGA TGTTAATAGG

184751   GCTAGTTTAG TTAAATAAGA ATAGGGGATC TCAGGTTTAG GAGTGATGGG

184801   TTGTTGCTCG ATTACAATGA TGGTTAATGG AAGAAGAGCG TTTCTAGAAA

184851   GTGCATCTGC TTCCTCGTCT TCTTTAGGCA ACAAGCTCAA GATGAGAAGC

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184901   ACGAGCCCGA TGGCTAATCC CACGAGTGTG ATAATACCAG CAATGCTATA

184951   CGCCTGTATT AGAGGGAAGC CTAAAGCTAA GAAGGTAACG AACGTGATTC

185001   CAGCTGCTAA CATTAGTGCA GCGAAAAGTA TGTAAAGAAC AGCACGCGCA

185051   ATTTGAAGAG CAAGACTTTT ACTTCTGAGT GTGCCTTCTG TAGCTTGGGT

185101   TTTGTTAGCT TCAATCTCAG CGAGTTGCGC TTTTTTTGGC TTCACTGGTT

185151   CGTGAACTTT ATGATTAGTT GATGCGCCTA ATTTCATAGA AAGTCTTTAA

185201   GCTTAATTTT TTCCTAAAAA TTGTAGTTTA CATGTTGTTT TTCATCAAGA

185251   AGATTACTGA ATTCTGAGTG GGTTGGAACG AAGCATGTTC TTCTAGAAGC

185301   TAAGGTCCTT AGGGGAAAGG AAAAGAAGCT TGGCTGGATC TTTTTAATCT

185351   CTGGGTAGGA GAAGGACGGC GGTTACATTA TTTCTATTTT TTGAATGTTG

185401   GCCTGTGAGA TTGGGATCGG GATGGTGAGC AAGGTACCTT GAAGAAAAGA

185451   AAGCGTCGTG TTCCGTGTAG GTACAGAGGT CTGAGATAAA AATGCGGTCT

185501   TTAGAGATTC CTAAATTCGT AAGTTGCTTG CGAGCAATCG CACGCAGGTC

185551   AAAATGGTTT TTGGGATTCA TAAAGGGAAG AAAGCTACGA GGAAATAACG

185601   TAGCGTAATC GGGATAGATA GCATAATCTG GACCGATGGA AGGGCCGATA

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186001   TTTTGAAAAG ACTCCGTGGC GTATAGGCAA ACCATCGAAT TCTTCGAAAG

186051   TCCAATAGTT CAGAGGGTGA GTGTGGAAGG ATAGAGTCAT ACTGTCAACT

186101   TAGTTTCTTC AGGGTCTTTC CATACCCCAT GTTCTTGTAA AAGTCGAATT

186151   AATTCTTCTT CAGCATCTTC CATGGGTATG TGAGCTTTTA CACAAGTATG

186201   TTTTACATAA AGATCGATCA TCCCTGTTTT GGAACCTACA AATCCAAAAT
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186251  CTGCATCTGC CATTTCTCCA GGGCCATTCA CAATACAACC CATGATAGCG

186301  ATCTTAAGTC CTGGTAGGTG CTGCGTTCTC TTGCGGATAC GTGTGGTGAC

186351  TTCTTCAAGA TCAAAGAGGG TCCGACCACA CATAGGACAG GAGATGTACT

186401  CTGTTTTTAC AAGGCGCACC CCTGCATTTT GTAGAGTGCC AAAGGCAATT

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187451  TGCCTAGTCG CTTACATTTC TCTACTAAAG GAGCAAACTT TTCTTCAAGA

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187551  GAACATGTTC CTCTTATCTA TGTAGTTGCC TGGATTGATG CGAACCTTGT
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187651   GCAACCAAAG GGATATTTAA CCCTAGAGCA ATCAGACGTT CTTTAATTTT

187701   TTCACAGGCT TGTGCTTCCT TGATTCCCTG TACAGTCACT CTGACAATAT

187751   CACAATTATG TTCCGCTAGA GCGTAGATTT GCTCTACTGT ACTGTCAATG

187801   TCTGTGGTTA ATGTCGTTGT CATTGATTGG GTTTTTATTG AGTGGTCACT

187851   GCCTATGTAT AAGTTGCCTA TTCTTACTGT ATGGGTTTTG CGTCGCGAGG

187901   AATTGATGGC AGGGGTAATG AGTGTCATAA AAATCTCAAA AATTTCAGAG

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188501   AAGCCGCAAA GGCAATTTTT ATGCATCGTC CTGATCCCGA TAACCTTTCT

188551   AGGAATTCTC CAAGCTTTGT TTGTTCAACT GGAGATGCAC TTGATGTTCC

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188701   AATTAATCTC CTACTAAAAT AGGAGGAGAC ACTCTCATAT TTTCTATGAC

188751   CTAGGGAATA AAATATTTTA TTTATAATGA GTGAAAAACA CCGCTGTTTG

188801   TCTAAGAAAT ACTTTTAGAA GAGAGTTTAC GTTTTATCTG CTGTTCAGCA

188851   GTTGTTCCTT CGGTTTTGTT TACAAGGGCA AGCTTTATAA CAAGAAGAAG

188901   CACACAGAGT ACTGTTGTAA GAATAAGGCC TCCTAGGATA ATCAAGCAGA
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189001  ATTACTAGAA TGGCAACAAG GATTTTAACT AAAAGTTTAA TCGTCTTCGT

189051  CGTTTTATCT TGATGCTTTG CTTTTAGAGC TTTGGAATTT GGTTCCATGA

189101  GGCCTAGATT TCCAGAGGAA GGGCGGTGGC TTGTGGGTAG GGGGGCTGAG

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189701  GCCCTAGAAG TTGTCCTAAG AATTGCGGTA GTCCTGCTTT ACCTGCATTC

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189951  AGTTTTATAG CGAGGCTTTT CAATGGGCCC TAACGTAGAG ATCAAAGTCA

190001  GGTTTGAGTT TTTCAAATGC CAAGCATAAC CGGTTTGATT GTCAGCAGCG

190051  ATGAAAGGCA TATCTGTGTT AGCCTGTAGA TCAGGTATAC GGTCCCAATT

190101  TTCTTGTAAC AGTGTTTGAT GGGTTCTAGG GGAAGGAAGC GGGGGCTCTT

190151  CTAGGACAGC TTCCGTAGGC ACTGGGGTGA GTGCTAGGGG CGGGACAGGA

190201  GGAAGGTCTG TATCTTTTAT GATGGGCGTC GGCTGATGCG TTACGCTTAT

190251  AGGACTTTTA GGTTCTCTTA AGAGAAAATA GAGAAGAATA CTAAAAGCCA
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190301　AGACTGCTAG AGCGGTAAGA ATAAATAATA GAGGAATGCC TAAAATTATA

190351　GCAGCGGTTC CAGAACTTAC AGCAATTCCT ATAATTAGAA TAAAAGCGAC

190401　AAGGTCCAGA CCTTTGAGCT TATGAGATGC GAGTTGCGTG GGCATGCTTT

190451　CGCTGCTGAT CAGCATGGTT AGATTTACGT TAGTCAAATT GGGTTCTGTG

190501　GTGGACATAA AACTTTTTAA ATAAAAAACA AAAAGTTTAA AAAAGATTCT

190551　TTTTTATGTG AAGTTATTTA TATTTTAAAT AGAAGTTGTT TATTTAAAAT

190601　AATAAATAGA CAACATTTTC ACTTTAAAAA GTATTGGATG CGGCTTAGAG

190651　CCAAGAATCT AGGGGGTGCT TGTGATCAGG ATAAATTGGC TGTGTTTTTA

190701　GAAAGCTGTT CGATTGGAAG CACGGACGCT TTCCGACATA GACTAGGGAG

190751　TCGTTAGATC GAAACGGGGT GGAATGATGG GAGGCTGGTC CTTGTCTGTA

190801　AGGATGATAA TTTTTTGCTC TTCCTGGTTG TCTTGTTCCC ATCCAAAATC

190851　TTGAAGAGAT GTGATGAGTG CCAATTTTAT AGCCTCGATC CATTCTGCTC

190901　TTGTTTTCCC GAGGTTTAGA AGTCTTGATG GAGCAAATAG ATTACATCCA

190951　ATGAGGGGGA GTTGAATCAC ATCAACGCCT ATGATTTCAG CTTCTTGGAA

191001　CAGGTTATGA AACGCTTTCT TGCTTACTTC AAATGCTTGC TTAGGATCGT

191051　TGTTACACTT AGCAGCTTCG GGACCAAGCA GTTGTGCTAA GAAGTGTGCT

191101　TTGCCTGGGA CATGGTCGTT TGAGGTGTGA TCACTATTTT CCCATTTTGC

191151　TGAGCGGCAT TCTCCTGGCT GTAGTTGGGA TCCAGAACGA GAGTGCGCTC

191201　TAGGGAGCCT AGATGCGTTC CAACACTGTA GACTTGTAGC CAGGGATAGA

191251　GCTTTATTCG TTCCCCCTCC TTCTCGGGAG ATGTTCTCGT TTGCTGCGTT

191301　AACAATCATC ACCCTGCCTT GAGTTTTGAT TCTTGGAACT GCAATATCTC

191351　CTGAGGTAGA TATAAAGATA AGCTTCGAGT CTTTAAGCTT CCAAATAAAA

191401　CAGGGCTGCT GAGGTGTTTC TGTAGTAAAC GATGGGTCTA CAGCGGCTAA

191451　GCTCGGAAGA AGATCCCAGT TTTGTTCAAG AAGAGCCTCA TAGCCAGGAG

191501　TGACCGTGAT AGCGGTAAGT TCTTCTGGGG GTGTGGTTAG ATCAGCAAGA

191551　GAGACTTCGG GGAGTGATTC GGGATCGGGA AGTGGATCGA TCTGCAAAGG

191601　GAGGTCCTGT TGCTCAGGAG GCTGGGGAGA GGGAGACAGA GAACTTTGCT

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191651   CAGATTCGGG TTCGATTTGA GGAAGAATCT CGTATAATTT AGGTTTCTTT

191701   AAAAGGGAGT AAAGTGAGAC CGCAGCAATT GCTAATGTTA TGACAACTAC

191751   GGCAGAAAAA ATAGGCATAG CCAAAATGCC AGCAGCAATG CTAAAGCCCA

191801   AAGCGCACGC TAGGGCTAGT GTGAGGGTGA CAATTTTCAG TATTTTCTCG

191851   ATTCTATCTG TACGGTTGAG AGGGAGTCTA ATCGGATAGG AATGTTTCGC

191901   AGGAGTTCTG TAGAGACTGG CGTCTGTATA AGAGGGTAGG GGATTAGAAT

191951   CTGTCATAAT ATTTTATTAA TAGATCAATT TTCAACTATT ATATTACTAA

192001   TTTGTATTTT TATTAGATTT TTTTATAAAA CAAAATTAGT TTATTAATGC

192051   ATCCTATTGA AATAGATCTT TTTAGTTAAA AGGGACCATA AGTAGCTGTT

192101   TGTGGTCTGT AAGGATTATA GTCATGGGAG TTGAGGGGTG CTGCGCAGCA

192151   AAGGAGCGAA GAGCTTCCAT AAGACCTTTC TTTATATCAT TTACCCACTA

192201   CGTACGGATG TGGTAAAGCT TATATGCACT GCTATTAGGC TTTGTTTGGT

192251   TTACGGGTTC TAGTTCCAGC TTTCCTCCAG GTGAGTATAT AGAGGAAGAG

192301   ATCAGAGGCA CTTGGACCAC AGTGGCTTGG TTATTGAGAG CTTCATCAAA

192351   ACAGTTCAAA TAGGCTTTCT TAATAACATT GCTTAATTTC TCAGGATGTG

192401   CTTTCAATTC TCCTTCATAT TTAGGACCAA GAAGTTGTGC TAAGAAATGT

192451   GCTTCTCCTG GGTTCGTATC ATTTATTCGT CCAGTCTCTA TTGATCCAGG

192501   GTGCTGAGCG GCATTCACCC ACAGATAATC CTTTGCCAGT GTTTATTTTT

192551   CCCCCAGATG TTCTCGTATT GTTCCAACAA GTAGGGTGTG TGGCTGCTGA

192601   GAGAGCAGCA TTGGTTCCGG CTCCACCAGA TTGCATGTTC GAATTCGCTG

192651   CGTTAACAAT CATGACTCTT CCTGAGGTTT TCAGGCGTGG TTTAGCGATG

192701   TCTCCTGTAG TGGCTACTAA GGTAATTGGG GCTCCTTGAT GTTCCCAGAC

192751   ATAGTATCTT TGATTAGGAT CTTGGAGAGT CCAGGATATA TTGATTTCTG

192801   AGAGAGTATT GACTAGGGTC CATTCATTTC TCAGCAGCTT TTGGTAATCC

192851   AGAGGGACTG AGGGTTGCAC TTGAGCTGCA ATATCCTTGG GGACATGTTT

192901   TTGGGGCCCA AGGAGCTCTT CTGTCGGTTT GGATGGCTCT CTTCTTCTTA

192951   AAAGAAGACA AGAGAGTACG ACTGCTGCAA GGAGAGCAGC ACCAGTGGCT
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193001   ATAGCCATGA GAGGCATACC AAGAACTCCA GCAACAACTG CAGTCCCTAC

193051   AGCTATGGCT AAAGCAAGAA TAAGAGCTGT GAGTTTTATT ATTTTAGCAA

193101   TCACTTCTTT CTTAGTAAGC ACGGGTGATT CTGAGATCAA TCTCTCATCT

193151   ACAGACAAAT GTGATTGATT CTCGTGTACA TCTGGGATTG AAGTGGTTTT

193201   AGTCATAAAA TATCTATTTA AAGGAAAAGA TTATATCTTA ATTTGTTGTT

193251   TTTTACAAAA AATCTTTTTC TTTGATAATA AAGATTTTTA TAAATTCTTT

193301   TTAATTTCAT TAATTTTAAT GAGTTAAGGC GTAGCAGGCG CACCTTATTG

193351   TTTAGTTCAT AAGAGAACTC TAAGTGGGTG CCACACAGAG TTTTTTCTCC

193401   ACTTGGTTCA AAAGGGTGGC GTTTGTGGTT TTATGGGGAA CGATTCTACC

193451   CCAGCCATGG GATTCAAAGA CTTCTTAGAT CGACAATACT ACTTGAGATT

193501   CTAATGGGGG GTGAAGACAT GTGTATTTCA TGGGCATGGG TAACGGAGGA

193551   CATCAGGTTT ACTTTCGAAG GCCCATATAT CATCTTCAGA GGTCAATAAA

193601   AGGGGGGGGT AGGGAGAACG ATGTTTTACA ACAGTGTAGA AATTAACTAT

193651   TTGTGAAATA TTTTCATTTA ATAACAATTT AATGAGTTTT AATTTGAAGA

193701   CACAGGCAGT GGCTTATCTT TTGTCTATAA GTCGGTACAG TCAGACTTAT

193751   AAGAATTGCC GCTTTTTGGG TCTTCATAAT CTCTATCTTA AACAAAAAGG

193801   AGGTCAATCA CAAACTGGGT GAGTTGTAGA GGTCTCAATA AGAAAGTTTG

193851   TAAGGTTAGG AGAGCTATAA TTGCGCCTGG GATTCTGCAT AGACGATACC

193901   TGAAAAGATA GTGCCTAGGG TCGGTGTTTG CTGATGAGAA TGCCAAGAAG

193951   CATAGTCATC AACCGTCTTA ACATATTTAT AAGTTTTCTT AGCAGCGAAT

194001   GGCACAGCTG CTAGAAAGCA AAACAAGATG ATAACAGCCA CCAATAGAAT

194051   TGTTCCTGAG ACAGCAAGGA CTGCAATGGC AGCTGGATGT CCAGTTTCTA

194101   GAGTGAATTG CAGAGCAGGG CGGATTGCCA ATAAACTAAG AACTATGAGG

194151   CAGCATCCGA TCACTAGGAG AACTTCCAAT ATGACAGAAG TGATTGTCCG

194201   TGGAGAAGAC TCAGCTTGCT GCTTCCCCTT GAGTTCTATG AGTTTCTGAT

194251   TTTGTGTGTT TGCGCTATTG ATTAAGGGAG CGGCTGGACT TTCAAAAAGA

194301   ACGTCCGTAG CAGATACTGG AAGATATCCC ATTTATTTTA ATATCCTTTA

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194351   ATTAAAATTT GCGCAGATAT TATACCTTAA TTTAATTTTT ATTAGAGAAT

194401   AAAATTCTAT ATTTTCTTTT GTGTAATATT TTTTTATAAA AACATGAGTT

194451   TTTAATTTAA CTTAGAAGAG AAGTGTTGCA ATATCTTTTA TTAAAACAAG

194501   AGTACCTAAG AATTCGTGCG TAAAATATTA CGTATTTGAT TTGTATAAGT

194551   CGTGAGAGTG TTTTTTCTAT TATTGAGGGG CTATTTGAT TTTTCTTGAA

194601   TTGCGTCATG GAAAGATCTT GGAGGCTTTA GGAGCCTTTT TGTCCCTCAT

194651   CATCTCGAGA TAACCAAACT GAAAAGATGC GTACCAAGAG TTTGTTTTTT

194701   CGTTCGCGAA TCTACTGTAC CCTTGATTTT AGGATAGCCG TTTTGAGTGA

194751   GATAGAGATC CTAAGAGAGA TCCTCAATAC TTTCTTGAGG TAGTTGGGCT

194801   AAGGATCTTT CAACACAAGC AATAGTTAGC GGATATTCTG GGTGCAGCTC

194851   GGCCATGTAT TTTACTGCTG TAATCATAGC CAAAGATTGT TGCATTCTTG

194901   ATTGCGGGGG CAATTCTCTA GAATAGAGAT GCTCCCTCAA GCTGTATAAA

194951   GGGATTTGGA TAATTTGGGT GTTCGTATTG ATCGCAGTCT GGATATAAGT

195001   GACATAGAGT GCATAGTAGT ATTGGTAGAT GGCTTCAGGA GTTGTTGGTA

195051   TTTGTGGGAG GAAGACGCGG CCTCGGAAAT CGGGTTGCCA GTATAAACGT

195101   TCTCCTGAAT CTCCCGCAGG GAGTTCTGTA TTTATTTCTA CCCTGGTTTC

195151   CTGAATTGCC TCATTGAGCA AGGATTTTGG GGAGGGAGTG GTATCTACGT

195201   AGGAGGATAT AGGCGCATTT TGCGAGGTTT CTTCAATTAA CAGAGTCTTT

195251   CCTAAATTTT CGGAAGCTGA AATTAAGAGA TGTTCTGGAT TGCCTCCCGG

195301   TAGGAGGGAT ACTAGGGAAA ACAGTGAATG TTTAGCTTTC CATATCTCGT

195351   AAGGGTTATC TGTGAGTAAT GCAGAGGGTG CGGGGAGATT CTGTAGGTCC

195401   TTGGGTTGGT GTTCCCAGTT TTCTTTAGAA CGATTGATTG CGATAGAGAT

195451   AGAAGAATAC TGTAGGTTGG TGGAGACCCT TTTTGGTTTT ATTTCTTTGT

195501   GTTTGCCACA AGCACGCGGT TTTAAGAGGG TGGTTGCTCG TTTATAAAGG

195551   ATAAAGTTGC TAAGAACAAC AGCAATAAAT GAAATTCCTG TGAGGAAATA

195601   GATAACAGGA ATATTTAAAA GCAAACCAAT AAGTAGGGTC CCTATAGTAA

195651   CTAAGACAGC AAAGATTGCA GTAATCAATA GAATTCGAGA CTGAATCTTA
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195701  TCAAAGTTGC TGCAGGATTT TTTTTTAGTG TCTACTAGGG GATGATCTAC

195751  AGTTAAAGAT ATGGGTGAGA TTGTAGCCAT AATTAAGGAA TTCACCTGAG

195801  TTCCTTTAAA TTATATCTCT TTTATTGATA TTTAAATAAT TAAAAACATT

195851  TCTGCATTTA AAAATATTTT TTAATTTGTC ATCTTTCTAA GTAAATATAA

195901  AAAATAATAA GTTTATTTAG TTAAATTTTT TTTGAAAACA AGAAAGATAG

195951  GGGAAAGGCT CGCGAGTAAA TCAAGCCTTT CCTGAATGCA AAGAGTCGCA

196001  TAACTACTTA GAAAAGAGTT CGTCAGAATA GAAGTTGTAT TAATATAAAA

196051  TTTTTATTTT CTAAGATTAG AAAGTAACTT TGACACAGCC ACCTTTGATG

196101  CGGCACTGAC AAGCAAGACG TTCGTTAGAG TCTTCGGGTT CTCCTAGAAA

196151  ATCGTATTCT GGTTCCGTAA ACTCAGAAAG ATTCTCACGT CCTTCTAAGA

196201  CCTCTATCAC ACAAGTTCCA CAGACACCTT CTGTACAAGC AAAGGGAATG

196251  CCCATGGATT CACAAGGCTC TGCGATCTCA CTATTGTCTT CTAACTCGAA

196301  CTCTTGTTGT TCATCATCAG AGGTAATGAC TAGCTTGGCC ATGGAGTTTT

196351  CCTTCTACGT ATTGTCGGAT AGATTAAAAT GAAGTTCGGA GTAGAGGGAT

196401  TCGAACCCCC GACCTATTGC TCCCAAAGCA ACCGCGCTAA CCAAGCTGCG

196451  CTATACTCCG TAAAATAAAA TTTTCGAGTA AAAGAGATCA ACGTTAGCAT

196501  AGAAGGAAAT AGTCGACAAG ATCAAAGATG CTTCATAACG TCTCTTTAGA

196551  GTTTTACTTG CAGATATATG GAAGAGGGAA GTATGAGAAA AGGCAGGGAT

196601  TCTCTAGGAG GCTGTTTTTG TGTCTGGGAA GAAAGATGGT GTAAGGGGAA

196651  TGATCTTTGT CCCTCTTAGC ATCCTAGTAC TAATCTTTTT ACCTCTTCCT

196701  CAGATCCTTC TTGATTTTGG ATTGTGTATT AGTTTTGCAT TGTCTTTACT

196751  AACGGTCTGT TGGGTCTTTA CCTTAAATTC AAGCAATTCA GCGAAGCTTT

196801  TTCCTCCATT TTTCTTATAT CTTTGCCTAT TGCGGTTGGG ATTGAATCTT

196851  GCATCAACAC GATGGATTGT CTCTTCAGGA ACCGCCTCTT CTCTGATTGT

196901  TTCTTTAGGC AGTTCTTCT CTTTAGGAAG TCTATGGGCA GCAACGTTTG

196951  CGTGCCTCCT TCTTTTCTTT GTGAACTTTT TGATGGTTTC AAAGGGTTCG

197001  GAAAGAATCG CAGAGGTCCG TTCGCGGTTT TTCTTAGAGG CTCTTCCAGC
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197051   AAAACAGATG GCTTTAGATT CTGATCTTGT TTCTGGAAGA GCTTCTTATA

197101   AGGCTGTCAA AAAACAAAAA AATGCCCTTA TAGAAGAAGG GGATTTCTTC

197151   TCTGCCATGG AGGGGGTCTT TCGTTTTGTT AAAGGGGATG CAATTATTAG

197201   TTGTATCCTT TTACTCGTGA ACGTAGTTTC TGTAACTTGT CTTTATTATA

197251   CTTCGGGTTA TGCTCTTGAG CAGATGTGGT TTACAGTTTT AGGAGATGCT

197301   TTAGTGAGTC AAGTACCTGC TTTACTTACT TCGTGTGCTG CAGCCACTCT

197351   TATTAGTAAA ATCGATAAGG AAGAGAGCCT TTTAAATTAC CTGTTCGAAT

197401   ACTACAAACA GTTGCGTCAG CATTTCAGGG TGGTGTCGTT ATTGATCTTT

197451   TCTTTGTGCT GCATTCCCAG TTCTCCAAAA TTCCCTATCG TTTTGCTCGC

197501   GAGTCTTTTA TGGTTGGCGT ATCGAAAAGA AGAGCCTGCA TCAGAAGATT

197551   CTTGTATAGA ACGTGCGTTC TCTTATGTTG AGGGGGCCTG CCCTAAGGAA

197601   CAAGAATCAC AGTTCTATCA AGTATATCGT GCAGCATCCG AAGAAGTATT

197651   TGAAGATTTA GGAGTTAGAT TGCCTGTGCT TACTTCTCTA CGTATTGAAG

197701   AGCGTCCTTG GCTCCGAGTA TTTGGCCAGA ATGTATACTT AGATGAAATG

197751   ACTCCAGAGG CTGTGCTTCC TTTCCTTAGA AACATCGCTC ATGAGGCTCT

197801   CAATGCCGAG GTAGTTCAAA AGTACCTTGA GGAATCAGAG AGAGTGTTTG

197851   GCATCGCTGT TGAAGACATC GTTCCTAAGA AAATCTCTTT AAGCTCTCTT

197901   GTAGTTCTTT CTCGCCTCCT TGTTAGAGAA AGGGTATCGC TTAAGCTTTT

197951   CCCAAAGATT CTAGAGGCCG TTGCGGTATA CCAAAATTCT GGAGACAGCT

198001   TGGAGATCCT TGCGGAAAAA GTGCGAAAGT CTCTCGGATA TTGGATTGGG

198051   AGAAGTCTCT GGGATCAGAA ACAAACCCTT GAGGTAATTA CCATAGATTT

198101   TCATGTTGAA GAATTGATAA ACAGCTCATA CTCAAAGTCT AATCCTGTAA

198151   TGCAAGAGAA TGTGATCCGT CGAGTAGACA GTCTTTTAGA ACGGTCGGTA

198201   TTTAAAGATT TTCGAGCCAT AGTTACGAGC TGTGAAACAC GATTTGAGAT

198251   GAAAAAAATG CTCGACCCAC ATTTCCCTGA TCTTTTGGTT TTATCTCATG

198301   ATGAGCTTCC TAAAGAAATC CCTATTTCCT TCTTAGGGAT CGTTTCAGAT

198351   GAGGTTTTAG TTCCTTAATT TAATTTAATC TTCTGTAAGC ACTATTACTT

147

198401 TCGTATTTTT TTTGTTGGTG TAAATATTGT TTAAAAATTT TTTTTGAATT

198451 AATCTAATAA ATAACTAGAT AAAAAAAAAT TTGTGAAAAC ACAGCAAACT

198501 CAAAACATCA TAGAGGTTTG GAACTTCTAC TGGGAGACTC AGGAAATAGA

198551 GTATCGCGAT AGCTTAATTG AGTTCTATTT GCCTTTAGTA AAAAGTGTGG

198601 TTCATCGTTT GATTTCAGGG ATGCCTTCCC ATGTAAAGAC CGAGGATTTG

198651 TATGCTTCGG GTGTTGAAGG TCTCGTCCGT GCGGTGGAAC GTTATAATCC

198701 TGAGAGAAGT CGTCGTTTTG AAGGTTATGC GGTATTTCTG ATTAAGGCTG

198751 CCATTATTGA TGATCTGCGT AAGCAAGACT GGGTTCCTCG TAGTGTCCAT

198801 CAAAAAGCGA ATAAATTGTC AGGAGCTATG GATTCTCTTC GCCAGTCTTT

198851 AGGCAAGGAA CCCACGGATC TTGAACTGTG TGAGTATCTC AATATTTCGC

198901 AACAAGAGCT TTCGGGATGG TTTGTATCTG CCCGTCCTGC ATTAATCGTG

198951 TCTCTGAATG AAGAGTGGCC TTCACAAAGT GATGAAGGAG CCGGAATGGC

199001 TCTTGAAGAG AGAATCCCCG ATGAACGTGC CGAGACAGGG TACGATGTTG

199051 TAGATAAACA AGAATTTTCT TTATGTTTAG CCAATGCGAT TCAGGAACTT

199101 GAGGAAAAGG AACGCAAGGT CATGGCCCTG TACTACTATG AAGAACTTGT

199151 CCTTAAGGAA ATCGGTAAGG TCCTTGGGGT AAGTGAGTCT CGCGTCTCTC

199201 AAATTCACTC TAAAGCATTG CTTAAGCTTC GCGCAGCACT CTCTGCATTT

199251 CGATAAATAC AGTTCTCAGG TTTTAAGAGC AGTCCTAGAG CTAGGAGAAG

199301 CCCTCCTACG ACACAGAGTA ATCCGTAAAG AATTTGTTTA GTCAACGCCA

199351 TAACAATGCA GCCAGCAATT GTGAAGATTG CTCCTACAAT CAAGAGAAGA

199401 ATGCGGGGCA GCCATTCTTT AATACGTTCG GCTAGGGTAG AGGTAGGAAG

199451 GGGTGCCTTG CTAGTTGTGG CATTTAGACT AGTTGCGGCG TTTAGCATCG

199501 ACGGAACCCC AATTGGAGAT GTAGACATAG CGACCTAATC TTTAGAGAAG

199551 ATAGAAGTTA TGGTATCTCA GCAAAGGAAT TATTCTCAGC GTACAATCTT

199601 TTCTTTATTG TTAGATAGGT GGTGCCTTGC ATATAAGCTT TAGGATCGAT

199651 AAGATAGAGC TTGGCAATTC TTAATTATGT ACGATCACTC ATGCAATCCT

199701 GGTTACAATC TTTACAAGAG CGAAATATTT TAGAGAATTT TACCGCAGGT

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199751   TTGGAATCCG TAGAGGGACC TATCGCCGCT TATTTAGGAT TTGATCCTAC

199801   CGCACCTGCT CTACATATTG GTCATTGGAT TGGGATTTGT TTCTTGAAGA

199851   GACTCGCTGC TCTGGGGATT ACCCCCATAG CTTTAGTCGG GGGAGCCACA

199901   GGTATGGTTG GAGATCCCTC AGGGAAACAG AGCGAGAGAT CGTTACTTCA

199951   GACAAGTGAA GTTTTTGATA ACAGTCAAAA GATCACGGCG TGTCTCCAGC

200001   GCTATCTTCC CGGGGTGACT CTTGTAAATA ATGCAGACTG GTTGCAGGAG

200051   ATCTCCCTGA TTGATTTCTT AGGGGATATA GGAAAACACT TTCGTTTAGG

200101   CCAAATGCTA GTGAAAGATA CAATAAAGCA GCGGGTGCAT TCTGATGAAG

200151   GAATTAGCTA TACCGAGTTT AGCTATTTAA TCCTGCAATC CTATGATTTT

200201   TATCACTTAT TTAAAAATTA TGGCACGATC TTGCAGTGCG GTGGTAGCGA

200251   TCAGTGGGGG AATATTACTT CAGGAATCGA TTTTATTCGC CGTAAAGGGT

200301   TGGGTCAGGC CTACGGCCTT ACCTATCCTT TATTAACGAA TGCTCAGGGG

200351   AAAAAAATAG GGAAAACAGA GTCGGGAACT GTATGGCTCG ATTCAGATTT

200401   AACCTCTCCT TTTGAGCTGT ACCAATACTT ACTCCGTTTG CCCGATGATA

200451   CCATCCCTAA AATTGCTCGT ACGTTAACTT TATTGAGCAA TGAAGAAATT

200501   CAAGATATTG ATAGGCGTGT ACAGACGGAT CCAGTTGCAG TGAAGGAATT

200551   TGTAGCCCAA GATATCTTAA GTGCTATTCA TGGAGATCTA GGGCTTGAAG

200601   AGGCTCTTTC TGTAACTCGT AGCATGCATC CAGGGAATCT TTCATCCTTA

200651   TCGGAAAAAG ATTTTCATGA ATTGTTTGCA GGAGGGATGG GGGCCTCATT

200701   GGATAAATCC GAGGTGTTAG GGAAACGTTG GTTAGACCTA TTTCTTGTTT

200751   TGGGACTATG TAAATCTAAA GGGGAAATTC GAAGGCTAAT TGAACAAAAA

200801   GGGGTATATA TTAATAATGT GCCCATCGCT AATGAGCATA GTGTTTGTGA

200851   AGAACAAGAC ATCTGTTATG GTCACTATGT GTTGTTGGCT CAAGGTAAAA

200901   AACGAAAGCT TGTTCTATAT TTAAATTAGT TTAAGGAGGC TAGGTAGCTT

200951   TGCAAACGAA TATTGGTCTT ATTGGCTTAG CTGTCATGGG GAAAAATCTT

201001   GTCTTAAACA TGATAGATCA TGGTTTTTCT GTCTCTGTCT ATAATCGGAC

201051   CCCAGAGAAA ACGCGGGACT TCTTGAAAGA ATACCCTAAC CACCGAGAGC
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201101   TTGTAGGGTT   TGAATCTTTA   GAAGATTTTG   TGAATTCATT   GGAGAGACCA

201151   CGAAAGATCA   TGTTGATGAT   TCAAGCAGGG   AAACCTGTGG   ATCAGAGCAT

201201   TCATGCGTTA   CTGCCTTTTC   TAGAACCCGG   CGATGTGATT   ATCGATGGGG

201251   GGAATAGCTA   TTTTAAAGAT   TCCGAACGAC   GATGTAAAGA   GTTGCAAGAA

201301   AAGGGGATTC   TCTTCTTAGG   CGTGGGGATT   TCTGGAGGAG   AAGAAGGTGC

201351   ACGTCACGGC   CCATCAATTA   TGCCTGGAGG   AAATCCTGAG   GCGTGGCCAT

201401   TAGTGGCTCC   TATTTTTCAA   TCAATAGCAG   CAAAAGTACA   GGGCCGTCCC

201451   TGCTGTTCTT   GGGTAGGAAC   TGGCGGTGCA   GGCCACTATG   TAAAGGCTGT

201501   TCACAATGGT   ATAGAATACG   GCGATATCCA   GTTGATATGC   GAAGCTTACG

201551   GTATCTTAAG   AGATTTCCTA   AAGCTCTCCG   CAACTGCCGT   TGCTACAATT

201601   TTGAAAGAGT   GGAATACTCT   AGAGTTGGAA   AGCTATCTAA   TTCGTATTGC

201651   TTCTGAAGTC   CTAGCATTGA   AAGATCCGGA   AGGAATCCCT   GTTATTGATA

201701   CGATTTTAGA   TGTCGTGGGC   CAAAAAGGTA   CAGGAAAGTG   GACCGCAATC

201751   GATGCTTTAA   ATTCTGGAGT   TCCCCTTTCC   TTAATCATAG   GAGCTGTTCT

201801   TGCTCGTTTC   CTTTCTTCTT   GGAAAGAGAT   ACGCGAGCAA   GCTGCCCGTA

201851   ATTATCCAGG   AACCCCCTTA   ATATTTGAAA   TGCCCCATGA   TCCCTCGGTA

201901   TTCATACAAG   ATGTCTTTCA   TGCTTTATAC   GCTTCCAAGA   TCATCAGCTA

201951   TGCTCAGGGA   TTCATGCTTT   TAGGAGAAGC   TTCAAAAGAA   TATAATTGGG

202001   GATTAGACCT   AGGAGAAATT   GCTTTGATGT   GGCGCGGGGG   ATGCATTATT

202051   CAAAGTGCAT   TTTTAGATGT   TATACATAAA   GGATTTGCTG   CCAACCCAGA

202101   GAATACCTCG   CTCATCTTCC   AAGAATATTT   CCGTGGAGCA   TTACGCCATG

202151   CGGAGATGGG   ATGGCGTAGA   ACAGTAGTGA   CTGCAATTGG   TGCAGGGCTA

202201   CCTATTCCCT   GTTTAGCAGC   AGCAATCACG   TTTTATGATG   GCTATCGTAC

202251   AGCAAGCTCT   TCAATGTCGT   TAGCTCAAGG   ACTGCGAGAT   TATTTTGGAG

202301   CTCATACCTA   CGAGCGTAAC   GATCGCCCTC   GAGGAGAGTT   CTATCATACC

202351   GATTGGGTGC   ACACGAAAAC   TACAGAAAGA   GTGAAGTAAA   AATAAAAAAT

202401   CTCGAGAAGA   CCCTAGGTAG   CTCGAGATTT   AGTTCACCAC   TACCGAATTT
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202451  TCAATTGTAA GCAGTGTGCT GATTTTAAGC GTCAATGTTA ATCTAATTTT

202501  AGAACTTCAA TGAAAGCTGT ATTGGGAATG GAAACTTTTC CAAATTCCTT

202551  CATACGTTTT TTTCCTTTCT TTTGCTTTTC CCACAGCTTG CGTTCCTAG

202601  TAATATCTCC GCCATAACAC TTTGCGGTCA CGTTCTTAGA AAGCGCACGA

202651  ATCGTTTCTC TGGCAATGAC TTTTTTGTTA ATGGCAGCTT GGATGGGAAT

202701  CTTGAAGAGT TGTTGTGGAA TCACGTCCAC AAGCTTTTCG CAGATACTTC

202751  TTCCACGAGA TTCTGCTTTA TCTCTATGGA CTAAACAAGA AAAAGCATCT

202801  ATGGGCTCCT CGTTAATAAG AACCTCTAAT TTGATGATCG ATCCCTTACG

202851  GTAATCCCCA AGACGGTAGT CAAAGGATCC ATAACCTTTA GTTACTGACT

202901  TCAGCTTGTC ATTGAAATCC GAGACAATCT CATTTAAAGG GAGTTCGTAA

202951  GCAAGAACTA GACGGTGCTG ATCTAGCATT TCTGTTTTTA CGCAGATCCC

203001  ACGTTTATCT AAACAGAGGT TCATAATGTT GCTCAGATAT TCTTGAGGGG

203051  TGATAATATT CACATGAACC CAAGGCTCTT CCACATGCTC GATGATCGCA

203101  GGATCCGGAT ATCCTGAGGG GTTATCAATA TCTAGAACTT TCCCGTTTTT

203151  TAAGACGACT TTATAGATGA CACTTGGAGC CGTTGCAATA ATATCTAAGT

203201  CAAATTCTCG AATGATTCTT TCAAAGATAA TCTCAAGATG AAGAAGTCCT

203251  AAGAAGCCAC AACGAAAACC AAAGCCTAAA GAGTGACTGC TTTCTTGTTC

203301  TATAGTTAAA GCAGAATCAT TGAGCTGTAG TCTTCCTAAA GCATCTTTCA

203351  AAGTATCAAA ATCAGAAGAA TCTATAGGAT AAATTCCAGC AAAAACTACC

203401  GGATTGATCT CTTTGAAGCC TTCCAAAGGA GTTTTTGCAG GATGTTTTGT

203451  TTTCGTGACT GTATCGCCGA TCTTCACATC CTTCACTTTT TTGAGATTGG

203501  CAATAAAAAA ACCCACCTGA CCAGGGCGTA AGGAACCTTC TATAAATGTT

203551  GCTTTAGGGA GAAAGGCCCC TATACCTAAG ACTTCAAACG AGGAGCCTTT

203601  AGCCGCCATA AAAGTAATGC GGTCTCCTTT TTTTAATTCC CCGCTAATAA

203651  TGCGTACGTA GACCATAATG CCAACGTAAG GGTCATAATG AGAATCAAAG

203701  ACTAAAGCTT TAAGCTCTGT TTCTGCAGGT GCTTTTGGAG GAGGAACAAG

203751  ATCGATAATT GCTTTCAGGA TTGCAGGGAT CCCCTGACCT GTTTTTGCAG
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203801   AACAGGCAAT AATGTTCGTA GTGTCTAGGC CTATATAATC TTCAATCTGT

203851   TGAGCAATTC TCACGGGATC AGCGGCAGGT AGATCAATCT TGTTTAATAC

203901   AGGAATGATC TCTAAATCTC TTTCAAGGGC CAGGTAGACA TTAGCAAGAC

203951   TTTGTGCCTG CACCCCCTGG GCGGCATCTA CAATAAGTAA GGCGCCCTCA

204001   CATGCAGATA GAGATCGAGA GACTTCATAC GAAAAGTCCA CGTGACCAGG

204051   GGTATCAATC AGGTTCAGTT GATACACCTC TCCTTCATAT AGATACGTCA

204101   TGGTGACAGG ATGAGCTTTA ATTGTAATGC CACGCTCTCT TTCAAGATCC

204151   ATGGAATCTA AGAGCTGCTC ACGCATCTCC CGTTCTTCTA CTGTGCTCGT

204201   ACTTTCTAAA AGGCGATCAG CAATTGTAGA CTTCCCGTGA TCAATATGCG

204251   CTATGATTGA AAAATTGCGA ATGTTCTCTA TCTTATATTC TTTCAAAATG

204301   TACTGTAGTG TTATCTAGGT TTATTCCTGG TTTCATAAAG CTGCATTGAG

204351   AAGGCTCCTT CAGACAAAGA CCAGCTTCTC AAATACTTTT GCGGACTGCA

204401   TCTCTTTATT AGCAAAATGA TCATGCGGTC ATCTTTAGCT TTGGATAGAT

204451   GAAAGTATAA TAGATGAGAT GTAGAAACCA CAAGGGTTTA AAGTCGAATC

204501   TGATTTGAGG TAGAGTTCCA GAGTGGCTAG CAGTAGAAAA AACTAAGTGA

204551   GAAGAAGTGC TCTCCGTTAG TATGAAACTG ATTCCCACTC AGGATTCTAT

204601   AGAAAGGGAA ACCGATTCTA AAAGAGATAA AAAAATATTT ACCATTTACA

204651   TATGTTCATC TAAAGTCCTT GCGGGTCATT TTTTCAGTCA TTTAGACAAG

204701   CATAATAAAA TTCATGAAAG CATTGGGGTT TGAGATAGTT AAATCGACTC

204751   GATCCAAGAG TATAAGAGAG GAATGAGTGT TCTTATGTCC GAGATAGTGC

204801   TCTTCAATGT AGTGAAGAAC TGGAAAGTCA GGAGATCTAT TTGAGTAGGA

204851   GTTCAGGTCT TCGCAATCGA TTTTTTCAAG CTCTGGAGTC TATGTGAAAG

204901   AAATTTATAG AAGTAAAATA ATTCCATGAA TTCTAAAATG ATTAGGAAAA

204951   TAATATAACA CGCTGATACT CAAGTCACAA TGGAGCTTCT ATGGTTAATA

205001   TACAGCCTGT GTATAGGAAT ACCCAAGTCA ACTATAGTCA GGCTACCCAA

205051   TTTTCGGTGT GCCAGCCAGC GCTTAGCCTG ATTATCGTTT CTGTTGTTGC

205101   TGCTGTACTC GCTATTGTAG CTTTGGTATG CAGTCAATCT CTTTTATCCA

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205151   TAGAGTTAGG AACTGCTCTT GTTCTAGTTT CTCTTATTCT TTTTGCTTCT

205201   GCTATGTTTA TGATTTATAA GATGAGACAA GAACCTAAGG AGTTGCTGAT

205251   CCCTAAGAAA ATCATGGAAC TCATCCAAGA ACATTATCCA AGTATTGTTG

205301   TTGATTTTAT TAGAGATCAG GAGGTTCCA TTTATGAGAT ACATCACTTG

205351   ATCTCTATTC TTAATAAGAC GAATGTTTTC GACAAAGCAC CAGTATATTT

205401   ACAAGAAAAA CTCTTACAGT TTGGCATTGA GAAGTTCAAA GATGTACATC

205451   CAAGTAAGCT CCCTAATTTT GAAGAAATTC TTCTACAGCA TTGCCCATTG

205501   CATTGGTTGG GACGTCTGGT ATATCCCATG GTATCGGATG TCACTCCAGG

205551   AACCTATGGA TACTATTGGT GTGGTCCTTT AGGACTGTAC GAGAACGCTC

205601   CCTCTCTTTT TGAACGTCGA TCTCTTCTAT TGTTAAAGAA AATTAGCTTT

205651   GGAGAGTTTG CTCTTTTAGA AGATGGTCTC AAGAAAAACA CGTGGAGTTC

205701   TTCGGAACTC GTTCAAATCA GACAAAACCT TTTTACAAGA TATTATGCTG

205751   ATAAAGAAGA GGTAGATGAA GCAGAGTTAA ACGCTGATTA CGAACAGTTT

205801   GATTCCCTCC TTCACCTTAT TTTTTCTCAC AAGCTCTCTT GAAAGCAAGT

205851   GCAATTATTT CAATATATGA ATGAGTCCGG ATGGGATTGG CTTTGTGATT

205901   TTGATTCTCA AGGCGAGGGA TTCCAGTTAT CACGTCTGGT TGGGCTGTTA

205951   CATTCGTCCT GGGCATTATA CGAAGCAAAA GAGCAATTTT ACCTTCCTGA

206001   GGTTTCTCTA TTGACCTGGG AAGAACTGAT AGAAATGCAG TTATTAAGCA

206051   AACCAACAAA ACACGGGGTT GCAAAGATC TTTGTAATGT ATTTGAAAAA

206101   CACTTTCAAA GGTTTAGACA GTACCTAGGT TCCTTAGATC TAAATCAAAG

206151   GTTCGAAAAT ACCTTCTTGA ATTATCCTAA ATACCATTTA GATAGGGAGT

206201   GAGAAAAAAA TCCTAGGTCA GCTTGGCAGA AATTTTTGAA ATCCTTAAGT

206251   GTTCGATCTG CATTTTTTTC GGGGATTGTA AAAAGTTTGC CTAATCTGAA

206301   GGGTAAGAGA GAGCTATTTT TCATGGGATT TTTTATTACA GGAAATTCTT

206351   GAATTAGAGA TTTTTATTTA CACATAATCT ATACTGCCTT CAATAGATCT

206401   ATATCTAAGG AGTTGGCTAT GAGCATGACG ATCGTTCCAC ATGCTTTATT

206451   TAAAAATCAT TGCGAGTGTC ATTCTACCTT CCTTTGAGT TCAAGGACTA
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206501   TTGTAAGAAT AGCCATTGCC AGCCTCTTTT GTATAGGTGC ATTAGCAGCT

206551   TTAGGCTGTT TGGCTCCTCC CGTTTCTTAT ATTGTTGGGA GTGTTTTAGC

206601   TTTTATTGCC TTTGTCATTC TTTCTTTAGT AATTTTAGCT TTGATTTTTG

206651   GAGAGAAGAA GCTTCCACCA ACACCAAGAA TCATTCCTGA TAGATTTACT

206701   CACGTGATAG ATGAAGCTTA TGGCCTTTCA ATCTCTGCAT TTGTAAGAGA

206751   ACAGCAGGTA ACATTAGCCG AGTTTAGACA ATTTTCTACT GCCCTGTTGT

206801   GTAACATATC TCCTGAAGAG AAAATCAAAC AATTGCCTTC TGAATTGCGA

206851   AGTAAAGTAG AGAGTTTTGG TATTAGCAGG CTCGCAGGTG ATTTAGAAAA

206901   GAATAATTGG CCAATATTTG AAGATCTTTT AAGCCAAACC TGCCCGTTAT

206951   ATTGGCTTCA GAAATTTATA TCAGCAGGAG ATCCACAAGT TTGTAGAGAC

207001   CTAGGTGTCC CTAGAGAATG TTATGGGTAC TATTGGCTAG GGCCTTTGGG

207051   ATACAGTACA GCTAAGGCTA CAATTTTTTG TAAAGAGACG CATCATATTC

207101   TTCAACAATT AACGAAAGAG GACGTTCTTT TATTAAAAAA CAAGGCTCTT

207151   CAAGAGAAAT GGGATACTGA TGAAGTCAAA GCAATTGTAG AGCGTATCTA

207201   CACTACCTAT ACGGCACGAG GAACTCTAAA GACCGAAGCA GGGGGACTTA

207251   CAAAAGAGAC AATCAGTAAG GAATTGCTAT TGTTGAGCTT GCATGGCTAT

207301   TCTTTTGATC AGCTACAGCT GATCACTCAA CTTCCTAGAG ATGCTTGGGA

207351   TTGGCTGTGT TTTGTAGATA ACAGTACCGC ATACAACCTT CAGCTTTGTG

207401   CTCTTGTAGG AGCTTTGTCA TCCCAAAATC TTCTTGACGA ATCTTCTATC

207451   GATTTTGATG TAAACCTAGG CCTGTATGTG ATTCAGGATC TAAAAGAAGC

207501   TGTTCAAGCA TTTTCTGCTT CTGATGAGCC AAAGAAAGAA CTAGGTAAAT

207551   TCTTGTTAAG GCATTTGAGT TCAGTTTCTA AGCGATTAGA GAGTGTATTA

207601   AGACAGGGTC TTCACAGAAT AGCTCTAGAG CATGGAAATG CCAGAGCTAG

207651   GGTTTATGAC GTCAATTTTG TAACAGGAGC TAGAATTCAT AGGAAGACGA

207701   GTATCTTCTT TAAAGACTAA ACCAGGTAAC TAGCTTTTTA GTCTCGAAAG

207751   GGGCTACGAG AGGGAGTAGA ATTTTTCTTA TTCCAAAATA GAAATCTCTA

207801   ACCTATCAGC AGGGAGGACT CGTCTTCTTC AGGTTGGGAG AAGACGCTTC
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207851   TCTTGAGTGG ATGGACTGTT ATAGGTGGTA AGCTTCTAAA GGTGGAATTA

207901   TGAGTTGCTA AATTCTCAAG GAACATCGCT ATATTGGTTG ACTGACGACG

207951   GATCGTTTTA AACTGATCTA AACTAAGGAG TGTCAATGAA GAAAGAAATG

208001   CTTCGCTTTC TTTATGAATT AGGCCTTGTG TGTAGAGAGT ACCAATTAGA

208051   GAGGCAAATT CCATGTCTTG GGGTCGTCCT GTATGGTCTA AAGTCAAGCA

208101   ACAGAGGTTT TCCCATAAAT CAGCCGGGAC TGTTTTTATT AAGGACATCT

208151   GCTTCCACGA GTACCTATGC TTAAAAATAC ACAAGAGCAG GTTATAGAAT

208201   TCATCCTCTT GAAGAGAGGG TTGAGATAGA TGTTTATAGG ATTGATACGC

208251   CGCATGATAT TTAGCAAAGA GCTGCTGTTT CATAGTATTT AGATCACTAT

208301   GATTCAGGTT CCACTCGCCA TTTAATGCTG CATACTTAAG ATGTTGAAAA

208351   ACATCACGAG TTAAGACTCT AGCTAAAACT AATGTGTGTA GATTTAGAAT

208401   AGAGGAATTT GTTGGTCTAA AATCTAAAGG AATCAACCAA TAGGTAGGAA

208451   GCATCTCTGG TTTTATATAA TCACTAAGGT CTTCTTCGAG GCTGCCTCCA

208501   ATTTTCTTAA CTCGATGGAG CTCTACAACC TTGCTGCCTG CAGAAATAAA

208551   CTCTCCTAAC CAGAAAAATG GAAATACCTT TTGTAAGATT TTTGGTAAAG

208601   AGGGGAAGAG GGGACGGGAA GAAGCAGCGC TTTCAAGTCT TTTAAGAGAA

208651   GCAGTACGGA CTTCATTTTT TAAGCGTGCG ATACCCTCGA ACGTATCTAT

208701   TTTCTGTTGT AGTTCTTCAG ATACGTTGTA ATTTGTAGAT GATCCAACTT

208751   CAGAGTGCAA TTGATTTAGA AGATCAATAA AACTTATGAG ATCTTTAAGA

208801   TTTGGTTTAG CTTCTGAAAC AAAATCAGAG ACAAATTTAG GATAGTGCGC

208851   CCTGATTCTA TTTACGAGTT CTTGGGGGAA TACTTGTTCT TTTGATGAAA

208901   TCATAGGCGT GATTTTTTTT ATTCCTAAAA TCACACCAAT CAAGGCTATT

208951   AATAATCCTA ATCCTAACAA TGCGCCACTT AGAATATAGG AAACAGGAGC

209001   TGCTACACAC AAGAAAGCTA TCAAAGCTCC GCAGAGTAAG ATGGCACTGA

209051   TAACAATATG AATAGTGGTT GAATTCTTTA ATTCAAAATA ATAATTACAA

209101   GAGCGATTAT TTTGAATAAC TGGCGAGGTT ATATTACTCA TACATTTCCT

209151   AGGCTCATCA ATTTGCGTAT TATATCGTAA ATTTAACAAA AATCCTATTA
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209201   ATAGAAATGT  TTTTATTTTT  AAAATTTTTA  TTGAAATTGT  TTTGTATTAT

209251   TGATGAAAAG  TTTTCATTGA  AGATAGCTTC  TAGAAGAAGA  ATAACGAGAG

209301   AGCTTGTTAT  GCTTTTTTTA  AAAAAGGGC  GAGCCCCTTT  TTGTTCTTTT

209351   CCCGATTGGG  AATAACGTAT  TCTTTTTATA  AAAATTAAAG  ATTTTTTTAT

209401   ATTTCTAAAT  CTCAATTATA  AAAAGTCTTT  CAAACGCAAT  TTGCTTGTAG

209451   GTATTGCAAA  TGATCAGACT  CCCCTTATAG  GGAAGATCGT  ATAGGGAGAC

209501   TGCTTTCTAT  TTTTTTCTCT  AGTTGTAGG  TTTGGGCGTG  GAAAGCATAC

209551   TGAGGTAAGC  TTGATGTCCA  TTGTGAACTC  GTATTACGAA  CAAATTGCCA

209601   TCGTTTTAAC  AGATTTTGAT  GGTGCGTTGT  ATTTACGCAT  ATCTTCTGAA

209651   CAAGAGCACT  CGCTGGGTGC  ATAGGACTTT  CTTTTACTTT  CTCTAGTAAA

209701   ACCTTCAATT  CTTTCCACGT  CATGAAGTTC  ACTGTAGGTT  CATAGTTAGA

209751   GGATACTGGA  TCGAACATAT  TTGTTTCAGT  ATTCAAAAAG  CCTCCAAATG

209801   TTGCCATGGA  ACAGTGGCCT  CCTGCTTTAT  CAAACTGACA  CAACATTTTC

209851   CAATTATCAG  GATTTATAAG  TTGAATCATC  TGAGCCTGTT  CCCAAGTGAT

209901   ACCATGAGAA  AAGAAAAGAA  ATAAGAATTG  TGAGATTCCT  TGAACATCCT

209951   TCCGGAAAAT  CATATTGTGG  GGGAGTTCCT  TGAATATTTC  TTCGCAGGTT

210001   TTTTTCACAG  AAGGAGAATC  CCATTGATTC  TTAGACGCTT  TACTATATAG

210051   GAACTTATAC  TGTGATTCTG  AGATTAATGT  TAGTAGAGGG  CGTGTATAAG

210101   AGTGGAAAAT  AGTTGTATAT  CCTTTATGAA  ACGCTAAGGG  CCCAAGTAAA

210151   CCATAAACTT  TTTGTGTTTT  ATTTAATCCG  ATTTCCCCAG  CAACAGATTC

210201   AGTTTGTCT  ATAAAATGGG  AGAGCCAGTA  TAACGGGCAG  TTTTGAAGAA

210251   GAATCTCTTC  GAACTCTGGA  AACAGGGTTA  AATCTATAGA  TTTTAGAATA

210301   TCGATCCCGA  AAGCCTCTGC  TTTTTTATGT  AAATTCGGAG  GCAGGTCTGT

210351   ACCGCTTTTC  CAGCAATTAA  TAAATATTTT  TAATTCGTTA  ACAGTCAGGG

210401   AGTGTGTTTT  CACGAAATAA  AAGACTTCTT  TAGGATAGCG  ATTGTAAATA

210451   ATCTTCTGAA  GTTCGTTGGG  GATGGGCAGA  ACCTTTGATT  TAGCTAGCAG

210501   TGCTACGACT  AGCGTTATAA  TCAAGATTAC  GATAGCGGCT  AAAGCTAAAG
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210551  TTCCTCCAAT AGCATAGCTA ATCGGCGCAG CAAGGAAAAC AAAAGAAAGT

210601  GCGCTAACAA GAGCTAGAAC AAGCCCAAGA ATGAGTCGGG CAATTGTCCT

210651  AATTTTTAAA GAACAAGATC TATGACATTC GCAGTCATTT TTTAAAAATA

210701  TATGGGGAAC TAGTGTTAAA GGACTACACT TCATAGTACA ACCAGAATGT

210751  CTCACGGTTA TTATAACCTT TTGATTGAAA AAAGCGTACG AATTCGTGAA

210801  ATGGGAGTTA ATAAAAAAAA TCCCTACCCA CTAAAAAGCA GGTAGGGATC

210851  AACAAGAGTA AGAGAAGCAA CTCTATGAAG AAGCAGGAGC TGAATCTTCT

210901  TGAGCCACTT CTTGTTCTTT AAGAGCAGAC TGCGCTAAGA ATAGTTTGTT

210951  TAACTTAGTT GCAGAAACCA ACCAAATAGC AATGATGAAA AGAAGAATCA

211001  CTGCAAGATA AGGGGTCATA GCTCCAATAC TTCCACAGAT AACGAGCAAA

211051  CCTTGTTGGA TTAAAGCTCC TCCTGATTTT CCGAAGCGGG CAGCAACTAC

211101  ATCAATAGCA GCCTTACCTT TGACTTTTTG CTCTTGGTCA AGAGGGATAT

211151  AGGCCATTTC TTTAGTTGAG TCAAAGAGAG CGTATTTGT GGATTCGAA

211201  AGAATATTCT GTATAGCTCC GACAACCACA GCTAGCATGA GAGGAGTTGT

211251  ACCGAACATA GCGACCAGCC CAGAAGCTTG GTTTCTAAAG ATAACAAGAG

211301  CGAAGAAAAC GATACCTGTT AGGAGAACCA TGACAGGAGT GACTAGGGCT

211351  CCAGTTAACC ATCCAAATTT ACGAATGACG TTACCACCAA CAAATAGCAT

211401  GATAAGTACG GATACTACGC CAGTCCAGAA GGAGAAGTTC CCCATGAACT

211451  CACTATAGTC ATTCATATTA GGATATTGCA GTTTCAGCTG ACTTTTCCAA

211501  GTCACTTCGA TTAAGTTAAT GCAAATACCA TAGGCAATAA CCAAGAGAGC

211551  TAATAAAAGA ATATAAGGAG ATCTAGCAAG ATAGAGGAAG CTATCTTTCA

211601  TATTCATTTT AGGTTTAGCA CCTTTTTTCC CCTTTTGCAT TTCTTCTGGA

211651  TTATAGAAGC GAGGATCGGT CAATACGTTC TTATTGATCC ACCAGTAACT

211701  GGCCATAAGA ACAAGTCCAG ATACAATAGT CATAGCCATC AAAAGACGTA

211751  AAGAAATTCC CCAAGGATCT ACACCTTCAG AAACGGAAGC TCTCAACTTT

211801  GAAGCCCAAA CAATTGCACG ACCAGAAGCT AGTAAAGAAA TATTAGCTCC

211851  GATACCGAAA AGAGCGTAGA AACGCTTTGC TTCGTGGATT TTTGTAATTT
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211901   CATTAGCAAA TCCCCAGAAC ATTAGAGATA GCATGACGCT TCCCCATAGT

211951   TCAGCAAGTA CATAAAATGC AGCAAATGTC CAGTTTCTTA AGATGGCAAC

212001   GAGTCCTAGC AATCCTGGAG GTAGGATGGC CTGTAAACGG TCAGCAAATT

212051   CTGTAGGATG TAAAACATCG CGTAGCGGAT AAATTACAGT CGGGAACAGG

212101   GCAAAGAAAA TTAAAAAGGG CGTTCCCACT GCATAAAATA AGGCCTGCTT

212151   ACTTAAAATA TTACTTAGCT TTGCATAAAT AAGCATAAAG ATAATAGCAC

212201   AGGGGACAAC AAGCCAAAAC TTGATGAAAG GTATTGCCTC TGCACCAGAA

212251   CCAGGAGCTC CCACAATAAG AGTGTCTTTT GTATCGCGTA ACACCGTATA

212301   GTTAAATGTA ATACAGAAGA ACATTAGGAA CATTGGCAGA ACTTTCTTTA

212351   GCTCGTGAGT ATGTATCGGC CACAAGAAAG AGCGCAATTT TCCAAAAGGT

212401   TTTTCTTCGG TTTTTGTCAT ATTTACCCTC TGAAATACTT TTATTTTCTA

212451   TTCTGATAGT TTTTTATTTC GTTGTGGACT AACTTGAATT GTTTCCATTT

212501   CGAAAGACCT TATAATATAC CATCTTTTCT CTCTATTGAC AAGAGGAAAG

212551   GGATACTCCT AAGGGATAAG AGTTCTTAGG CGACTTTATT GCTAAGTCGC

212601   CTGTAAAATT TATTTTTTAA TTAAACGAAA GGAGAGGTAA CTTCAAGGTT

212651   GGGAGAGCTT ACAGCCTTCA CAGCTTCGAC GTAGGCATTC CATAGCTCTA

212701   CGCTCACGAT ACCGTTGCGA ATCGAACGAA TTAACTCCCT TTTTAAAGAA

212751   GTTAACGGTT TTTTAGGGCT AAAGCGAGCG AGGAGGTCTT TGTCTCCAAC

212801   TTGTCTTGCC AGTTCTAAAA CGCGTTCAAT ATCTGTTTTA GTAAAGTTAA

212851   TAAAGTCACG ACGTTTTTTA GAGCCTCTAG GAGCTCTAGG CTTAGGATTA

212901   ATTGTGCGTG GGGTTTCCGA TTCTAAAATA AATGTTTTTA ACATTTTTAA

212951   AAGTTGTTCG GGAGCAGCGC TTTTCATCTT TTTTAGAGTG AAATGATGCA

213001   TATAACCGCC GCTAGGGCCT GGAAGATAGC GACATAAATC GTTTTCTTTG

213051   TTTCCGCAGA CTCTTTTAAT AGCTTTTCCG ATCAGTTTTT CTATTTCTTC

213101   TTTTATATGT GATTGTTCTA CGGCCATGAA ACCCACCTTT TATAATTGAT

213151   GCTTACATAT TTTACAAGAA AGAATGTGGC ATACTTTCAA TTTAATGTTT

213201   AGAGAAATAA AATTAAAGCG CTGTTTTAAT CAATCAGCGA ACATAAATTA
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213251   TATTGCAAGT TCTCCTTTTT GCAATATTTT TCCTCTCAGG ATCTTTTTGT

213301   TTCTTAACAA AATTCAAAAC ATAAAAATCG TAAAGTAAAG AAGATTTTTT

213351   CTATAACATT TTGTTTTCTT ATAAAACAAA CGGGTTTTCT AATTTTTTTA

213401   AAACTATCCT GAACAAAGAT ATTTCTTTCA TTTCTATTAG TTGTATTTCT

213451   TGCTGGATAA AATATATTTT GAATAGAACT TGTTTTTCTG GTACTTTAAG

213501   TGGTTTTTAA TGGATCTTAA AAAATGCTTC TAGAGAGATG GATGCGAAAA

213551   TGGGATATAT ATTTAAAGTG ATGCGTTGGA TTTTCTGTTT CGTGGCATGT

213601   GGTATAACTT TTGGATGTAC CAATTCTGGG TTTCAGAATG CAAATTCACG

213651   TCCTTGTATA CTATCCATGA ATCGCATGAT TCATGATTGT GTTGAAAGAG

213701   TCGTGGGGAA TAGGCTTGCT ACCGCTGTTT TGATCAAAGG ATCCTTAGAC

213751   CCTCATGCGT ATGAGATGGT TAAAGGGGAT AAGGACAAGA TTGCTGGAAG

213801   TGCCGTAATT TTTTGTAACG GCCTGGGTCT TGAGCATACA TTAAGTTTGC

213851   GGAAGCATTT AGAAAATAAT CCCAATAGTG TCAAGTTAGG GGAGCGGTTG

213901   ATAGCGCGTG GGGCCTTTGT TCCTCTAGAA GAAGACGGTA TTTGCGATCC

213951   TCATATCTGG ATGGATCTTT CTATTTGGAA GGAAGCTGTC ATAGAAATTA

214001   CAGAAGTTCT CATTGAAAAG TTCCCTGAAT GGTCTGCTGA ATTTAAAGCA

214051   AATAGTGAGG AACTTGTTTG TGAAATGTCT ATTTTAGATT CTTGGGCGAA

214101   ACAATGCTTG AGCACAATTC CTGAAAATTT ACGGTATCTT GTCTCAGGTC

214151   ATAATGCGTT CAGTTACTTT ACACGTCGCT ATTTAGCTAC TCCTGAAGAA

214201   GTGGCTTCCG GAGCATGGAG GTCTCGTTGT ATTTCTCCTG AGGGTCTATC

214251   TCCAGAAGCT CAAATCAGTG TTCGTGATAT TATGGCGGTT GTAGATTATA

214301   TTAATGAGCA TGATGTCAGT GTGGTTTTCC CTGAGGATAC TCTGAACCAA

214351   GATGCGTTGA AAAAAATTGT TTCTTCTCTG AAGAAAAGTC ATTTAGTTCG

214401   TCTAGCTCAA AAACCATTGT ATAGTGATAA TGTGGACGAC AATTATTTTA

214451   GCACCTTTAA ACATAATGTC TGCCTTATCA CAGAAGAATT AGGAGGGGTG

214501   GCTCTTGAAT GTCAAAGATG AGACTTTTTG GTCTGTACAC AACCTTTGTG

214551   TAAACTATGA GCATGCAGCC GTTCTTTATC ACATATCCTT TTCCTTGGGA
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214601 AAGGGGTCAT TAACTGCTAT TTTAGGTCCT AATGGAGCTG GTAAAAGCAC

214651 TCTCTTAAAG GCTTCCTTAG GCCTGATCAA ACCCTCTTCG GGGACTGTTT

214701 ATTTTTTTAA TCAAAAATTT AAGAAGGTGC GTCAGCGCAT AGCCTATATG

214751 CCTCAGAGAG CTAGCGTGGA TTGGGATTTT CCAATGACTG TCTTAGATTT

214801 AGCCCTTATG GGGTGTTACA GCTATAAAGG AATGTGGGGG AGAATTTCTT

214851 CGGATGATCG AAGGGAGGCC TTTCATATTT TAGAAAGAGT TGGTTTGGAA

214901 TCCGTAGCAG ATAGACAAAT AGGACAGCTC TCAGGAGGAC AGCAACAAAG

214951 AGCATTTTTA GCACGTGCTT TGATGCAAAA AGCAGATCTA TATCTTATGG

215001 ATGAGTTGTT TTCAGCGATT GATATGGCTT CGTTAAAAC ATCTGTAGGG

215051 GTTTTGCAAG AGCTGCGAGA TCAGGGAAAG ACTATCGTCG TTGTTCATCA

215101 TGACTTGAGT CATGTGCGTC AACTATTTGA TCATGTGGTT TTATTGAATA

215151 AGCGTTTGAT TTGTTGTGGC CCTACTGATG AATGTCTGAA TGGAGACACT

215201 ATTTTCCAAA CGTATGGTTG TGAAATTGAA CTTTTGGAAC AAACCCTGAA

215251 GCTCTCTCGA GGAAAACAAT TTGGATCGTG CTGATTATGC TCAGTTGTGT

215301 TTTTTCTGAT ACGATTTTCT TATCTAGTTT TTTAGCTGTC ACTTTGATTT

215351 GTATGACCAC AGCTTTGTGG GGGACAATTC TCTTGATTAG CAAGCAGCCT

215401 CTTTTAAGCG AAAGTTTATC TCACGCGTCG TATCCAGGAC TTCTAGTTGG

215451 AGCTTTGATG GCGCAATATG TTTTCTCATT GCAAGCTTCT ATTTTTTGGA

215501 TTGTGTTGTT TGGGTGTGCT GCTTCGGTAT TTGGTTATGG GATCATTGTT

215551 TTCTTAGGGA AAGTATGTAA ATTACATAAA GACTCCGCCC TTTGTTTTGT

215601 TCTTGTGGTA TTCTTTGCTA TCGGAGTGAT TTTAGCCAGT TATGTCAAGG

215651 AAAGTAGCCC TACGCTATAC AATCGCATTA ACGCCTATCT ATATGGGCAA

215701 GCAGCCACTT TAGGTTTTCT TGAAGCTACG TTGGCTGCGA TCGTCTTTTG

215751 TGCTTCGTTA TTTGCTTTAT GGTGGTGGTA TCGACAAATT GTTGTGACTA

215801 CTTTTGATAA AGATTTTGCT GTTACTTGTG GCTTAAAGAC TGTTCTTTAT

215851 GAAGCACTCA GTCTAATTTT TATATCGTTG GTGATCGTAA GTGGAGTTCG

215901 AAGCGTAGGG ATTGTTTTAA TTTCTGCTAT GTTTGTGGCT CCTTCTTTAG

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215951  GTGCTCGTCA GCTTTCCGAT CGTCTAAGTA CAATTCTTAT CCTTTCTGCA

216001  TTCTTTGGAG GGATTAGCGG AGCTTTAGGA AGCTATATCT CTGTAGCATT

216051  CACATGTCGT GCTATTATAG GGCAACAGGC GGTGCCTGTA ACCTTGCCTA

216101  CGGGACCTTT GGTTGTCATT TGTGCTGGAT TATTGGCCGG TCTATGTTTG

216151  CTTTTTTCTC CAAAATCTGG GTGGGTCATT CGTTTTGTCC GTAGGAAGCA

216201  CTTTTCGTTT TCAAAGGATC AAGAACACCT TTTAAAGGTG TTTTGGCATA

216251  TTTCTCATAA TCGTTTAGAG AACATTAGTG TTCGAGATTT TGTCTGTAGT

216301  TATAAGTATC AGGAGTATTT TGGGCCTAAG CCTTTCCCTA GATGGAGAGT

216351  TCAGATTTTA GAATGGCGGG GTTATGTTAA AAAAGAACAA GATTATTATC

216401  GACTCACAAA AAAAGGAAGA AGTGAGGCCT TAAGATTAGT TCGTGCTCAC

216451  AGATTATGGG AATCGTATCT TGTGAATTCT TTAGATTTTA GCAAGGAAAG

216501  TGTTCATGAG TTGGCTGAGG AAATAGAGCA TGTTCTTACT GAAGAATTGG

216551  ATCATACCTT GACAGAGATT CTCAATGATC CTTGTTATGA TCCTCATCGA

216601  CAAATTATCC CAAATAAAAA AAAGGAAGTC TAATGGCTTT GGGACCTTCT

216651  CCTTATTATG GAGTATCTTT TTTCCAATTT TTTTCAGTAT TTTTTTCGAG

216701  ACTGTTTTCT GGAAGTCTTT TCACGGGTTC TCTCTATATT GATGATATTC

216751  AGATTATAGT ATTCCTTGCT ATTTCCTGTT CAGGTGCTTT TGCAGGAACT

216801  TTTTTAGTCT TGCGAAAGAT GGCTATGTAT GCGAATGCTG TCTCTCATAC

216851  TGTCCTTTTT GGTTTGGTCT GTGTTTGTTT GTTTACGCAT CAACTGACGA

216901  CCCTCTCTTT GGGTACCTTG ACTCTTGCAG CAATGGCAAC AGCTATGCTG

216951  ACAGGGTTTC TTATTTACTT TATTCGTAAT ACTTTTAAAG TTTCAGAAGA

217001  GAGCAGCACC GCTCTAGTCT TTTCTTTATT ATTCTCTCTG AGCCTTGTTT

217051  TGTTAGTCTT TATGACAAAG AATGCTCATA TAGGAACGGA GCTTGTGTTA

217101  GGAAACGCAG ATTCTTTAAC GAAAGAGGAT ATTTTCCCTG TCACTATTGT

217151  GATTTGGCT AATGCTGTAA TTACTATTTT TGCGTTCCGT AGCTTAGTTT

217201  GTTCTTCTTT CGATTCTGTA TTTGCCTCTT CTTTAGGAAT TCCTATTCGG

217251  TTGGTTGATT ATTTGATTAT TTTTCAACTT TCTGCATGTC TTGTAGGAGC
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217301   TTTTAAGGCT GTAGGTGTAT TAATGGCACT TGCTTTTCTG ATCATTCCAT

217351   CGCTTATTGC TAAGGTTATT GCAAAATCGA TAAGGAGTCT TATGGCTTGG

217401   TCGTTAGTTT TTAGTATTGG TACAGCATTT TTAGCTCCTG CATCTTCGAG

217451   AGCAATTCTT AGTGCTTATG ATTTGGGGTT ATCGACTTCG GGAATCTCTG

217501   TAGTGTTCTT GACGATGATG TACATCGTGG TTAAATTTAT AAGCTATTTT

217551   CGAGGCTATT TTTCTAAAAA TTTTGAAAAA ATAAGTGAGA AAAGTTCTCA

217601   ATATTAGCAG TGATTTAAAA GAATGAAATT TTAGAGTTTA GTCCACTTTA

217651   GTTAGAAATA GTATCAATAG AGAATTGACA ATTCCTCGAC TTGCGGAGTA

217701   TGATTCTCTT TTTCACCTAG TTAAAGGTAG CATGCTTGAA ACATTTAGCC

217751   GTTCTTGGGT CAACAGGTAG TATTGGCCGT CAAACATTAG AGATTGTGCG

217801   GCGCTATCCT TCAGAATTTA AAATTATTTC TATGGCTTCT TATGGAAATA

217851   ATCTAAGGTT ATTTTTTCAG CAACTAGAGG AGTTTGCTCC GTTAGCCGCA

217901   GCGGTCTATA ACGAAGAGGT TTATAACGAG GCCTGTCAGC GATTCCCCCA

217951   TATGCAATTT TTCCTAGGCC AGGAGGGTTT AACCCAACTT TGTATCATGG

218001   ATACAGTCAC TACTGTCGTT GCTGCTTCTT CAGGAATCGA GGCGCTACCC

218051   GCGATTCTAG AGTCGATGAA AAAAGGAAAA GCACTAGCTT TAGCAAACAA

218101   AGAAATTTTA GTTTGTGCTG GCGAATTGGT TTCTAAGACT GCAAAGGAAA

218151   ATGGTATAAA AGTTCTTCCT ATTGATAGCG AGCATAATGC TTTGTATCAA

218201   TGTTTAGAAG GCAGGACGAT TGAGGGAATC AAGAAACTGA TTCTTACAGC

218251   TTCTGGAGGG CCTCTGCTCA ACAAGTCTTT AGAAGAGCTT TCTTGTGTAA

218301   CAAAACAAGA TGTTTTGAAC CATCCTATAT GGAATATGGG TTCAAAAGTG

218351   ACTGTGGACT CATCCACATT GGTCAATAAG GGACTCGAAA TTATCGAGGC

218401   GTATTGGCTG TTTGGTTTAG AAAATGTTGA AATCCTGGCT GTAATTCATC

218451   CTCAGAGCTT AATCCATGGT ATGGTAGAGT TTTTAGATGG GAGTGTGATT

218501   TCTATCATGA ATCCGCCTGA TATGCTCTTC CCAATACAAT ACGCTTTAAC

218551   AGCTCCAGAG CGTTTTGCAT CTCCTAGGGA TGGTATGGAT TTTTCGAAGA

218601   AACAAACTTT AGAATTTTTT CCGGTAGATG AGGAGCGATT TCCTAGTATC
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218651   CGTTTAGCAC AACAGGTATT AGAGAAACAG GGGTCTTCTG GAAGCTTTTT

218701   TAATGCAGCC AATGAAGTAT TAGTGCGGAG GTTCCTTTGC GAAGAGATTT

218751   CTTGGTGTGA CATTTTACGC AAATTAACGA CTCTTATGGA ATGTCATAAG

218801   GTTTATGCCT GCCACTCTTT AGAAGATATT TTAGAAGTAG ATGGTGAGGC

218851   TAGAGCTCTT GCTCAAGAAA TATAATCGAG TAGGTATATG ACAATAATCT

218901   ATTTTATTCT AGCAGCCCTA GCTTAGGGA TTTTAGTGTT AATTCATGAA

218951   CTTGGTCATC TGGTAGTAGC AAAAGCTGTA GGAATGGCTG TAGAGAGTTT

219001   TAGCATAGGC TTTGGTCCTG CTTTATTTAA AAAGCGTATA GGCGGCATAG

219051   AATATCGCAT TGGATGCATT CCTTTTGGAG CTATGTTCG TATCAGAGGT

219101   ATGGAACGTA CCAAAGAAAA AGGGGAGAAG GGAAGATAG ACTCTGTCTA

219151   TGATATTCCT CAGGGATTTT TTAGTAAGTC TCCTTGGAAA CGCATTCTGG

219201   TTCTTGTTGC TGGTCCTCTT GCCAATATTT TATTAGCTGT CTTGGCTTTC

219251   AGCATTCTTT ACATGAATGG GGGAAGAAGT AAAAATTATA GCGACTGTTC

219301   TAAAGTGGTA GGTTGGGTCC ATCCTGTTTT ACAGGCAGAA GGATTGCTCC

219351   CTGGAGACGA GATTCTTACG TGTAATGGTA AGCCTTATGT GGGAGATAAG

219401   GACATGCTAA CAACCTCTTT ATTAGAGGGG CATCTCAATC TAGAAATCAA

219451   ACGTCCTGGC TATTTGACAG TTCCTAGCAA AGAGTTCGCT ATTGATGTTG

219501   AGTTTGATCC CACAAAATTC GGGGTTCCCT GTTCTGGAGC GAGTTATCTT

219551   TTGTATAGCA ACCAGGTGCC CCTAACGAAG AACTCTCCTA TGGAGAATTC

219601   AGAGCTACGT CCGAATGATC GTTTCGTTTG GATGGATGGC ACACTTCTTT

219651   TCTCAATGGC TCAGATATCT CAGATACTCA ATGAGTCTTA TGCTTTTGTG

219701   AAAGTAGCAC GGAATGACAA AATCTTCTTT TCTCGTCAAC CTAGGGTATT

219751   GGCTTCCGTT TTACATTACA CTCCCTACCT TCGTAATGAG CTTATAGATA

219801   CGCAGTATGA GGCTGGACTT AAAGGCAAGT GGTCTTCGTT ATATACATTG

219851   CCTTATGTAA TCAATAGTTA TGGATACATA GAAGGTGAAC TTACTGCTAT

219901   AGATCCAGAG TCTCCTTTGC CACAACCTCA AGAGAGGCTA CAGCTTGGGG

219951   ATCGCATTCT AGCTATTGAT GGAACTCCTG TTTCTGGAAG TGTAGATATT
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220001   TTACGTCTTG TTCAGAACCA TCGGGTCTCT ATTATTGTTC AGCAGATGAG

220051   TCCGCAAGAA CTTGAAGAGG TGAATTCTCG AGATGCTGAT AAGCGGTTTA

220101   TCGCCTCTTA TCATTCCGAA GATCTGTTAC AAATTTTGAA CCATTTAGGA

220151   GAGTCTCACC CAGTAGAAGT CGCGGGTCCT TATCGTCTTC TTGACCCTGT

220201   TCAGCCTCGT CCTTGGATTG ATGTTTATTC TTCGGAGAGT TTGGATAAAC

220251   AGTTGGAAGT AGCTAAGAAG ATTAAGAACA AGGATAAACA AAGATACTAT

220301   TTGGAGCGTC TTGATGCTGA GAAGCAAAAA CCATCTTTAG GGATTTCTTT

220351   GAAAGATCTT AAGGTGAGGT ATAATCCTTC ACCTGTGGTT ATGTTATCAA

220401   ATATTACTAA GGAAAGTTTG ATCACCTTGA AAGCTTTAGT TACTGGACAT

220451   CTGAGTCCAC AATGGCTTTC AGGACCTGTG GGTATTGTGC AGGTTTTACA

220501   TACAGGATGG TCGGTAGGGT TTTCTGAAGT GCTCTTTTGG ATCGGTCTAA

220551   TTAGTATGAA TTTGGCTGTC TTGAATTTGC TTCCTATTCC TGTTTTGGAT

220601   GGAGGTTATA TCCTTCTATG TTTGTGGGAG ATAGTCAAAA GAAGACGTTT

220651   GAATATGAAG ATTGTGGAAA GGATTTTGGT TCCGTTCACT TTTTTATTGA

220701   TCATCTTCTT TATTTTTCTA ACTTTTCAGG ATTTATTTCG TTTTTTTGGT

220751   TAAGGCTCCA TTTTTTTGGA AATCCGTAAA GGTTGTAAGG ACGAGAACCA

220801   AAGCAGTGTA TAACGTAGAT GTCTTGGTTA GGGTAAGGCT TAAGTCTTGA

220851   GTTCTTTTGT TTGTCTTCCA TAACAGTTTG TTCTAAAGCT GCTTCGGGAA

220901   CGTGCTCGAT TATCGGGGTT GTATTTCCTT CTTTTAAAAA CTCTTTCATA

220951   AGATAGAGCG ACTTCCGATT AGTAATGATG TAGGTATGAC TCGTGTGGAT

221001   CACGTAAGCT TTATGTGGAG TATCTAGCTT TGTCTCTATA GTGCATACCT

221051   TACCATCGTT TTCATAGGGC AGGCGGAAAG GAAGGAATTT GCTATGTCTG

221101   TTCCCACTAA GAATGAGAAC GTCTAAAGAC GAAGGGAGTT TCCCGACATT

221151   TAACATCTTT GTGGGGCAGT AGGTAAGAAG CTGTCGTCCT AATTTTCCTC

221201   CAAATACGAA CTGTACGAAT TTCACACAGC GGTAGCGTCT AGCTAGTGTA

221251   GACCCTGCGT TCGGAGGAGC CATGAGAATA GCTTTTCTTT TTTGGCTTCT

221301   TCGGGGCAAT CAGGGTGAGC GAGTGCTACA CGAACAATGA CTCCTCCAAT
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221351   AGAATGAGTT ACGAAGTTTA TAGGGACTCC AGGCTTAAGT TCAGCTATTT

221401   TTTTCAGCAA GCGATTGAGA TGTTCAGCAT GCTTTTCTAG AGTAAACTTG

221451   CGCGTCTCAT AATTCCAAAT AAAGACATCG TAATGTTCTT TTTCTAGAAC

221501   GCGAGCAATA GGTTTTAAAG ATGTATAAGA TCTTAAAAAC GCATGCACGC

221551   AGACCACGGA TTCTTTTTGT TTTGAGGTTT CCTTTAATCC CCCAATTCCA

221601   GATGGAAGGG TTTGGATTAC CGAGGTTTCC GAGAATAAAG GATTACCCAC

221651   AGCTAAAAAG AGTATAGTTA ATAAAAATTT CTTCATGTGT CACCGATATA

221701   ATTATTTTAA ATAAGTTTTT TATTAAAAAA GAATATGTTT ATTAAAACTT

221751   ATTTATAAAA ATAACTAATT CGCTTACTTT TAACGCAAAA GAAAAATGAT

221801   GTTATTGTTT TAGATAATTT GCTCAGAAAC TTGAGCGTTC TCGATACTTA

221851   AAACAAGGCT TGTTTTTGGA AGTTCCCCAT GCATATGGGT GGAAGTAATC

221901   AGAGTCTGAC CCAGAGTTGG GGCAGGGTCA AGGAGTTGAC CGACACGTTC

221951   ATTATCTAAT CCAGCATGGA TATCATCTAG ACAGACTAGA GGGGAGACGT

222001   GATGAGATTG CTTTAGATAT AGGCACTCAG CAAGCCTTAA GATTGCCAAA

222051   AGACTGTGTT TCTGCCCTTC ACTAGAGAAT TGAGACACAG GCATTTGGTT

222101   CATAGTGAGT AGAAAGTCTT CGCGATGAGG GCCAACGGAA GTGCTTCCTC

222151   ATTCGAGATC TCTAGGAAGT GATATAGAGA GCTGTTTATG AAATTCTTCG

222201   GCAACAGCAG TTTCAGAAAT ATCAGAATTT TTAATTAAGG AACTTTTAAA

222251   TTTTAAGGCC AATTGTTCTT TTAGGTTGTT AGACCAAAGT TCTTTGGATA

222301   AATCTGAAAG TTTCTGACTA CAGAGAAACC GTTGGATGGA TAGGTAGGTG

222351   CCGTGTTTGA CCAACTGTTC ATCCCAGAGG CCACGGTTGA GGTTTGCTTG

222401   CTTTTTAAGA GAGCATTTCT CTGCTGAAGA GCGCGATGAT AGTACGATAA

222451   GCAGAGGGTA TAGTGGTTAT CGCATTGAGA TAAAAGCAGA TTTAGGAAAA

222501   GGCGACGATC CGCAGGAGCT CCTGAAATTA GAAGGCGGTC TTTTGAAGAG

222551   AAAAGCACAA TAGGTACTTT CCCTATCAGC TGCGATAAGG TTTTTATAGG

222601   AAGTTGGTTA TAGCAGATTT TTTTTCCTTG CTTGTCTGTA TAGATGGAGA

222651   GAGCTTGGGG AAGGTGGTCT TTCTCAAACT GTGTTTCTAA GAAGAAATGG
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165

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222701   GAAGATCCGA AGGTGATGGT ATCTGTGAGA TGTTGCGTGC GAAAAGACCT

222751   TCCCAAGGAC AAAACATAAA GCGCTTCTAG GAGGTTTGTT TTTCCTTGGG

222801   CATAATTGAG TTTAGGAGCC AGTGAGATTT CTAAATCACT GTGGTTACGA

222851   AAATTTTTTA GCTTCAGAGA GCAGATTTTC ATAAACATCG GCAGGGTAGT

222901   GACCTAAAGG ATTCTCCTTA GGGAGTTTAT TAATCATCAT GTAGCCTCAT

222951   AGGCATGATG ACAAATAATC CTGAGGCAGA ATCGGTAATG ATTCCAGGAT

223001   TATAGGAATC CGAGATCCCT AAGCTGACTA ATTCATCCTT ACTATGCTTC

223051   AGGATATCTA AAAAGAAAAA GGGATTAAAG GCAATTTCTA GGAGTTCGCC

223101   AGAATAATTT ACAGCCATGC TTACCTTTCC TTCACCCACC TTAGTACAGT

223151   TGGCTGTTAG AGTGAGCTCT CCGGGTAAGA AAGAAAACTT CACGGAGTGA

223201   GAGGACTCAT TTGTAAATAA AGCCACTTGT TTGAGCAGAG TAATTAGTTC

223251   TTCGCGATGC AGATCGAGTT TTACGTTGCT TTCTGTAGAT ATGACGGGGG

223301   AGAAATCTGG AAATTCTCCA GAAAGAAGTT TTGTGATCAG GAGAGTATTG

223351   TCACATTCAA CCGCAATCTT ATCTTGATCC AAGAAGATCG CAGCTTCACC

223401   TTCATCGGAG CACATCTTTA TAATTCTTC TACTGCTTTG ATAGGAATAA

223451   TATATTCCCC AGAAAAACTT TTATCTAAAG TAACTTCAGC ATCTATTTTT

223501   GCTAAACGCT TTCCGTCAGT CCCTACGATG GTAGCCACGC CATTGGCGAT

223551   AGCAAGCAGG ACTCCAGTAA GAACATAGCG GCTTTCTTCT CTAGATACAG

223601   CGAATGAAGT TCTCTGTAGC ATGGTTTTTA GCTGCTCTGC AGGCAAGGAA

223651   AAACGCAAAG CATTTGTAT ATCAGGGAGC ATGGGGAAGT CTTCTTTTTC

223701   CATGCTGAGT AGGCGAAAGC ATGAAGATCC CGAGGTGATT TGTGCCATTT

223751   CCCCTGCTGA AGAGGAAATT TCTAAATTTG CCTCTGTTAA TTCTTTTACT

223801   AATTGAAAAA ATCTCTTGGA GGGAATGGAA ATAGCGCCTT TCTCATAGAC

223851   TTTAGCTTTG GTGACGCAAC GTGTGCTCAC TGTCAGATCC GTAGCAGTGA

223901   AAACTAATTC ATCATTATAA GTTTCAATCA AAACATGGGT GAGTACTGGA

223951   ATAGGTGTGT TTTGAGGGAC GACACTTTGA ATTTTTTTGA TAAGGTTTCC

224001   TAGCTCATTT CGGGATACAA CGAATTTCAT ATTTTCCTAT AACCTGAGTC
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166

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224051   TAACTTTATA TGAAGGGCTA CGCCTCTCTA GGAGAGACGG TAGAGGTACG

224101   ATCGGGATAT TACTACAAAG TGATTTTCTG GTCTTCTAGA TATTTTACTA

224151   ATAAAAAAGG CTTTAGATTG AGGAAATCTT CCCTGGAAAT CAAGGAAAGA

224201   GGATTCTAAT CATTGTCTTA AGAAGGAAAA ATTGCTTTTT GTTATACTGG

224251   TTTTTGTCCC CAATTATGGG GGAGGATCTT ATGGCACAAA AAGAAATTGT

224301   TTCTAATCGC AAGGCTCTGC GTAACTATGA AGTTATAGAG ACTTTAGAAG

224351   CAGGCATCGT TTTGACTGGG ACTGAGATTA AGTCGTTGCG CGATCATGGG

224401   GGAAACCTCG GTGATGCTTA TGTCATTGTT TCTAAAGGTG AGGGGTGGTT

224451   ATTAAACGCG AGTATTGCTC CCTATCGGTT TGGAAATATC TATAACCATG

224501   AGGAGCGTCG TAAACGTAAA CTCCTTCTTC ATAGATATGA ACTTCGTAAG

224551   TTAGAGGGTA AGATTGCTCA AAAGGGCATG ACTTTGATTC CTCTGGGAAT

224601   GTTTCTGAGT CGCGGCTATG TTAAGGTACG TTTGGGTTGT TGTCGTGGGA

224651   AAAAAGCTTA TGATAAGCGT CGTACGATCA TAGAAAGAGA AAAGGAACGT

224701   GAAGTTGCCG CTGCTATGAA GAGGCGCCAT CATTGATATA GGTTAGGATA

224751   TGGTGTTCTT CAGCCCACTG TTTTGCTTCT ATTTTAGAAT CAAAAGTCAT

224801   GAGGACTGTG GCAATAGCGT CGGCGTATGC GCAGCTCGGA TGGACTACTG

224851   AAACACTTTG GATAGGATAG GAGCTTAGCT CTAGGGGTTT CCCTGTACGA

224901   GTATCAAGAA TATGGGTGTA AATTTTTCCT TCAACACACC ATTTTTGAAT

224951   ATGATTTCCA CTTGTTGCAA TTGCCATATC ATCGATATCT AAGATCGTAC

225001   CTGCTGCTTC AGAAAAAATA CGCCAAGGTC TTCCCGAGGG ATGATGCCCT

225051   GACGTTTTGA TCTCTCCTCC CCACTCTACA TAGTTGTTCG GACAAAAGGT

225101   ATTGCAAATT TCATTTAGAC AATCTACGGC ATAACCTTTG ACAACACCAC

225151   AGAGGTCGAT TTGAACATGA GGATTCTTTT TGATTAGAGT TTTTGTGTTT

225201   GACTGAAACT CCAAGTGTTG CCAGCCCATG TCTTTATAAT GTTGTTCCCA

225251   AACGTCTTTA GGGGGGAGGG TTTGACTTTT GAGATGTAGA AGCCATAGGG

225301   TTTTTAAAGG TCCTACAGTA GGGTCAAAAC GTCCTTCTGA AAGTTTGTAA

225351   AGTGTATCTA CCTGATCTAG AAACTCGGAA AGTTCTACAG ATAAAGTTAT
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225401   GGGGACATCT GCTGGAGCTC GGTTGATTAT CGAGAGTTCA GAATAGGGAT

225451   TCCAGTTGTT ATAAATCGAG TCGATCTTAT GAAAGCATCT ATCAATTTGT

225501   TGGGATAAAG ATGCTTTTTC TTTTGCGGAT AAAGAGGTTC CCAGAACAAT

225551   GCGATAGAAG ATTGTCATCT GCTCTCCTTC GATTGTTGTC GTTTTTTGAG

225601   AGCATGAACA GAGTCCAAGA CATAAAAGAA CTAAGAAAAA TTTTGGTAAC

225651   ATCGCCATGT ATTGCTCATG AGCATAGCGA CAGTCATGGG ACCAACGCCT

225701   CCAGGAACTG GAGTGATTGC TGCGCATTTT GTCACAACGT TATTAAAATC

225751   TACATCCCCA AGAAGAGTAT AGCCTTTCGC ATTGTCTGCA GGGACTCTTG

225801   TTGTTCCTAC ATCTACGATC ACAGCATGTG GGGCTACCAT AGTTTCCTTT

225851   ATAAAAAGCG GTGCTCCTAG AGCAGCAATA ATGATATCAG CTGTCTTTAA

225901   GATTCTGGG AGGTTTTCCG ACTGGCTATG AAGAACTGTG ACTGTACAGT

225951   TAGTTTGAGG ATGCTTTTGC ATCATGAGGG CCGCTAAGGG TTTCCCCACG

226001   ATGTTGCTTC TCCCTACAAT AGCGGCATGG CGGCCTCGAA GAGGAATTTC

226051   ATAATAGTTC AGGAGTTCAA TAATTCCTGC AGGAGTGCAG GGTAGAAGTC

226101   CATCAAAATT TCCAAGGAGC AACTTTCCCA TGTTCACAGG GTGAAGCCCG

226151   TCCACATCTT TGTCTGGGGA GATCGCTTGG AGAATCACTT CGCTGTCCAA

226201   GTGTTTGGGC AAGGGAAGTT GCACGAGGAT GCCGTGGATG CTAGGATCTT

226251   GATTCAATCG TTCTATGAGC TTAAGGACTG AGGAGAGGGT AGAGTCAGAG

226301   GGTAACTTGT GCGCTTTGGA GATAATTCCG ATTTCTGTAG CTTTTTTGAC

226351   TTTCATGCCA ACGTACACCT CAGATGCGGG GTCATTGCCA ATCAGGACCA

226401   CAGCAAGCCC CGGAGAGGTA GGACTTTGTG AGATTTCCTC TTTGAGTCTC

226451   TGAAGGATTT TTTCAGCTGC AGGAATCCCT CTCAGTAACA TACCAATCTC

226501   CTAAAAAAG ATATCATTTT ATGGATTCCT GAGTTTATTG CGCAAGGAAG

226551   TATATAGATT ACAGAAGTGA AGATGAGATT ATCTAAGAAA GAACATTTTA

226601   GAGGTATCAT TAGCACATCT ATTGACCAAC GGACTTCATG TCCGAACAAG

226651   GCGCACATAG GAATGGTTAG GAGTAAAAAG ACTCCATAGA AAATCATATT

226701   CACAATGACC AAGGCGGCTT TGCTCTCTTT TGAAAAAATG AGGTGTGCCT

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226751  TATGGGTGAT CAGAGCAGTT AGAGGGTAGA GCAGTAGAAA TACACCGCGG

226801  CTTCCTAAGG CAAGATCACT TAAGACACCA CAGCCTAGAG CGAGTACCAG

226851  TCCCTTATCT TTTGAGAAAC AATAGAAACA AAGAACAATA TAAGGGGAAA

226901  AAAGGATCAG ATGTGCTTTA GGGAAGAGCG TTGGAAGGGT GAACATGGAT

226951  AAAATACACA AAATAAAGCA TTTGCGCGGT GTTATGTGGA CAGACATGGT

227001  TTACGCTTTG AATTATGATT ATCGATTCA AAAGGTTTTG CAGACTTGTA

227051  TATAGCAAAG CATAGGATTC TTAGCTTGAT TTTTTATGTT TATCTAAACT

227101  GCTTTTAAAC AATTATTTAT ATAATATTTT ATTTTTAGAT TAAAATTAGT

227151  TTATTCTTAA TAAGTTTTTT AATTAAAATT AGTTTATTAA GTTGATTTTT

227201  TTGTTTTTGT ATTTTTTATG GGGAAGCCTA AGAAGAGCAG AACGGATAGG

227251  GCTTTGGCTC AGGAGATTCA AAAGAAATCA ACGGAAGTGT TGAAGAAGCC

227301  TGCGCGGATA AAAGCTAAAA ATCGTCGTAA ATTTCTTATT GCTAAGGAAC

227351  AGAAAACTCT TAAACACCGT GCTCAAGAAT ACGATCAGTT AGTTCGCTCT

227401  CTCTTAGATT CTCAGAAGAA GGACACCGAT AAAGTTTTGA TTTTCAATTA

227451  TGAGAATGGG TTTGTTTTTA CTGACAAGGA CCATTTTAGT AAGTACTCTA

227501  TCCGTCTTTA GGCGGGGTTA AATTAAAAAA AAATCGCAGA ACGGGACTAT

227551  CCCGTGATGG AACGACAGGA AGCCTGGGTA ATTAATTTAG AGTTAGGAAC

227601  TGTCTCGGTA TTAAGATCTC CAAAATCTTA ATACCTAGAC AGTCGGATCC

227651  GAGTGATCCC TCTAGCTCGA CAGCGATGCA CTTTGTTGCA TCTACTCGCT

227701  GTTCTCTGTC CTCCCATAAG TTTTTTTACG CAAGGTGTTT CACCTTGCGT

227751  TTTTTTTTGT TTTTTAGATT TTTAAAATTT GTTTGTAAGT TCTTTTTTTT

227801  AAATTAATTA TTTTTTGTTT TAAAATTATA AGTAGTTATA AGTTTTATTT

227851  TTTAAATTCA GAGAATCATT ATGGCAGTTT CAGGTGGCGG AGGGGTTCAG

227901  CCTTCTTCGG ATCCAGGAAA GTGGAATCCT GCTCTGCAAG GAGAGCAGGC

227951  AGAAGGCCCG TCTCCGCTAA AGAATCTAT ATTTTCTGAA ACCAAGCAGG

228001  CCTCCTCTGC TGCGAAGCAG GAAAGCTTAG TGCGTTCAGG ATCTACAGGA

228051  ATGTATGCAA CAGAATCTCA GATAAATAAG CTAAGTATC GTAAAGCTCA
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228101    AGATCGATCA TCAACCTCTC CAAAATCCAA ATTGAAAGGT ACATTTTCTA

228151    AAATGCGCGC TAGTGTGCAA GGATTCATGT CAGGATTCGG ATCTCGGGCT

228201    TCGAGAGTGT CAGCAAAGCG TGCTTCCGAT AGTGGTGAGG GAACATCCTT

228251    ATTGCCGACA GAGATGGATG TTGCTCTAAA GAAGGGAAAC CGTATTTCAC

228301    CTGAAATGCA GGGATTTTTC TTAGATGCTT CGGGTATGGG AGGGAGTTCC

228351    TCTGATATTT CTCAGCTTTC TTTAGAGGCT TTGAAATCTT CAGCATTTTC

228401    AGGTGCCAGG AGTTTAAGTT TAAGCTCTTC AGAATCTAGT TCCGTGGCTT

228451    CGTTTGGATC TTTCCAAAAG GCCATAGAGC CTATGAGTGA GGAGAAGGTA

228501    AATGCTTGGA CAGTGGCTCG TTTAGGAGGG GAGATGGTCA GCTCTCTTCT

228551    CGATCCCAAT GTTGAGACCT CATCATTAGT GCGCAGGGCA ATGGCAACAG

228601    GCAACGAAGG CATGATAGAT CTTTCTGATT TAGGACAGGA AGAGGTCAGT

228651    ACAGCCATGA CATCTCCCAG AGCAGTAGAA GGAAAAGTAA AGGTATCTTC

228701    TTCTGATTCT CCAGAAGCGA ATCCAACAGG AATTCCAAAT TCTAATACTT

228751    TAGAAAGGGC GGAAAAGGAA GCAGAGAAAC AAGAAAGTCG AGAGCAGTTG

228801    AGTGAGGATC AGATGATGCT TGCACGTGCT ATGGCTGGGC TTCTTACAGG

228851    GGCAGCGCCT CAAGAGGTAT TGAGTAATTC TGTTTGGTCT GGTCCTTCTA

228901    CAGTATTTCC TCCTCCCAAG TTTTCAGGAA CTTTACCCAC CCAGAGATCG

228951    GGAGATAAAT CAAAGCATAA ATCTCCAGGA ATAGAGAAGA GTACGAACCA

229001    TACGAACTTT TCTCCTCTTC GGGAAGGTAC TGTGAAGAGT GCTGAGGTTA

229051    AAAGTTTGCC TCATCCAGAA AGTATGTATC GTTTTCCTAA AGATAGCATC

229101    GTTTCCAGGG AGGAACCTGA AGCCGTTGTT AAAGAATCTA CGGCATTCAA

229151    AAATCCAGAG AATAGCAGTC AAAACTTTCT CCCTATTGCT GTGGAGAGTG

229201    TTTTCCCTAA GGAAAGTGGT ACGGGAGGGG CTTTAGGAAG TGATGCTGTG

229251    AGTTCCTCAT ATCATTTCCT TGCGCAACGT GGAGTGTCTT TACTCGCTCC

229301    TCTACCTCGT GCTACTGATG ACTATAAAGA GAAGCTCGAA GCTCATAAAG

229351    GTCCTGGAGG TCCTCCAGAT CCTTTGATTT ATCAGTATCG AAATGTTGCT

229401    GTTGAGCCGC CAATTGTTCT CCGTTCTCCC CAGCCGTTTT CAGGATCTTC
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229451 ACGTCTATCG GTTCAAGGAA AGCCTGAAGC TGCTTCAGTT CATGACGATG

229501 GTGGGGGGGG AAATAGTGGT GGTTTTAGCG GAGATCAAAG AAGAGGATCT

229551 TCGGGCCAGA AAGCTTCCCG TCAGGAAAAG AAGGGAAAAA AATTATCTAC

229601 GGATATTTAG GGTTTTAAGT CGGTTTGATG TGATGCGTAT AATTCGTTTT

229651 GATCCTTATG GTGCGCTATC TGCACAAAGC ATAGCTAAAG ATTCCCGTCA

229701 AAACTCTCCT TTAGTAGAAA AAATTTCTGA GGAAATTGCT ACGAATGAAG

229751 CGATTCGGCT TGCCTTGCTA GCTATTGGAG ATCGCGAACA AGAGGAGAAG

229801 AAACAGAGGC ATCGTTATAA GCTACTCGGA CAAAAGCAAG CCAAGGTCTT

229851 GCTTTCTCAG TTGCGTCATG TGCATTTAGA TTTTAAAAAA CTATATTGCG

229901 ATAGTAAGAA AAAAGAAGAT CAGGAAAAAG ACGAAAAAAA CAAACAGAAG

229951 CGATCTATTA AAGTTACAAA GAAAAAAAAG GGCATCTCTT TAGGGGCTGC

230001 CGCTTCTCAG GCAATTGCAG CAGCAGCAGA AGCTTGGGTA ATTGCTAGAA

230051 ATAAAGGAGT CTTAGAAACT GCCTCCACTC TTTTTTATCA AAAGGATGAA

230101 GAGGCCTAGA CATACTTGAA TCACGAGCTA GGCCTTCTTC TGTGACTATT

230151 TTAGATCATC ACGCTGCTTC TTGCTCTTCT ACTGGAAGAC TTTTTTCTAT

230201 AATTTCTTTT TCTTCATCGT CTACTGTAGG ATGTTCTGAA TGCTTAGCTA

230251 GATCTTTCCA AATCATTCGA AGTTCTGAT TTTGTTGTTT GGTCAGGTTT

230301 TCCAGTATGA TCAAGCTTTC ATCATTTAAG GAGAATCTTC CTTTAGACCA

230351 ATTTATAGAT CCTGCAAGTA GAGTTTTATT ATCTATAACT GCAAACTTAT

230401 GGTGAAGAGT ACAGGGTGCG GTATTTATAG AAACAAAGTC TTTATTGATA

230451 TTTAATTGTC GTAATTGCTT AAAAGTAAGT TTGCTATGAC TTCTATCAAT

230501 GATAATATCT ACATGGATTC CTCGTTGTTT TGCTTGATGT AAGGCTTGAA

230551 TAATCTCCGA GTGGGTCAGA GCAAACATAG CAACTTGGAT GGTTTTCTGA

230601 GCTGTCTGGA TTTTTTCGAG TACAGCTTGT ATTGCAATTT TACGATCTTG

230651 AGGAAGAACA AAATACTTTC CTGTTTGATC CTTTATAGAA AAGTCTCCAG

230701 AGGTATTTGT GATAATGAGA TCACAGAGCT CCGAGCTATG CATTCCTAGA

230751 ATGAGATTAT TATCTAAACG TAGAGAAAGA TTGGTGTAGT TCGCAGATCC

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230801  TAGCCAAGCA TCTTTCTTAT CTATGGAAAG AGCTTTTTGA TGCATCAGTT

230851  TACGCCCTGC TGGAGGTTGC TCGACTAAAG TTACATTGCT GGCTTGCTTT

230901  AAGATTTGGG GAATTTTAAA TTTTTGATAG TAGATCGTAA CTTTGTTTTT

230951  TGCTTGAGCT TGTCGAGTTA AACTCTGTTG GATCTTGGGT TCTGAGAGGT

231001  TATAAATACG TAGGAAGATC TCTTCATCAG CGTGTTCTAT AGCATCGCAT

231051  AGAATTTTAC GCATGTCCTC ATTGCATTGA TTTGAGTAGA TGATAGCTTC

231101  TTCAGACTTT AAAAAAGTCT TAAAAGTGTC ACCACGAGGA GCTCTTGCAA

231151  AAATTCCTAC TAAAATCAAC GTGCTAATAA TAACACAGAT TTTTAATTTA

231201  TCTTTTTGTC TTTTATTCAT TTTTTACTCT TAAAATAGCT TTTTTGTTTT

231251  TATATATTTT TAAAAATAAA AATAACTAAT TTAATTAAAC GTTTAATAGA

231301  ATAAGATTCT TATTAAATAT AAAAAGTTTC TTTATTGGGG AAATATGCGT

231351  GCCATCGTTC GGAAACCTTT TGTTTTGTAG ATGGGTCGAC CTCTACTTCT

231401  TTAGGATAGG AAGGCTTCAT CAGGGCATCG ATAACGAAGG GAAAGTTGTA

231451  ATTAGGACGG TGAGTAGCAA AATGGCTGTG GAGCGCGTGA AGATCATTTG

231501  CTGGGGCACA TCGTGTGAAG GTCCTCCAGA GAAAATCTTT TTCACTTTGA

231551  ATGGTTTCTC TCAGATTATC GGCAAGGATA ATCAGAGGCC ATGATTTTAG

231601  ATCTGGATGG TGAAGGAGAG ATTTAATACA TCGGTCCTCG AGGGATGTTT

231651  CCAACACTAG GCAACCACGA CAAAAGGGAG CGATGTCTTG AACTCCATGG

231701  ATTTTTCCTC CCTGATATCC ATGGGGAAGG TCTCGGATGG CTTTTCCTAT

231751  TCCCATGAAG ATTCCCTTGG AGCCCTTATT TAAGCTTGGT CCTGTATAGT

231801  CTAACGTATC GTTTGCAGTT TCTGAGAAAA TAATAAGATC TCGGTCTGGC

231851  TGTAGACGCT CTAAAATGGT TTCTAGAACC ACGGAGAACC TGTCGAGAGG

231901  CACCTCTTGG TCTGTGACCA TTAGGAATTT CGTTAGGGAA AGTTGGCCCT

231951  CTCCAAGAAT TCTAAGAGCT GTGGTTAGAG ATTCTCTCCA ATAGCGTTCT

232001  TTAACGACAG CGGCAGTCAG TGCATGAAAC CCTGATTCTC CGTAACTTTT

232051  AAGTCTACGC ACACCAGGCA TAACTAACGG AAATAAAGGG GAGAGGTATT

232101  CTTGGAGTTT GTTCCCTATA TAAAAATCTT CTTGGTAGGG TTTGCCGACT
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232151   ACTGTAGCAG GATAGATTGC ATCTTTTCTG TGATAGATTT TATGACAGTG

232201   GAATTCAGGG AAGTCATGTT GGAGACTGTA GTATCCGAAA TGATCGCCAA

232251   AAGGACCTTC AGGACGACGT TTCCCGGCCG GAGATTCTCC GACCAGGATG

232301   AATTCCGCAT CGTAGAGTAG AGGGTGGGGA TGGTCGTTTG TTTTTTTATA

232351   AAGGAGCTTC GCTCCTTGGA GGAAGGTAGC AAAGAGAAGT TCCGAGACAT

232401   TCTCAGGTAG GGGGGCAATC GCAGAAAGGG TTAAAAAGGG GTTTCCAGAC

232451   AAAAATACCG AAACAGGAAG GTTTTGCTTT TTTTGCTCTG CTTCATACAG

232501   ATGCATCCCT CCGCCCTTCT GGATTTGAAA ATGGAGGCCC ATGGTGTTTT

232551   GATTGAACCG TTGCACGCGA TACATCCCAA GATTGGGTGT AGTAAGAGTC

232601   GGCGATTCCG TATAGACAAG AGGAAGTGTG AGAAAGGCTC CACCATCTTC

232651   AGGCCAGCTT GTGAGTAAGG GAAGGTGATC TAAGTTAACT GAGGACATAG

232701   AAACAAAAGG AAAGCGACGG AATCGAGCTT TTTTGAGCCC TAAAGAGCTT

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232951   TTCAATAACA CGACGATGAA TCTCAGCTAA CTCGAGGTTA GGACTTACGG

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233251   GTCTTCCCTG TCACTTTCAA ACCAATTCCT TTTTTCTTTT TAGCAATACC

233301   TCGAAGTGTA TAGCTATAAC CACGGCGAGG TCTCTTTCCT GTAAGTGGGC

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233651   GCCGAACTCG ATACGACCAA TTCTTTTTAG AAATTGTCCC AGGTGTATTA

233701   ATGCGTTCTC TTTGTAGATT TTTTGATACT AAATCAGGGC AGAGGGCGAG

233751   ATAATCGTTA AAGAGGTTGA TATGAAAGAT AGATGCTGAT TCATGAGAAA

233801   GTTTTAAGAT GTCTATTTGA GTTTCTGTAG TCAGGGTTTT TTGAAAAGGA

233851   AGATGTAGAA ATTTAGCAAA TTGCTTAGCT TCCTTAGGTG AATTGAGCCA

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234001   CGTTCCCATC GTGGAATCCG GGTTCCACAG ATTCCTAAGT GTGTTAATGT

234051   CGTTTTGACG TCTTGGGGTA TAATCCCTAA ATCTTCTCCG ATAGGTAACA

234101   TAGAAGAGGC TCCGAGCATA GTAGAAAGGA TCTCCGTGCC CTGCTTTATA

234151   TAGTCTTTAG GATTGTCTGG AATGAACCTT CCTCTTCCTG AAGAATCCCA

234201   AATCCACAAA CGGAAAAATC CTATAATATG ATCTAAGCGA TAGACGGAAT

234251   AGAAGTTTTG AGCATATCGC AGACGCTCTT TCCACCAAAT GTAGTCGTCT

234301   TTGGCAAGTT GTGAAAAATT ATAAATAGGC AGATGCCAGT TTTGTCCTTC

234351   AGAATTGTAG AGGTCAGGAG GAGCTCCTAC AGACCTTGAT GAAGAAAAGT

234401   AGTCTCGGAA ATACCAAACA TCACAGCTAT CCTTGCTAAT AAGAATAGGG

234451   AGGTCTCCTT TAAGCAGGAC GTGGTGTTGA TCTGCATAGG CTTTCACTTC

234501   GCAGAGCTGT TGGTAACAGA GAAACTGTAG ATAGGAAAAA AAGAGGACTT

234551   CATCATGGAA TTTTTTAGTT AAGTCCGGAA AATTCTCCTG ATCTGTGAGC

234601   GACTTCGGCC AGTTATTAAT AGGTTCTCCG TGCATATGAT GTTTGATTGC

234651   ACGAAAGGTC CCATAGGGAT AAAGCCAATA GCGCTCGCTT TCTAGAAACT

234701   CAGAAAAATT TGAGTTTCCT TCGAGGGAAG ACTTGCAACA TTTTTGGTAG

234751   TACTCTCTTA AGAATGCCCA TTTTTTTTCT TTAACTTGAG TATAGCTGAC

234801   TGATGGAGTC GAGCATAACT CATGCATATC TTGAAGTTTC TTGGCAACTT

234851   CAGGGATGGT ATCGATATTT GGAAGAGAGG ATAGGGAAAG GAATAGGGGA

234901   TTCAGGGCTA CGGAAGAGAT GCTGTTATAG GGACTCGTAT CTTCACCAGT

234951   ATCATTTAAA GGGAGAAGCT GAATAACGCT GAAGCCCTGT TTTTGGCACC

235001   AAGAGATCAG AGGAATGAGA TCTAAAAATT CACCGATTCC ACAGCTATTT

235051   TTTGTGTGTA TTGAAAATAG TGGGAGATAA ATCCCGTGTT TAGGAGAGGT

235101   TCCTATAAGT TTCCAAGCAT GTGCTGAGGG TGAGTGTTTT GTGTATTTTA

235151   AAACATTCAC GCGACGTAGT AGATTCCCAA AACATGAAGG TCAGGAAGAT

235201   TCCCTGTTCT TAGGGATTCC ATCCAAATCT TAGCATGCAA AGAAAAGAGC

235251   TTGAGATACT CGAATAACTT TTCTCCATTT AGGTAGTTCA TACTCAGGAT

235301   ATCTGAAAGA TAGAGCTGTT GAGTGACCTC ACCGTAGCCT AGAATTCCCT

235351   TGATGCTGGA TTGGAACGAG CCATTTACAG AGAGAGCAGC TTTGAAAATA

235401   CGCTCGCGAA ATACGTTTTC AGGAAGAGTA CCTAGTAGTG TCGATACTGC

235451   AAGATCTCCG GAATTTCCAT CTTCTTCTAT TTGCACAGGG ACATGGGTAT

235501   CGCTGAAACG GATTAAACAA GAGTTATTTT TATCTGGAGC AAGTGTCGTA

235551   TTTAATAGGG GTGCTAAGGA TTCTAGTAAT TGCTCGTATT GGTTTTGCAT

235601   GGCAATCCTT TTTTAATCAT GACCAAGGAT AGGGTTTAGG GAAGTCTGAT

235651   GCTTTGGGAT AATCTTCATT GTTTATATTT ACAGCATCTA AAGCATTAGC

235701   AATCATAGCT CCTAATTGCT GACGTTTGTC TGCTGAAGAG AAAAGGCGTG

235751   ACGACGTTTG ACGTAAAGCA GAAAAGAATA AGTTCAAGAC ACCGGTCACA

235801   GAATCAACAT CGTCTCCTAT GAGATTGCGG ACTTCTCGTT CTACTTTAGA

235851   TGCTGTTGGG AACTTATCGT TAATGATTTT ATGGTAGGAC TCAGCTACCT

235901   TCACAAAGTT TAGATCAGAA GGAGTTTGGA TTCCCTCAGC TTTTAAGCTA

235951   TCGAGTAAAA TAGGAACGCG ACTTTCAAAG TAATCGTACG AGGTAAGAAC

236001   TGCTTGCAGG TTACGAGTTT CTGTCATGAG AACTTGTAGT TGCGCACTGG

236051   GTACGTAGGG ACCCTGCCTT TTTAATTCTG TTGCCATTCC TTTCATTAGA

236101   AAGGAGCTGA CAATAGCCAT ATCTTGGTAG GTATAGCGGT CTTGAAGCAT

236151   AGAAAGTAGC TGATCACAGG TATGTGTGTC TCCAGTCACT TCTAAGTACA

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236201  AAGAGCGAAG  CCCTGAAGGA  GAAACATTCA  GTTGGTCTGC  ATATTCTTGA

236251  GAGGCAAATA  AGATGTTTTT  CGCACCAATA  GCAGTTCGTC  CGAATTGCTC

236301  CGTATGAGTA  TTCCTTGCTT  GGATAAGCGC  TTCTTTTAAT  TTACCTTGGG

236351  AGGGTGGAGT  CGTTTGAACC  AGGTAGTCCA  AAGCTGTGGA  TTGCAGAGCT

236401  GGGTCTTTAA  TTTTCTCTTG  TACAAGAGCA  AGAATGTCTT  CTGGAGAAGC

236451  ATCGTCTCCT  ATTGCATCAC  GCAGGCCGCG  AAGTTCTTGA  CCAGAGATTT

236501  CAGAATTCCC  AGAAGCATAC  TTATCAGCAA  GATCTGTGTC  AGGCTTCTCT

236551  TCTGTAGATT  CAGATTTTTT  CTCAGCCTTT  CCAGCTTCTC  CTTTTTTCCG

236601  AGATTCTAGA  GTTTGAAACT  TCTCTTCCTT  TTTTTTCGTG  CGTGTTGCTG

236651  CTGCGGGATT  TGTCAGGTCC  TGAGATTGTT  GAATCATGTT  CATCTCAGAA

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236751  TTCTACAGCT  GCAAGGTTGA  CACCCTGAGT  GCCTCCTAAA  CCACCTGTGC

236801  CTCCTGATGC  TGCCATATGC  CTCCTATGAG  CGACAACGTA  TCAATTAGAA

236851  AATCTGAATT  CTTCCTAAAG  GCTGGATGCG  GATTTCTGGT  AGGATTTCTT

236901  GATAAGAAAT  CACAGCAATG  TCAGGGAATT  CTGTTTCTAT  TAATTTTCGT

236951  ACATATCTTC  TTACATCAAT  TGCTGTCAAT  AATACTGGTG  GTTGGCCTCC

237001  TGCAGGTGTT  GGCGTGATCG  TATTCCTCAT  AGATTTTAAA  ATTAGGTTCA

237051  CAGAATCAGG  ATCTAGAGCA  AGGTAAGAAC  CTGCCGATGT  CTGTTTAATT

237101  GCTCCACGAA  TCATCTCTTC  AATTTCTGGA  TCTAAGAGAT  AAACAGAAAT

237151  TGCTGATTGT  CCTTGAGAGA  ACTTGAAGCT  GATATAAAGC  TTTAAAGAAG

237201  ACCGTACATA  TTCTGTAAGC  AAAACTGTAT  CTTTCTCAGT  TTGCGCCCAC

237251  TCGCTCAGAG  ATTCTAAGAT  TGTACGTAGG  TCTTTAATTG  AGATTTGCTC

237301  TTGAACCAAT  CTCTTAAAGA  TTTCCGTAAG  CTTTTGCAAT  GGAATAAGCC

237351  TTGTGACTTC  CTTCACTAAG  TCCGGGAATG  AACGTTCCAT  AAATTCGATC

237401  ATAGAACGTA  CCTCTTGAAT  TCCCAAAAAC  TCTTGAGAGC  TTTTATGGAA

237451  AAAGTACGAA  AGATGGAGAA  TGATCACTTC  GAGCGGCGTC  CAATATTTAA

237501  TTGCTGCCTT  CTCTAGAATA  GCTTTTGCAT  CTTCACTAAC  CCAAGCTGAA
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237551   GGAAGACCCG CAGCATTCTT ATAGGTAATG AAAGGTAGAT TATAACGGCT

237601   GAGATTGTCC TCCACCTCAT TGGTTAACAC ATGGTGCGGA GGAATTTTTC

237651   CTCGCACATA AGGGACTTCA TTAAGCAGAA TCATATAATC GTATCCTTCT

237701   AAAGAAGGGG AATCTGTGCG AACATGAATG CCAGGGTATC GGATTCCGAT

237751   ATCCTGATAG AGAGCTTGCC GCATTTTAGG AATCATATCA TCAACAAAGC

237801   TTTGTCCTGA TTTTGTCTTG TGTTGGATAA GCTTAGAGAG ATCTTTTCCA

237851   AGTTCTAGAA TTACGGGAAG AGTTAGAGAA TAGTCATCGG GATTATCCCC

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237951   AGCCACCACC TTTTTTTCCT GCCGCTGATT TCTTAGTCAG TAGGAGAATC

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238251   TGTAGACGTG AGCTGCTTGA GCGAGGTCCA TGCCGTGCAT AGCCACCCCA

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238401   CACTTTCCTT TTGGATTTGA GCCCTTTTAT CACGAGCTTG TGTGGCATCA

238451   ATCATACCAG CTCGTAAGTC CGCATCAATC GCCATCTGTT TACCTGGCAT

238501   CGCATCCAAT CGGAATCGGG CAGCAACTTC GGCAACACGC TCGGCACCCT

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238651   ATGACCCGCA TACGCTTTAA GGAGAATCTG TCGAGAAGAG GAAATATTAA

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238751   AGCTGCAAAG CACTTGGAAT ATAAAGAGCC ACCATCAATA AGAATACAGA

238801   GATCGATAAG TTGATGGTGA TCATCAAGTC AACGATAGGC GGAGGCAAAG

238851   GAATAATGAT CATTAAGACA ACGCCCATCA TCCAAAGAGC AAGGATTAAG
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238901   TCGCTGGACT TATTGATCAT GTTTAAGGCG GTATCGCCAC CAAGTGTTCT

238951   GCTGACGAAA TTGAGTAGCT TATTCATTAT AAATGATCAG GTTGGTTAGT

239001   ATTTTTATTA TTAGGATTTT GCGCATTCAG TGAAGTGATA TAGAGTAGAA

239051   TTTCTCCAAT AGCTTCGTAA GTAGATTCTG GAATAAATTT TAATTCCTTC

239101   CCTTCATCCA AAAGCTGATG TGCTAAAGGT ACGTTTCGCA TAATGGGAAT

239151   TCCGTACTTT TCAGCTTCAT CAAGTATCCT TTTAGCTCGT AAGTTGATGC

239201   CCATGGCAAT GATCCAAGGT GCTTTATATT TTTCAGGCAT GTAGCCAATA

239251   GCAACAGCAA TATCTTTGGG ATTAGAGACT ACGGTGCTTG CATGTTTCAC

239301   CTGTGATGAC GAGTCTTCAT AGGCAATTTC TTGAGCAATT TGTCGACGAC

239351   GGCCTTTAAT CTCAGGATTT CCTTCCGTGT CTTTAAACTC CTGCTTAACC

239401   TCAAACTTCT CCATCTTTAA TTCTTTAGCG AAATTGTGGC GCTGATAGAC

239451   AAGGTCAAGA ATCGCAACAA TCAAAAGAA AATTCCTATC GAGGTTACTG

239501   CTTTATAAAA AATTTCTTTG AAGATTTGAG CAGTAATTAT AGGAGAGACT

239551   CCTGCAGTTT CTATAATTAA AGAGACTTTG CTTTTTAACG TTATGTATAA

239601   AATTAAGGCT GCTCCAAAAA TTTTTAAAAT CGATTTGATC AGCTCTATGA

239651   GAGTCTTTAT TTTAAACTTT TGTTTGATGT CTCAATAGG GTTGAACTTC

239701   TTGATATCTG GTTTAAAAAC TTCGGTAGAA AATGTAGGAC CAACGATAAG

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240101   ATCTGCAAAT TACCTTATGC TCTTGTTTTT CTCAAGAGTG AAGCCCAAAC

240151   GTTTTGTTCT TAGTAAGATT ATAAATGAAT CTTAGAGATA AAGAAGAATA

240201   GTAGAAAAAA AGAACAATAA CGAAAAGTTG TTGAATTTAG CAATACTTTA
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240301 TCAATCGATT ATAGTGGTTT TTTATCATTT TCAAAGCACT CTTGATTTTG

240351 AAGGTACTAT TTTTCTAGCT ATTGTGCTTT TTTGAAACAG AAGAGTTGTC

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242801 CTCGGCAGCT GATAATACTT CTTCGAGACT AGGAATCTTC TTAGATCTTC

242851 CTACAACTTT GCCGTCGCAA TCATAAGAAT CGGTAGTTGT CCCTAAATGG

242901 GCAATTGCTT CGTATTCCTT GTCTTCAAAA AGTAAAATAT CAGAAAGTCT

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242951   AGTAAATTTA CGGCCAATCA ACATGACCAT AACGCCAGTA GCGAAGGGAT

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243051   GCGCGGATAA GGCTAAACGA AGTTCTCCCT TGAGGCTTGT CTACAAGAAG

243101   AATGCCCTCT TTTAATTCTA CTGCAAGATC CATAGTCATG TCTTTAATAG

243151   TATTCAAGTT CCCAAAAAAT ATAGTTATT AACTCTTTTC TTTCTCTTGA

243201   ATCTGCCAAA GCAGGTTTTC TATATAATCT TGAGGTGAGA AAATATCATC

243251   GAGATAAAAA TGAAGTTCTG GGAAATATTT AAGGACGACA TTTTTCGAAG

243301   CTCTATGAGC GATAAAACCA GCAGAGACTT TTAAAGCTTC TAAAGCCTCT

243351   TCCTTGGTAT CTCATGAGG CATTACAGAT ACATAAACAC GTGCAGAGTG

243401   CAAATCCTTA GATAGAGAAA CACGAGTTAC CGTGATCCAA AGATTAGAAA

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243501   AATAAAGCAT TTACCCGTTT AATACGTCTA TTTTCTGTCA TACAGTACTT

243551   CAAGTTATAG TTTTTGTGGA TGATAGATAA CTTCATAACA TTGTAGGACA

243601   TCACCTATTT GAGCTTGCTG GTATCCTTCT AACAAAATTC CACACTCTAA

243651   ACCTTTGCGA ACTTCTTTGA CATCTTCTTT AACACGTTTT AATGAAGATA

243701   ACGTACCTTT CCAAAGGATC TCTTTATTAC GTAATACTCG GACTTTATGA

243751   TTGCGAGTCA TAATTCCTTC AGTAACTATG CAACCGTAAA TAGATCCTAC

243801   TTGTGAAGAC CTAAAGATTT CTTTAATCTC AGCAGAACCT TCATCTTTTT

243851   CTTCAGCAAT AGGATCTAAT AGAGAAGTCA TAATTTCTTT AATTGCATCA

243901   ATAGCATGAT AGATGACGGT AAATAGTTCA ACTCGGACTC CTAAGCTCTT

243951   AATTAAAGGT TCCGCATGAC TTTCTATTCC TGTATGGAAA CCGATGAGAA

244001   CTGCTTTAGA GGCGGCAGCT AAACGAATGT CTGATTCTGA AATTTCTCCT

244051   ACACTGTTTG TTAAAATTTC AACATCTACT TTTTCTGATT TAATCTTAGA

244101   TATTGAACTG ACCAAAGCTT CTATGGAACC TTGAACATCA GCTTTAATCA

244151   TAAGCTTAAG AGTCTTTTTA TTCTGTAACA TAGAATCAAA GTTAGGCCGC

244201   TTCTTTTGCT GTAAAGCAAA ACGCTGTTGT CCTGCGGATC TAGCTTCAAT

244251   AATGTCTCTA GCCGTTTTCT CGTTTTTCAC GACGAAGAAA GGATCGCCAG
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244301  CTTTAGGAAT GTCCGATAGA CCTGTGATCA ACACAGGAAT AGATGGCCCA

244351  GCTTCTTTCA TCAATTCATT ATGTTCGTTA TGCATAGTTT TCACTTTGCC

244401  ATAACAATCA TTGAAGACGA GAGCTTCGCC CAGTTTTAAG CTTCCATTTT

244451  GAATCAAAAC AGTCGCAACA GGTCCGAGAC CCTTGTGCAG TTCTGATTCA

244501  ATAACAAGTC CTCGAGCACG TGCTGAAGGA TCGGCTTTTA GCTCCAAGAC

244551  TTCAGCTTGT AAAGCTAACA TCTCTAAAAG TTCTGAAAGA CCTTCTCCTG

244601  TTTTTGCGGA GGTATTTACT GTAACAGTCG AGCCTCCCCA AGCTTCTGGC

244651  AATAGATTGA TTTCAGAAAG TTGTCTATAG ATGGTTTCGG AATTAAAATT

244701  AGGCTTATCA CACTTGTTGA TAGCTACAAC AATAGCGATA TCAGCAGCTT

244751  TTGCATGTTC AATAGCCTCT AAAGTTTGTT CTTTAATTCC TTCGTCTCCA

244801  GCGACTACAA GCACAACAAT ATCACAAACT TCAGCTCCAC GGGCTCGCAT

244851  TGCAGAGAAA GCTTCGTGAC CAGGAGTATC TAAAATTGTT ATGTCTCCCA

244901  CTGGGGTGGA GCAGCAGAAG GCTCCCATGT GTTGGGTAAT CGCTCCAGCT

244951  TCTGTTGCAG CGACATTACT TTTCCTTAAG GAGTCAATGA GTGTTGTTTT

245001  TCCGTGGTCG ACGTGACCCA TAAACGCAAC AATAGGGGAG CGAATCACAA

245051  GCTTGCTGGG ATCTGTAGAT TGAATTTCGT CTCTTACAGT GTCATTGCTT

245101  AGGCACAACT TATCTTGCTC AGAATAGTCG ATGTCAATTG TACATCCAAA

245151  CTCTAAGCCA ATAAATTGTA CTGCAGTTTC GCTGTCTAGA ATATCATTGA

245201  CTACATAGGT CATTCCATGA ATGAATAACT TTTGAATGAC TTCTGAAGCC

245251  TTGAGCTTCA TTTCTGCTGC CAGATCTTTG ACGGTAATTG GCAAGGAAAT

245301  TTTGATATGC GTAGGTCGCT GGATAGAGGC TTCGTCATAG TGTTTTTTAG

245351  GCTTATAAAC ACGTTTTTTT CGCCATCTGT CTTCTTCTCC GCCTTCATTT

245401  AATCCGTAAC GATCTCTTCC TGTAAAAGCC TTTAGGCTTT CATCAGATTT

245451  CTTAGAACGA TCACGAAAGT CGGTAAGATT TTTCTTCCCA GCATCTCTTT

245501  TTGGACCAGA AGCAGGACTA CGGTTAGCAG GATTGAATTG TTTTTCTCGA

245551  TTATTCTGTT CACCACCTTC AGATGTTCCA GGTTTCCCTG TTTTATCTGA

245601  AGCAACGGGC TTTGTGCTTT TCGAGCCAGC TACGACTTTC TCTTCCTTGG
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245651   CAGGAGCCTT GAATGTTTTT GCTAGGAGAT GATTGATATG CTTTCCTGTA

245701   GGGCCGAACT TAGATTTAAT CATTACGACG CTTTTAGGTT CAGCAGGCTT

245751   CACAGGCTTA GGCTCTAATT CTTTTTCTTG AGGTGGGGTT TCGGGCAATA

245801   CGGGTTGCTC AGGAAGAACT TCAGCAACTG GATGAACCTC AGGACTTTCG

245851   TCACAAACCT CATCGACTAC TTCTAACTCA GGCTCAGGAT CTGCTATGGA

245901   GACTGGAGCA GGTTCAGATG TATCCACTGG AATATGAGCA GAAGACTCTT

245951   CTTCGGATGA TGAGAACGAC GAACGATTTT TAGCACGAAT GCGACGTGAA

246001   GTAGACTCTG GTGAAGCTTG TTCCGCACTT GCCGTAGGGG TAGAAGTTGC

246051   GGCAAGAGCT ACTTTTACAG ACTTTTCTTT CGCAGAAGGT TTTTCTGAAG

246101   AAGATTTAGC TTCAGAAGAT CCTGCTTGGG CAAGTTTTTG TTTTAGCTTA

246151   TCCAGCCCCG CGGCTTTCGT TAATTGAGCA TTCTTAATCT TCAATTTCAG

246201   GTTTTTCGTC AACTTTACTT TCTCCATATT TGCTGACTTG CTCAAGGATC

246251   TTATAAGCAA GCTCTAAACT GATCCCAGGA ACAGATGCCA GATCATTAGC

246301   ACTCGCTAAT AATACTCTTC TAATTGTGTC ATATCCAGCA TGTTCTAAAT

246351   TTTGGATGAC TAGCTTACTA ATCCCTTCCA TTTCTAAGGG TTGATCTAAG

246401   TGCGGACTAT CGAATTCTGC TAATTGAAGG CGTTGAATTT CTAGCAACTT

246451   ATTGTACTCA CTCATACGTT GTACTTCGAG CTCGTAGTCT AGAATGTGGC

246501   TAATTAAACG AGCGTTAATT CCTCGTTTAC CAATAACAGT AGCGTAGTCT

246551   GCATCATTAA CGACAATTGC AATCACTTTG TCGTCTTCTA AAATAGCAAT

246601   CTTTTGGATT TCTATTGGAT AAAGAAGATT CTGTAATAAC TCTGTAGAGA

246651   CGGGGGAGTA ATTGACAATG TCAATTTTCT CATCGTTCAA TTCTCGAATG

246701   ATATTTTTTA CTCGAGAACC TCGCATACCT ACAAAAGCTC CAACAGGATC

246751   AGTTTTAGGG TCTGACGATC TTACAGCTAG TTTCGTGCGG TACCCAGCTT

246801   CACGAGCTAT CTTAACAATC TCCACAGAAC CTTCTTCTAG TTCTGGGACT

246851   TCTTGAATAA ATAATTGTTT AACAAATTCT GCGTGACTAC GACTGAGGAT

246901   AACTTCCGCT CCACCATTTT CAGACTCTTG AACTTCATAG AGTAGGGCGT

246951   AAATTTTATC ACCGATCTTA TGTTTTTCTG TTTTAGGATA AAACCGGGTA

183

247001   GGAAGAATTG CTTCAACTTT TCCTAAGTCA ATAATTAAAT TAGAACCTTT

247051   AGCAAAACGT TTGACAACAC CAGATAAAGT TTCATTTACG CGATGGCGAT

247101   ATTCTTCATA AATAACGTCT CTCTCAGCAT GTCTTAGCTT TTGACCGATA

247151   ATTTGTCGTG CTGCGTGAGC AGCTATCTTC CAAAATTATC AGAAACAAAA

247201   GGGACATCCA TGTACTGACC AATCTGACAG TCCGGATCGT ATTCTCTGGC

247251   TTTATCTAAA GGAATTTCTT TGCTAGGATT CTGACAAATT TCTACTATTT

247301   CCTTTTCACA AAAGACTTCG ATGTCACCAG TACGAGAATT AATGTTTACA

247351   GATATGTTCG CGTCATCTCT TAAGGTTTTT TTAGCAGCAA TTTTTAAAGC

247401   AGATTCGATA GCTCCTATAA TAGTAGAGCG CTGAATCCCT TTTTCTTTCT

247451   CCATGTAGTC AAAAATAGCT ACAAGATTTT TATTCATTAT ACTCCTCTTG

247501   TAAATAAGGA AATCAGTAAA TAGCTAAATT AAGGACGTAT TATTTAGAAC

247551   TAAATAATAC GATCCTCTGC ATTACCAGCA TTAGATGCTA TTTTCCTTTT

247601   TTCTTTCTCT CTTTAGGGCC TTGAGAATCC TTGAAATCTA ATTCAGTCCT

247651   AGAGTCTTGA TCATAAGCAT TGTCAGCTAA GTATTCTTTT ACAGAAAGAG

247701   AAACTTTTTT ATGATCTGGA TCTAGCTTAA TTACTTTTGC AGAAACATTT

247751   TCTCCAATGG AGATAATATC TTCAATTTTT GCAAAGGGCT TGTCAGAAAG

247801   TTCTGAAACG TGAATCAATC CTTCAATCCC GTTTTGTAGC TCAACAAAGG

247851   CTCCAAATGC AGTGATTTTA GTCACAACTC CTGAAATTAC TGTGCCAGCA

247901   GGGAACATAG CTTCAATTTC ATTCCAAGGA TTAGAACTTA ATTGCTTAAC

247951   TCCTAAAGTA ATTTTTTTAC TTTCTTTGTC TACTGATAAA ATAACAGCCT

248001   CTACAGAATT TCCTTTTTTG AATAGTTCTG AAGGGTGAGA GACTTTTTTA

248051   ATCCAACTCA TGTCAGAAAT ATGAATCAGA CCCTCAATTC CTGGTTCTAA

248101   TTCAACGAAA GCACCGTAAT TGGTTAAGTT CTTGATTTCA GCATTGACAT

248151   GGAGACCTAT AGGATATTTT TCTTCGATAT TGTCCCAAGG ATTACGTTCT

248201   GTTTGCTTTA ATCCTAGAGA AATTTTTCCT TCGTCCTTCT GAATAGATAG

248251   AACAATGGCT TCAACTTCAT CGCCTTTATT TACGACTTCA CTAGGATCTA

248301   CAATATTTTT CACCCAAGAC ATTTCAGAAA TGTGAATTAG ACCTTCAATG

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248351    CCCTCTTCAA TTTCAATGAA AGCTCCGTAG GGGAGAAGCT TCACAATTTT

248401    ACCAAGAACT CGTTTTCCAG GAGGGTATTT CTTCTCAATA TCTTCCCAAG

248451    GATTATGCTC TTTTTGTTTG AGACCTAGAG CAACTCGTCC TTTTTCTTTA

248501    TCTACGCTTA AAATAATTAC TTCCAACTCT TGATTCAATT CGACCATTTC

248551    GGAAGGATGT CGTATGCGCT TCCAGGTCAT ATCGGTAATG TGGAGAAGAC

248601    CGTCAATACC ATCGAGATCT AAGAATACAC CAAAGTCAGT AATGTTTTTA

248651    ACAACTCCTT TGCGGTATTC TCCGATAGAA ATTTGTTCAA TAAGTTCGGC

248701    TTTCTTAGAG ATTCTCTCAG CTTCTAAGAG TTCTCTTCTT GAGACAACAA

248751    TATTGCGACG TTCAACGTTA ATTTTAAAA TTTTGAATTC ACAAACTTTT

248801    CCGACATAAT CATCTAAATT TTTGATTTTC TTGTTGTCAA TTTGTGATCC

248851    AGGTAGGAAG GCTTCCATTC CAATATCTAC AATAAGGCCG CCTTTGACTT

248901    TACGTGTAAT TTGACCTTTA ACAATAGAAC CTTCTTCACA ATGAGCTAAG

248951    ATGTATTCCC ATTGACGTTG TCGTGTGGCT TTTTCTCTAG AAAGGACAAC

249001    TTTGCCCTCT TCGTCTTCGG CTTGGTCGAG ATAGACTTCT ACTTCAGCTC

249051    CAAGCACTAA ACCTTCTGAA GAGTCTATGA ACTCTGACAT AGGGATCACT

249101    CCCTCAGACT TCAGACCAAC ATCAACTACG ACAAAGTCTT TATTAATATC

249151    AACTACGGTA CCTTTTAGGA TGGCGCCAGG CTGTATTTCG TTATCAGATT

249201    CTTCTTCGCT CGAAGTAATT CTGTGTGCCG TATAAAGCAA ATCTTTAAAT

249251    TCGGCAACGT CTTCTGTGAG GCATTCTATA TTGTCCAGAA TTTTTTTAGA

249301    TCCCCAAGTA TATTCAGCTT GTTTTGGCAT TTATTGTTAT CTCCTAAAA

249351    ACTACAAAGT CAAAAAAGAC AGTGTAAATA TAAACCTTAA AAAAGGCAAG

249401    ACCTCCCTTG CAGGAGACGA TTAGTTCTAT ATAATCGAAT TAATCGTAAA

249451    ATCCTATACT TCCGTTCTAG AGATGTATAA GGCCTCTTTT TTAACTTTTC

249501    TATATTACCA GATTTTATAA AATACGTGTG GTAATTATCA TAAATGTGCC

249551    TTGTCATATG TAGAGAAACA GGATTTGGCG CATAGAAAAC ATATCGTTTT

249601    TTTCATAAGC ACCCCATAAA TTCTCGTCCC AGATGGGCTA CATCAGCTTT

249651    GTTCTTAAGC CTGATAGATC TTTTTGGTTG CTGCTCAAGA ACCAAGTGCA
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249701  TTCAGAAGTA GAACCATACT TATTGAGGGT TAAATAATAG GATGGGTCTT

249751  GGTTTCTTAG CTCTAAGAAA ATTCTAAAGA TTAATCACAG AAATGTAGGT

249801  GTTATTACTG GAAGATGAAG ATCTTGAGAT TTGAAACTTT AGTCTTAAAT

249851  CCGTATAAAT TAAAACTAGA CAAAAGCTAT TCAAAAGCAA GTTTTTTGCA

249901  TAGAGAAACT GACGCATAGA CGCTAAGTGT TGTTTATTAG ATAGGCTAGA

249951  ATTAAGTGTC TTTTTTCTAG TAGATCAAGA ACAGTGTTCT CAATTTCTAA

250001  AGTTAGATAA GGAAATTATA AATGATTCAT TCCCGGTTAA TTATTATTGG

250051  TTCAGGTCCA TCTGGATATA CAGCGGCAAT TTATGCATCA AGAGCGCTTT

250101  TGCATCCTCT TTTATTTGAG GGGTTTTTCT CTGGGATCTC TGGTGGCCAG

250151  CTTATGACTA CAACAGAAGT TGAGAATTTT CCAGGGTTTC CTGAAGGGAT

250201  TCTTGGGCCA AAACTTATGA ATAATATGAA GGAGCAGGCT GTGCGGTTTG

250251  GGACCAAGAC ACTAGCTCAA GATATTATTT CCGTAGATTT TTCTGTTCGC

250301  CCTTTTATTT TGAAATCAAA AGAAGAAACC TATTCTTGTG ATGCCTGTAT

250351  CATAGCTACA GGAGCTTCTG CTAAACGTTT AGAAATTCCT GGAGCAGGAA

250401  ACGATGAATT TTGGCAAAAA GGAGTGACTG CTTGTGCCGT TTGCGATGGG

250451  GCTTCTCCTA TTTTTAAAAA TAAAGATCTT TATGTGATTG GGGGAGGGGA

250501  TTCTGCTTTA GAAGAAGCTC TTTACCTGAC TCGTTATGGA AGCCACGTAT

250551  ATGTAGTTCA TCGTAGAGAT AAACTGCGGG CTTCTAAAGC TATGGAAGCT

250601  CGGGCGCAAA ACAATGAAAA AATTACATTT TTATGGAATA GCGAGATTGT

250651  AAAAATTTCT GGAGATAGCA TTGTCCGTTC CGTAGATATT AAGAATGTTC

250701  AGACTCAAGA AATTACAACT AGAGAAGCTG CGGGGGTGTT CTTTGCTATA

250751  GGCCATAAGC CAAATACGGA TTTTCTCGGA GGACAGCTGA CGTTAGATGA

250801  GTCGGGCTAT ATTGTGACTG AGAAAGGAAC GTCCAAGACT TCTGTCCCTG

250851  GAGTATTTGC TGCTGGAGAT GTTCAGGATA AGTACTATCG TCAGGCGGTT

250901  ACTTCTGCAG GAAGTGGTTG TATAGCAGCA CTAGATGCTG AAAGATTCTT

250951  AGGCTAATGC GATTGCAGTT GCTGTGGCAT ACTCTTTGCA GTGGCTTATA

251001  GAGAGAATGA CTTTAGAAAT TCCAATTTTT GCATAGACAT GCGAAGGGAG
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251051   GAGAACTTCG GGTCCGTGAG ATACTTTAAA GACTTCGATG TCTTTCCAGG

251101   CAACAACGCT CCCTATGCCA GTTCCTAAAG CTTTTGCTAC AGCTTCTTTT

251151   CCAGCAAAGC GACCTGCAAA TGAAGGGATG GGATCGGTCT TTTCTAAGCA

251201   ATATTTCTGT TCTGCTTCTG TAAAGATTCT ATTGAGTAGT CGATTGCCGT

251251   GAGTTGCAAT TGCCTCGCGA ATGCGGCTAA TTTCAATAAT ATCGGTTCCT

251301   ATATGAATGA TTTCCATAGA GTTCGCACTA ATTTCCTTCA GGATTTTCCA

251351   TTAGGGCATT CTGTAATTTT GAGAAGTAAG CGATGGCAGT TTTAATGAGA

251401   GCATAGCCCA CTGTAGCTCG AATCACGAAT AAGGCTTGAG GATTGCTGAT

251451   ATAACGACGA AGGACTAAAG AGAAGGCAAT CATAATGACC ATGATGAGAA

251501   ACCTTCTAGA GATAAAGGTC TGCTTTATAT AGGCAATCCA TGTAATTTTT

251551   TGTGAAAAGA ATTCAGAAGA TAGACTCAGC TGTTTCCTTA TAGTTTTGCT

251601   TAGCAAGTAG CGATGTTTTA GGGATGCTAA TCCCCAAGAA ACCATAGATA

251651   GAAGACAGTA GGTAAAAAAA GAAGAAAGGG GGTCTAGGGC TATTGCGGTA

251701   GCTTTTAGCA AGAGTTTCAT TCCTGCTGAT ATCCACAAAA TACCAGGAAA

251751   TAGTATCAGG AAATATTTGA TGTTTCTTGC CATAGTGCAT TACACTTAAT

251801   TTCTAAATAC TCTATTTTAC TTGGAGTATG AATTTTTTGC TAACTGGTAT

251851   TAAGATATGC GAGCTGAGAT GGCTGTGATC TATTGGGATC GCTCAAAAAT

251901   TGTCTGGTCT TTCGAGCCAT GGTCTCTAAG ACTTACTTGG TATGGCGTCT

251951   TTTTTACTGT AGGGATTTTT CTAGCATGTC TCTCAGCAAG GTATTTGGCT

252001   CTTTCCTATT ATGGTTTGAA AGATCATTTA AGTTTTTCCA AAAGCCAGCT

252051   ACGCGTGGCT TTAGAAAACT TTTTTATATA CTCTATTTTA TTTATTGTCC

252101   CTGGAGCTAG ACTTGCCTAT GTGATTTTTT ATGGATGGAG TTTTTACTTA

252151   CAACATCCTG AAGAGATCAT TCAAATATGG CACGGAGGCT TGTCGAGTCA

252201   TGGAGGCGTT CTTGGCTTTC TTTTGTGGGC GGCCATTTTT TCTTGGATAT

252251   ATAAAAAAAA GATTTCAAAA TTGACTTTTC TCTTCCTTAC AGACTTGTGT

252301   GGATCAGTTT TCGGAATTGC AGCGTTTTTT ATTCGTTTGG GTAATTTTTG

252351   GAATCAAGAA ATTGTAGGAA CACCGACTTC TTTGCCTTGG GGGGTGGTTT
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252401   TTTCTGATCC TATGCAAGGT GTCCAGGGAG TTCCTGTGCA TCCTGTGCAG

252451   CTTTATGAGG GAATCAGTTA CTTGGTCGTC TCTGGAATTT TATATTTTCT

252501   TTCCTATAAG CGTTATTTGC ATTTAGGTAA GGGATATGTG ACTTCTATAG

252551   CCTGTATTTC TGTCGCTTTC ATTCGTTTTT TTGCGGAGTA TGTAAAAAGC

252601   CATCAAGGGA AAGTTTTAGC AGAGGATTGT CTACTTACAA TTGGTCAAAT

252651   TTTATCTATA CCTTTATTTC TATTTGGTGT GGCCTTACTT ATCATTTGCT

252701   CATTGAAAGC TCGAAGGCAC CGTTCACACA TATAGCAGCA TCTTTTTGGC

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252801   AGATTCTCCT TTGGGAGATA ATGTGGGTTT ATGATATTTT GACCTCTTAA

252851   GTTTAATTTT TAGAGTTTAT CAAATGAATA AACGCACTTT GCTTTTTGTT

252901   TCTTTAATTG GGATTGCTTT TGTAGGATGT CAAATATTTT TTGGTTATAA

252951   TGAATTTCGT TCCTGCAAAA ATCTAGCAGA GAAACAAAGA AAGATTTCAG

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253051   GACACCGATG TAAACGGAGA AGAACATAAG AATAACTACG CAGTTCGTGT

253101   TGGAGACAAG TTATTTTTAT TACATAATGG AGAAGCTGCT CAGTCTGTTT

253151   ATTCTTCTGG GGAATCTTGG AGCTTGTAG ATCACAAGTG TGGTTTCGAT

253201   AATATTCACT TGGCTTTATA TCGTCAGCAG GGTTCTTCTT TCAATCCTAC

253251   GAATACGGGA AAAGTTTTTC TTCCTACGAA TCATGAAGGT TTACCTGTAC

253301   TAGTTGTTGA GTTTCGTAAC AATAAAGAGC CTTTAGTATT TCTAGGTGAG

253351   TACGCACAAG GAAGAATTTC CAATAAAGAT AGCACGATCT TTGGTACAGC

253401   GCTTGTCTTT TGGAGATCAG GAAGCGACTA TATTCCTTTA GGTCTCTATG

253451   ATTCTCGAGA AGAAAAGTTA GTTTCTTTGG ATCTTCCTAT TACACGAGCT

253501   GTAATTTTTG GTAATGACCA AGATTCGGCA AAGTCGTCAG ATACTGCGAA

253551   CCACTATGTT TTATTTAATG ATTACATGCA GATTATTGTT CTGAAGAGA

253601   GTGGTTCTAT AGAAGGTATC AATTTACCTT TTGCTTCAAC AAATAATAAA

253651   AGCATTGTGA ATGAAATTGG TTTTGATAGG GATTTAGCTT CAGAGAAATC

253701   TCCTGAAGCT CTTTTCCCTG GGCTGTCTTC AAAACTTCCT GATGGCCAAC

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253751   AAGCCAAAAA CTCGATTGGA GGTTACTACC CTTTATTGCG CAGGGGATTA

253801   TTAAGTGATT CTAAGAAATT ACTTCCTCTA GAGTATCACG CATTAAATGT

253851   GGTTTCAGGA AGAGAGCTAG CGACTCCTGT GGCTTTAAGA TACCGAGTTC

253901   TTTCCTATAC CCCCCATTCC ATTCAATTGG AAAGCTTAGA TAGATCGGTT

253951   CAGAAGGTAT ACAAACTTCC AGAGAATCCG GAAGAAAAGC CCTATGTTTT

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254051   CAGGAGTTCC TGAAGTGGAG ATCATGTCAA ATGCTTCAGC CCCAACCATT

254101   AAATACAGGG TTATCAAAAA AAATAAGGGG TCTTTAGATA AAGTTAAGCT

254151   TCCAAAAGTA AAAGAGCCTT TAGCTATACG TCGTGGTGTT TATCCTCAAT

254201   GGATTTTAAA TTCGAATGGA TATTTCGGTA TTATTTTAAC TCCGTTGTCT

254251   GAAATTGCTT CTGGCTATGG ATCTCTCTAC ATTTCGGGTT CTACGGCTCC

254301   GACAAGATTG TCTGCTATTT CTCCTAAAAA TCAACTGTAT CCAGTATCAA

254351   AATATCCTGG ATATGAGACC TTGCTTCCTT TGCCAAAAGA TGCAGGGACA

254401   CATCGATTTT TAGTGTATGC AGGTCCCTTG GCAGAGCCTA CACTTAAAGT

254451   ATTAGATAAG ACAATTACTC AGGAGAAGGG AGAAAATCCT GAGTATCTTG

254501   ATAGCATTTC TTTCCGTGGT GTTTTTGCAT TTATTACAGC TCCTTTTGCA

254551   GCACTCCTAT TTATTATTAT GAAGTTCTTC AAATTGGTTA CGGGTTCTTG

254601   GGGAATTTCC ATTATTTTAC TTACTGTATT TTTGAAATTG CTTCTCTATC

254651   CTTTAAATGC ATGGTCCATA CGATCTATGA GGCGTATGCA GATTTTATCT

254701   CCTTATATTC AGCAAATTCA GCAAAAGTAT AAGAACGAAC CTAAGCGTGC

254751   TCAGATGGAA ATCATGGGCT TGTATAAGAC AAACAAAGTG AATCCTATCA

254801   CGGGTTGTTT ACCTTTATTG ATACAGCTTC CTTTCCTAAT TGCGATGTTT

254851   GATTTATTAA AGTCATCATT CTTATTACGA GGAGCCTCGT TTATTCCTGG

254901   GTGGATTGAT AACTTAACAG CTCCTGATGT GTTGTTTTCT TGGCAGACAT

254951   CGATATGGTT TATTGGAAAT GAGTTCCACT TACTTCCTAT TCTATTAGGT

255001   ATAGTGATGT TCTTACAACA GAAGGTCACG AGTTTGCATA AGAAAGGACC

255051   TGTTACGGAT CAGCAGAAAC AGCAACAAGT TATGGGGAAC ATGATGGCGA
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255151 TGGCTTTCGT CTATGATTTT AGGAGTCGTC CAGCAGTGGA TCACTAATAA

255201 GATATTAGAT AGCAAACATC TTAAAAATGA AGTGGTTTTA AATAATAAAA

255251 AACATCGATA ATACTGAAAA AAAAGTCGAA TTGTCTTAAT ACAGGCTTAT

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255351 TTTCTTTTGC TACAAGAGAA AGAAATTGGC ACAAATACTG TAGACAAGTG

255401 GTTGCGATCT TTAAAGGTCT TATGTTTTGA TGCTTGTAAT TTGTATCTTG

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256201 GCATTCAAGA AACGGCCTTA GATTTTTTAA TTTATGCGCT ATCTTCCAAC

256251 GTAAAGACCT TACTGCATGC ACTGAATCTT TTAGCAAAGA GGGTAATGTA

256301 TAAAAAACTC TCTCACCAAT TACTATATGA AGATGATGTG AAAACTCTTT

256351 TAAAAGATGT TTTAGAAGCA GCAGGAAGCG TTCGTTTAAC TCCTTTAAAG

256401 ATTATTCGTA ATGTTGCTCA ATATTATGGG GTCTCTCAGG AGAGTATTTT

256451   AGGACGTTCT CAGTCCCGAG AATATGTATT GCCACGTCAG GTAGCCATGT

256501   ACTTTTGTCG TCAGAAGCTT TCACTATCAT ACGTGAGAAT AGGCGATGTC

256551   TTTTCAAGAG ATCATTCGAC GGTAATCTCA TCCATACGAT TGATTGAACA

256601   AAAAATAGAA GAAAATAGCC ATGATATTCA CATGGCTATT CAAGATATTT

256651   CTAAGAATTT AAATTCCTTG CATAAGAGTT TGGAATTTTT CCCTAGCGAA

256701   GAGATGATTA TTTAGAGGAG TAACGATCCT CTAATTTTTG CTTCTGGACA

256751   GTTGCAGCAG CCGGCGCAGA TATCATTTTC ATTGAGTTCA ACTCCGCTGT

256801   TCTAGCTTGT TTAAATTGTC TAATATGATT GAAAGCAAGG ACAAGAGCAA

256851   TACCAGCAAG TACTATCTGT ATAGCAAGAA CAATGCCGAT TCCTAAGGAT

256901   AGGGTGACTC CACTGGCAAT AACCAGTCCT AGGGTGGTTA AGGAAGCAAG

256951   GAGGAGACCT AGACTAACTA AAATAGGCTT AAAAAATACC CAGGAACAAT

257001   AACGATGTGT TGCCTTGTGA GATACTGATG GTTGTGGTTG TGTAGTCTGA

257051   GGTGTTTGTG CTACTGTAGC CATGTTGTTC TCCTGAGTAA AAAATTAAAT

257101   AATTTTAATC TGTCTATATA ATTGTTGTCA ATAATATTTT TATAGATATT

257151   ATTTTAATTT TATTAAAATT TATCAACTAA TTTTATTTAT AGTCTTTCTC

257201   TAGTTCAGAA CTATTAAGCT CTCTTAATAG GCTCTCTTTT ATTTACCAAG

257251   GCGAAGTTCT TTTTTTTTTT TCAAATTTCG CATATGGAGG GTTCTAGATG

257301   GTATTTGAAA TGGTTGCATT GTGGAAGATT TTTCGAGTTT TGATAAGAAC

257351   AAAGTCAGTG TTGACTCTAT GAAACGGGCG ATTTTAGATC GTCTGTATTT

257401   AAGTGTTGTA CAATCACCAG AGTCCGCATC TCCTAGAGAT ATCTTCACAG

257451   CTGTTGCAAA AACTGTTATG GAATGGTTGG CCAAGGGGTG GCTGAAAACT

257501   CAAAATGGCT ACTATAAAAA TGATGTAAAA AGAGTTTATT ACCTTTCCAT

257551   GGAATTTCTC TTAGGGAGAA GTCTAAAAAG CAATCTTTTG AATTTAGGAA

257601   TTCTAGATTT AGTAAGGAAG GCACTAAAAA CTTTAAATTA TGACTTTGAC

257651   CACCTTGTAG AAATGGAATC CGATGCAGGA TTAGGAAATG GTGGTTTGGG

257701   GAGACTGGCA GCTTGTTACT TGGATTCTAT GGCTACATTA GCAGTTCCAG

257751   CCTACGGCTA CGGTATACGC TATGATTATG GTATTTTTGA TCAGAGGATC

257801   GTCAACGGGT ATCAAGAGGA AGCTCCTGAC GAGTGGCTAC GTTATGGAAA

257851   TCCTTGGGAA ATCTGTAGGG GAGAGTACCT CTATCCCGTA CGATTTTATG

257901   GAAGGGTCAT TCATTATACC GATTCTCGAG GGAAACAGGT GGCAGATCTT

257951   GTCGATACCC AAGAGGTATT GGCGATGGCT TATGATATTC CGATTCCTGG

258001   GTACGGTAAT GATACTGTAA ATTCTCTAAG GCTATGGCAA GCACAATCTC

258051   CGCGAGGCTT TGAATTCAGC TATTTTAACC ACGGGAACTA TATCCAGGCT

258101   ATAGAAGATA TCGCCTTGAT AGAAACATC TCTCGCGTCC TCTATCCTAA

258151   TGATTCTATT ACTGAGGGGC AGGAATTGCG TCTCAAACAA GAGTATTTTT

258201   TAGTTTCAGC AACCATTCAA GATATTATCC GCAGATATAC AAAGACACAT

258251   ATTTGTTTGG ATAACCTTGC GGATAAAGTC GTAGTACAAT TAAACGATAC

258301   CCATCCCGCT TTAGGGATTG CTGAAATGAT GCATATTTTA GTCGATAGGG

258351   AAGAATTACC TTGGGATAAG GCTTGGGAGA TGACTACAGT CATCTTTAAC

258401   TATACCAATC ATACAATCCT CCCAGAGGCT TTAGAGAGAT GGCCTCTCGA

258451   TTTATTCTCT AAGTTATTAC CTCGGCATTT AGAGATTATT TATGAAATAA

258501   ATTCCCGTTG GTTAGAAAAA GTTGGCTCTC GCTATCCTAA AAATGATGAT

258551   AAGCGCCGGT CTTTATCCAT TGTTGAAGAA GGGTATCAAA AGCGTATCAA

258601   TATGGCAAAC CTTGCCGTAG TAGGTTCTGC AAAAGTAAAT GGAGTTTCGT

258651   CATTCCACTC TCAGCTGATT AAAGATACTC TCTTTAAAGA GTTTTATGAG

258701   TTTTTCCCTG AGAAGTTTAT CAATGTGACC AATGGGGTGA CTCCACGACG

258751   ATGGATTGCT CTCTGTAATC CTCGTTTGAG TAAGCTTCTC AATGAAACTA

258801   TAGGGGATCG TTATATCATT GATCTTTCTC ATCTTTCATT GATCCGTTCC

258851   TTTGCCGAAG ATAGTGGTTT CCGAGATCAT TGGAAGGGG TAAAATTAAA

258901   AAATAAGCAG GATCTAACAA GTAGAATTTA TAATGAAGTT GGAGAAATAG

258951   TAGACCCTAA TTCTCTCTTT GACTGTCATA TTAAGCGTAT TCATGAGTAT

259001   AAACGACAAC TAATGAATAT TTCTTAGAGT CATCTATGTT TATAATGACT

259051   TGAAAGAAAA CCCTAATCAA GATGTCGTCC CTACAACAGT AATTTTTTCT

259101   GGTAAGGCGG CTCCTGGCTA TGTCATGGCC AAACTCATTA TCAAGTTAAT

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259151   CAATAGCGTT GCTGACGTTG TAAATCAAGA TTCTCGAGTT AATGATAAGC

259201   TTAAGGTTCT TTTTTTACCT AACTATCGAG TTTCTATGGC TGAGCATATC

259251   ATTCCTGGTA CAGATCTTTC AGAACAGATT TCTACAGCTG GAATGGAGGC

259301   TTCTGGAACA GGAAATATGA AATTTGCTTT GAATGGAGCT CTGACTATAG

259351   GAACTATGGA CGGTGCAAAT ATAGAAATGG CAGAGCATAT TGGTAAGGAG

259401   AATATGTTTA TTTTTGGTCT TTTGGAGGAG CAAATTGTAC AACTGCGGAG

259451   GGAATACTGT CCTCAGACAA TTTGTGATAA GAATCCTAAG ATCCGTCAGG

259501   TTTTAGATTT GCTAGAACAG GGATTTTTCA ATAGCAATGA TAAAGATCTG

259551   TTTAAACCGA TAGTACATCG CCTACTGCAT GAAGGAGATC CCTTTTTTGT

259601   CTTGGCTGAC TTGGAGTCTT ATATCGCTGC CCATGAAAAT GTGAACAAAC

259651   TCTTTAAGGA ACCAGATTCA TGGACTAAGA TTTCTATTTA TAATACTGCA

259701   GGAATGGGCT TTTTCTCTAG TGACAGAGCC ATTCAGGATT ATGCCAGAGA

259751   TATTTGGCAT GTTCCTACAA AATCTTGCTC TGGAGAAGGA AATTAAGAAA

259801   TAGACAGGAT GGAATCAGGG ACTCTTTCCA TAGCCAAGGA GCTATAGAAA

259851   GAGTCCTTTT TGTTCAAAGA TTGCTAGTTT AATAGTAGGA CAGCCGGAGC

259901   TTCTAAGATC TTTTGTAATC GTTTCATAAA CATCGCAGCA GGATAACCAT

259951   CAATCACTCT ATGATCTACA GATAGGGTAA GATTGCAGGT AGATCCTATA

260001   GTAATTTCTC CGTCAAGAAC AAGAGCTTGT TCTGTAACAC TTCCTACGGC

260051   AAGAATCGCC GCTTGAGGAG GATTGACAAT CGCTGTAAAT TCAGTGATTC

260101   CTGTCATTCC TAAGTTAGAG ACACAGAAGG ACCCTCCTTT GTATTCAGTG

260151   TCTTGAAGAG ATTGATTTCT TGCTTTTAAC GCTAAGCTCT TAATTTCTGC

260201   TGAAATCATG CCGAGATTTT TACGGTCTGC GCAGCGTATA ATTGGCGTAA

260251   TAATTCCATC TGGAATGGCC ACAGCTATCG AGATATCGAT AGTATCAAAA

260301   CGGACGATTT TATTATCGAC ACTGTTAAAT CCTGAATTGA TAGAAGGGAA

260351   CTCTTTGAGC GCCAGAGCAC AGGCACGTAC AATGCAATCG TTAATAGAGA

260401   GTTTGATTCC CTGAGCTTGA AGTTCTTTGA GCAGATTAAG GAGAGGTGAG

260451   GCGTAGACCT GCTGCCTTAC ATAGAAGTGA GGAATAGAGA TCTTAGCAGC
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193

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260501   TTGTAGGCGT   GCAGCAATCA   CTTCCCGAAT   CGGAGAGAGA   TTCTCCTCAT

260551   GATAGGAACC   TGGAGGCACT   TCGGGAGACT   CAGGATAGCC   AAAACCAGCA

260601   ATGCTTTTAG   GAGGAGCTTT   CTCTAAATCT   TTTTTTACTA   TACGTCCTCC

260651   AGGACCACTC   CCTTGAATTG   ATGAGACATC   TATGTTTTTC   TCTTTTGCTA

260701   GTTGTCTAGC   TAATGGAGAG   AGATTATTCG   TAGTGCCTAC   GTGTTTGAAG

260751   ACTAAAGGCG   AGGAGAGAGG   TGGCTCTGGC   TTAAAAGTTA   CTGCTGTGAA

260801   TGTTGCTGAG   GCAGCTTGTG   GAGTTGTTGC   AGGCGAGACC   TCTTCAGAAG

260851   AACCTTTTGG   AGATGCTTCA   AGGTTAGAAG   GTTCTGTCTT   AGGAAGAAGT

260901   TCTTCTAGAT   TAAAGGGCTC   GTTGGCTTCT   GTAGAGAGTA   CCGCAATAGG

260951   GGTGCCTATA   ACGATTTTCT   CGCCTTCATG   ACGTAAGATT   TCACGAATCC

261001   AGCCATCTTC   ATTTGCTGTA   TGTTCTAAAA   TAGCTTTGTC   TGTAGAGATC

261051   TCTACAATGA   CGTCTCCAAA   ACTGACCTGA   TCATTACTTT   TTTTATGCCA

261101   TTTCACTATA   GTGCCCACTT   CCATAGTTGG   AGAAAGCTTT   GGCATTTTCA

261151   ATAAGGAGAT   CACAAACTTA   CCTCATGACT   TTTTCAATGG   TATCTAAGAT

261201   TCGGTTAACA   TTAGGCAAAG   TGGCCTGTTC   TAAGATTTTA   CTATAGGGCA

261251   TAGGCGTTTC   TTTTTGGCAT   ACCCTTAAGG   GGGGAGCATC   AAGAGAATCA

261301   AAAACATGCT   CAGTAATCAG   GGCAATAATT   TCAGAAGAAA   TCCCAGCGAA

261351   GTAGTGGCCC   TCTTCAATTA   CAATACAGCG   TGAAGTTTTT   CGTACCGATG

261401   ATAAAATTGT   TGATATGTCT   AAAGGTTTGA   TCGTTCTTAG   ATCAATAATT

261451   TCTATAGACA   AGCCCCAACG   TTTTTTGGCT   AGAGAACACG   CTTCTTTTGT

261501   AATGGAAACC   ATACGGCTAT   AAGTAATAAT   TGTAAGGTCA   TTTCCTTCTT

261551   GAACTCTATG   TGCTTTCCCA   ATAGGAACGA   GATATTCTTC   GGTGGGGACT

261601   TCCCCTTTTA   AGTTATATTC   TAGCTCGTTT   TCTAAAAAAA   GAACGGGGTT

261651   ATTATTTCTG   ATTGCTGATT   TTAATAAGCC   TTTAGCGTCG   TAAGGGTTCG

261701   AAGGGGCTAT   AATAATAAGA   CCTGGAATAT   TAGCATACAA   CGACTCAACG

261751   CAATGAGAAT   GCTGGCAAGA   TACCTGGGCT   GCAGCACCAT   TAGGGCCACG

261801   AAAAACTATA   GGAACGGAAA   ACTTCCCTCC   AGTCATAAAA   TGCATCTTAG
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194

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261851   CTGCATGAGA AATGATTTGG TCCAAGGCTA CAAAGGAAAA GTTCCAGCTC

261901   ATAAATTCTA TAATAGGGCG CAGGCCTGAC AATGCGGCTC CTATTCCAAT

261951   TCCAGAGAAG GCTGCTTCAC TAATAGGAGC ATCAATGACT CTCTTAGGGC

262001   CCCATTTATC TAATAAGCCT TTGGTGACTT TATAAGCACC ATTGTAGTCA

262051   CCAACCTCTT CACCAAGAAT ACAGACATTA GGATCGCGAG ACATCTCTTC

262101   GTCAATTGCT TCTCGGAGAG CTTCTCGAAT TTCTAATGTT TTATGTTTAG

262151   GCATAGACTC CTTCCTCTAA TGTGGTGACG GATGGATCTG ATGAGAGTTT

262201   TGCGTTAGAG AACGCTTCTA AAACAGCAGT TTTGCATTCT TGGCGTATAT

262251   TTTGAAATTC CTCTTCAGTC AGAACCTCTA ATCGAATTAG CCAATCTTTA

262301   GCTAGGACAA TAGGATCTTT TTTAAATAAA CACTGCATTT CTTCTTTCGA

262351   TCTATATAAA TTAGGATCTG ATATAGAATG CCCTCGAAAT CGGGAGCAGA

262401   GACACTCAAC TAAAACCGGA GATTCGGTAT CAACCATATA GCGATAAGCC

262451   TCTCTAAATC CTAAAGAGA GTTAAATAGA TCAAAACCAT TGACTGTGAC

262501   TGCACGGATA TCGTAGGAAC TTCCTTGAGA CTCTGCTATG GGCTGTTTTG

262551   CAACAGCACG ATTTAATGAC GTTCCCATAC TCCAGCCGTT ATTTTCAATA

262601   ATAAGCATTA GAGGGAGTTG GTGAAGAGAA ACAAAGTTCA GAGTTTCATG

262651   GAATACACCT TGAGCTACCG CACCATCTCC GATAAAGCAT AGAGAAACTC

262701   TATTTTTTTG TTCTTGATAT TTGATGGTAA ATGCGGCTCC AGCTGCGAGG

262751   GGAATTTGTC CTCCGACAAT ACCAAATCCT CCAGGGAAAT TAGGCCCACA

262801   CATATGCATG GATCCTCCAC GACCTAAAGC GCATCCAGTT TCTTTCCCTA

262851   AAAGTTCAGC AGCAATTTCT TGAAGGGGAA TGTTGAGAAG AATCGCAAGT

262901   GCGTGGCAGC GGTATGAAGA GAACACCCAG GGATCTAGTC CTGTGTTTGC

262951   GATTGCAGCA GTTGCTACAG CTTCTTGGCC AGCGTAAGAG TGGTAAAATC

263001   CACCCACTAG CCCTTCTAGA TAGGCTTCTT CTCCTCGGGC TTCGAATTCA

263051   CGAATCAGAA CCATCTGTTT TAAAAATTTA ATACAGGAAG CGGGCCCGTA

263101   AAGGTCTAAG ATCCTTTCTA CTGTGGATTT CTCTGTGCCC TGAGAAGCTA

263151   TATTATAAGG TGCTGAACTA TCCATAACTT TTTTATAAGG GAGACGCTTC
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195

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263201  GGGAGCGGTT TTTGATCTCA TTATAGGAGC CTAGGTTTCA AAAGACAAGG

263251  GCTATCCGAA GAAAAAATAA TTAAGTTTTT TTAAAAAATC GAAAAAATTT

263301  TAATATGTTT CTCGTGGCAA TTTAAAGAGA ACAAAAAGGA TTACATCACA

263351  TGGACGTTTC TCGTAAAATT AATCGACACA CTCAGTTTTA CGTGGATTCG

263401  ATAGACGGTG TCATCAAAAA CTTTGATCAT AAGCCTAGTG AAGATAAATC

263451  TCGAGATCAT GAAGAATTAG AGGAAAAGCT TTTAACTATA ACAAACGTA

263501  TTGTTGCTTC TGCTCAAGAA TTTCAGAATC GTAAGACGGA CTCTAAAAAC

263551  TACTACTTAA AAAAAACTCA ATGGTTGCCA TTCAAAAATG AAGAGTTGGA

263601  GCAAACTAAG GAATTGTTTG CCATGTTAAC TTCGATGGAT AAAAAAATAG

263651  CTCAGTTATT TTTTTATTCT CCCGGATGTA GTAGCGACTG GGTAGAATTT

263701  ACCGAAGTAA TTTGTCATTT AAATGATTCT ATAGGTTTGG GAGGGGTTTT

263751  ACTGTGTTGC GGATTATTCG AACAACAGTG TGAGCATGTT GTTACTGTGA

263801  ATAAAAAGCT AGACCTACCG CTTCTTTTAG GAACTACCGT TGTAAATAGT

263851  CTACGTTATT ATTTAACCTA TAGGAATATC TCTCTTTTGA ATTGTCAGAG

263901  CATGAGTGAG CTAGGCAAGG AGCTCGGGGA TGTTTTAAAG CAACATGGAG

263951  TTGCTTTCAC TTTAATTTTT AAAGAGATTG TGGATATAGA TTTATTAAAC

264001  TATGTGAAAC TAATTCAAGG ACTCAAGCGT AGTGGAAATA TTCAAGCACG

264051  TATTTATGAT AATGATGTGC CTACTTTACC TTCAGTTTCA TCGAGTCCTA

264101  TTGCGTTGAG ATATAGCTTA GCGAATACAA TTCGGGGCCT TGCTTTACAT

264151  GTAGATTTTT CTTCATTGAA GTTTATAAGC CCGTCTATAC TTTCCAATAC

264201  AGAGCACACT GCAAAGCTT TAAACTCTGG CGGAGAATGT TTTATCTTTT

264251  CTAATCTGGA TGAATTCAAT CTTGGAATGA AAATAGTCAT GCAACTATTG

264301  CGGACAGGGA AGATTAGCCC AGAAATTTTA AATAAAAATA TCATGAAAAT

264351  TCTCATGATA AAAGAAGAG TACGTTCTTT ATATATTTAA TTATTTGGTC

264401  TTTTTTTTGA TTTCAAAACT AATAAAATAA ATAGAATTTT AGATCTCTGA

264451  AGGAATCTCA GCAAGGCTGG GAGTCGATAG ATCTCTTACT TGTTTTTCTA

264501  ACTTACTTAG TCTTTCTTCA GTTTTAGGAA GGTTCCGAAT TTTAGCAATC
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264551  AACCGATGTG TTTCTTGATA AGGTCGTGCT GGAGCGCCTC CATAAATGCC

264601  TGGAGAGGTG ATAGATTTTG TGACTCCAGT TTGAGCAATC ATGATCACAT

264651  GGTCTGCAAT AGAAATATGC CCAGTAATTC CGGTTTGCCC TCCAATGATG

264701  ACATGTTCAC CAATTTTTGT AGAACCTGCA ATGCCTGCTT GGGCAACAAT

264751  AATACTATGC TTTCCAATTT CTACGTGATG AGCTACTTGT ACTTGGTTAT

264801  CTATTTTAGT TCCTTCATGG ATCACGGTGT TCTTGAATCG ACCACGATCT

264851  ATCGTAGTGT TGGCTCCGAT TTCTACATCA TCACCTACAA TCACATAGCC

264901  TAGATGCTTT AAAGGTTTGT GATGACCAAA AGCATTGTA ATATAACCAA

264951  AACCACAGGA TCCTAAAACA GCTCCAGGTT GAACAACTAC ACGGTTTCCC

265001  ATGAGGACTC TTTCTCGAAT CACCACCTTA GGGTGAATCA GACAGTTAGC

265051  ACCTAGAACG CTGTGAGCTC CAATGACACT TCCAGCTCCG ATGTATGTGT

265101  CAGAGCCGAT ATGGGCATGT TGACTAATGA CAACGTAAGG TTCTATGGTT

265151  ACATTTTTCT CAATACGTGC AGTAGGATGA ATCACTGCAG TAGGATGAAT

265201  ACCAGGAAAC CCTGATGTTA CGGGTTCAAT AAACAACTCT ATGCACTTTT

265251  GAAATGTTAG AGAAGGGGAT TCATTGGTAA TAAGAAAGTT TTTCTTTAGG

265301  TGGGCATGTT GCATTGCCTG AGATCTAGAT AAAATAATAG CACCAGCTTT

265351  GGTGTTTTTT AGAAAGCTAG AGTATTCTC ATTATCTAAA AAAGCAATAT

265401  GGTGAGGTTG CGCCTGACTA ATATCTTCAA CACCTGAAAT AGGAGTTTCT

265451  ATATTTCCTT GAACTTCGAC TTGTAGTAGC TCAGCTAACT GTTTAAGAGT

265501  GTAGACTGGT GCTTCGGACA TAGAAAACTC CTTAAACTTG GACTAGTTTT

265551  GTTTTTTGAA AGATTCGTTA AGAATAGCAA TAATTTCGGT TGTTTTATCA

265601  GTCCCAGGTG CTATTGCTAA GACAGCTTCT TCATTAAGGA TAGCTTCTAG

265651  TTTTTCTTTG GACCGCACTG ATTCTGCAGC TATTTTTACT TCTTGAATGA

265701  GTTTTTGAAT GCGTTTTACA TGTACTTTGA TTGATAGATT GATAGTACTG

265751  AGACTGGTAC GCATTGTACT CTCCTGAAAG ATCTTCGAAT TTCTTTCGCA

265801  ACTCTTCAGA GGCAGAATCC GATAGGCTTT CCATGTAATC TTCATCTTGC

265851  AACTTATTAT AAATAGAAGT GAGTTCTTCT TCTATTTTCT CAGCATTTTT
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197

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265901   TACAAACTGC TGTTTCATAG CTTCCAATTC TTCAGTTTCC TTTTTACCTA

265951   GATCGGATTC TTCAAGACAT CGCTTTAAAT TAACATAGCC TAAATTTGCA

266001   TGAGCTGCGC TTGTTGATCC TAAAACAAGA AGAAATGTAG AAAATAATAA

266051   TTTTTTCATA ATTACCTGTA CTAACTTGGG TATAGAAAAA GGGTACCAAA

266101   AGCCTTTTCT GAAACAACA AAGATTTCCT TCGATAAGTC CTTAATTTAT

266151   ATCTTAGAAC ATGCCCCCTA AAGCAAAGAA GAATCGCTGA GATACATCAA

266201   TTTTTTCTCC ATTCAAAGTC TCGGTTGGAC GGAAGGGCCA ACCAAATCCT

266251   AACATAACAG GAACATTATT CATTACATCG AAGCGCAGAC CAAATCCAGC

266301   ACTACTACGT AGATCTTTTA ACGAAATCTT ATACTCTTGT AAACCGACAA

266351   AACCTGAGTC TAAGAATACA AAGGCACTAA TATTAGGTTG TCTGATGAGA

266401   GGGTATTGAA ACTCTTCTGA AATAAGGAGC GAAGAGAGTC CTCCCTGAGG

266451   TTCTGTAGCA GAGTATTTTG GACCGATAAT AAAGGATTTA TATCCCCGAA

266501   CTGTAGTCTC TCCACCTAGG AAGAAGCGCT CACTGACAGG AACTCCTTCA

266551   GCTGTAGTAT TGCTATAGGG TTTAATAAAT TGAGCTTCCC CTTTGATTTT

266601   CAAAATACCT TTACGCGTAA GTTTTCTATA GATAGAGCTG TTTAAAGAGA

266651   GTTTTGTAAA ATGATAAGTT CCTCCCAAAC CAGAAACCTC AAAAGTCACC

266701   CCCCCGCGAA TCCCTGTAGT TGGAGTTCTA GGACTATCTA CAGAATCGTA

266751   ATTCAAGTTG ACACCTGCAG CAGAGACAAA TCCTTTATTG CTGTCTATAT

266801   TTGGCCCTAG GAGGAACTTA CGTTTTTCAT GTAAACTCGT TTGACTTCCT

266851   CGATAAAATA GACCGTATTT CAGGTGTTCG TTCAAGATAT ACGTTGTGCT

266901   GACGTTCCCG CCATAGGTTT GGACAGCATA ATCTTTAGAT AATGCTCTGT

266951   TAATTGATTT ATCTAATTCA ATTCCTAAAA TCCAAGGAGT GTTTAGAAAA

267001   TGAGGTTTGG TCCACTTCAA AGTATAGTCT GTGACTTTGT CCCCGAAGTT

267051   GGCTTTTAAG AATAGATGTT CTCCACCGCC TCTTAGACAA CGAAAACCTT

267101   TAGAAAATAT ATTTCTAGCT CCAAATAGAT CAAAATTACT TTCAGATAGT

267151   TCAATTCCTC CAAAAAGATT GTCAAGAGAA CTAAATCCTA AGAATAAGCC

267201   TAAGTTTCCT GTTGTTGTTT CTTTGACTTC TACAAAAATA TCTCGGTATT
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198

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267251  GATCCGCATT GCCCATAGGA TCAAGTTGAG AACGAACTGT ATAGACACTA

267301  ACGCTTTGGA AGTAGCCTGT ATTTCTTAAA CGTTGCTCAG TATCTTCTAG

267351  CTTTAAGCGA TTGAATGTAT CTCCTGGGAA GAGACTGGTT TCGTGTAAAA

267401  TAACGTCAGA TTTTGTATGG GTATTCCCAG TAATTTTAAT TAACCCAACT

267451  TTATAAGGAG ACCCTTCACT TACCTCATAA GTTACATCAT AAATAGGGCG

267501  GGTTGCGTGA GGGATGAAGA GAACGTCTAC ATTGGTATTG ATGTAGCCAT

267551  ACTTTGCATA AGTTTGTTTG ATCTTATGAG CCCCATCCCA TATTTTATCG

267601  GGGCAATAAA GATCATTGGG GCCGACTTGG GATTGCTTTT CTATAAGGCG

267651  TTTTGGCAAA ACCTCAAACC CTTGGATATG GACGTGTCCT AAGGTATATC

267701  GCGACCCTCG ATCAATATCC ATGTAAAGAA GAATATTCCC TTTGTCGTCA

267751  AGGTCATAGT GAGAGTTGAC TATAGCATCA GCGTACCCGT TATTATGTAG

267801  GTAATTCGTA ATTGCCAAGC TATCTTGTTC AACAATATCT GGGTGATAGA

267851  GTCCAGCTCC AGTAAACCAA CTTGTAGTTG TAGAGTGCTG CTTGGTTTGA

267901  ATAAATTCTT GGATATCTGA TTTTTCTGAT CGAGAGATTC CTGAGAACGT

267951  AAGCTGTTTA ATTTTCCCGC AAGGACCTTC ATTGATTTTA ATTAAAACAT

268001  CGATGTGACC TTTTTCTTGA TTGTGTTCCA GACTGTAGTC TACACTGGAT

268051  GCGAAATATC CTCGCTTGAG ATAATACGTT CTTAGATCAT CAAGACCCTT

268101  AAGAAATTTT TCTCGTTCAA AGAGATCATT ACGGTAAATT TGTAGGGTTT

268151  TAAGAATTTT ATGTTCAGGA ACGACTTGAT TTCCTGAGAT ATGAATATTT

268201  CGAATTGAGG GTTTAGCTAT TAGGTGAAGG GCTATGTTAG TTTTCCCTTC

268251  AGAAAATTCT ACTTTAGGCT CAACAGAGTC GTATTCTTTA GCTAGAATTC

268301  TCAAGTCTTC ATCAAAATCT AATTGAGAAA AAAGAGCCCC ACTTCTGGTC

268351  TTTAATTTGG GTAAGGGATG TTTATTTGAA GCATTTCTC CTTCCGTTAT

268401  GATTGTGATA GAGTCTACCA CCACATGGCC TTCTTTAACT TTTTCAGTAG

268451  AAAATAAAGT TAAAGGGGTT TGGATTAACG CTAGAATAGA TATTTGCAAG

268501  ATAACTTTAT TTCGCATGAT GAGCATTCCC AAGAGTCTTC CCTAGATAGA

268551  AAGCTTGTTT ATCAGATAAT GAGGTAAGCA CAAAAATAGG GACAAAGAAG
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199

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268601   TTTTTTAACA AGACCTTACT ACTTAGATTA TTTTTGTATT TCTAAAGAAA

268651   TTTAAATTGT GTTTGATTTT TTCCCGTCCT AACACCGGGA TTATTACTGT

268701   GCTCAGACTA GAGCCTGAAT ATTTCGGCGG GTTTTTTGCT TCCTTAAAAA

268751   GCTTAATAAA CCTTGTCGCT CAAATAACTC TACTGATTAC ATGGTTTTAA

268801   GGCAAATTCG ATAATTCACT GTGTCCTAGG GGAAAGTAAG AAAGACTAGC

268851   ATAGAAGAGA ACCTTGTTTA CTTTTAGGAT AAGAGAGCTG CTAATAGGAG

268901   TGTCGTCCAG AAAAAGCTCT TGCCAGTGTC CCTGAATCTA CATAATCAAA

268951   AGATAAGCCT ATAGGAAGAC CTAAAGCTAG ACGGGAAATA TTTACAGAGA

269001   AATGTTGTAA TTCTTGTTTT AGAAAAGGG CAGTAGCATC TCCTTCTAAG

269051   GTTGCATCAA TGGCTAGGAT AATTTCTTTT GGGCATAGCG TTTCTATGCG

269101   TGATTTTAAA ATGGAGAGAC GCTCGTTTTC TATATGTTTC CCTGTAATGG

269151   GCGATAAGAG TGAACCAAGA ACATGATAAC GTCCCTTGAA TACTTTAGAA

269201   CGTTCTAGAA AGAAACATC TTTTGGAGAA GCGACAATAC ATAGACTTTG

269251   GTTATCTCTT TCTTCTCTAC AAAAGTGACA GTCTGCCTCT TTAGATTCTT

269301   TGAGAGTAAA ACATAGGGGA CAGTGACTAC GCTCACTAGC AACATTATGA

269351   AAAGCGTTAC CTAATATTTT TAATTGTTCG CTGTCCCAAG AGATGAGTTC

269401   AAAAGCAAGT TTTTCTGCTG TTTTAAATCC AATTCCTGGA AGTTTTCGTA

269451   AAAAGAAAAT TAATTTAGAT AAGTAATCTG GATATCTTGT CATAGTGATG

269501   TGAATTTTAT TTTTACATTC GGGTCTGGGG CCTAAATTAA GGTTAGAGTA

269551   TAAACTCTCT GAATAGTATA CTAGCTTTTT TCTTTACATG TGGTTCTCTG

269601   TGAATAAAAA CAAAAAAGCA GCAATTTGGG CAACGGGTTC CTATTTGCCT

269651   GAGAAAGTTC TTTCAAACGC AGATTTAGAA AAAATGGTAG ATACCTCTGA

269701   TGAGTGGATC GTGACCAGAA CGGGGATCAA AGAGCGTCGT ATTGCTGGAC

269751   CTCAGGAGTA CACTTCTCTT ATGGGAGCCA TCGCTGCAGA GAAAGCTATA

269801   GCAAATGCGG GTTTAAGCAA GGATCAGATT GACTGTATCA TTTTCTCGAC

269851   AGCAGCACCA GATTATATTT TCCCATCAAG CGGAGCTCTT GCTCAAGCAC

269901   ATTTAGGCAT TGAGGATGTC CCTACATTTG ATTGCCAGGC GGCTTGTACT
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200

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269951  GGGTATTTGT ATGGTTTGTC TGTAGCTAAG GCTTATGTAG AATCAGGTAC

270001  ATATAACCAT GTATTGTTAA TTGCTGCTGA TAAGTTGTCT TCTTTTGTAG

270051  ATTATACAGA TCGGAATACC TGTGTGTTGT TTGGAGATGG AGGAGCTGCT

270101  TGTGTCATAG GGGAGAGTCG GCCAGGATCT TTAGAGATTA ATAGGTTGTC

270151  TTTAGGCGCA GATGGTAAGC TAGGAGAGTT ATTAAGCCTT CCTGCTGGAG

270201  GTAGTCGTTG TCCTGCTTCT AAAGAGACTT TACAATCAGG CAAACATTTT

270251  ATTGCTATGG AGGGAAAAGA AGTTTTTAAG CATGCTGTGA GACGTATGGA

270301  AACGGCAGCT AAACATTCGA TAGCCCTGGC AGGCATTCAG GAAGAGGATA

270351  TAGATTGGTT TGTACCTCAT CAAGCTAATG AAAGAATAAT AGATGCTTTA

270401  GCGAAGCGTT TTGAGATTGA TGAGTCTAGA GTGTTAAGA GTGTACATAA

270451  GTATGGAAAT ACTGCGGCCT CGTCTGTGGG CATTGCTTTG GATGAATTAG

270501  TTCATACAGA ATCCATTAAG CTTGATGATT ATTTACTTTT AGTTGCCTTT

270551  GGGGGCGGTT TGTCTTGGGG CGCAGTAGTT TTAAAGCAGG TCTAATAAGG

270601  ACGATAATTT CATGAAAAAA CGTTATGCTT TTTTGTTCCC AGGACAAGGG

270651  AGCCAATATG TAGGTATGGG ACAAGACCTA TATATGGAGT ATCCTGAGGT

270701  TAGAGAGCTT TTTGATTTTG CTAATGAAAG GTTAGGATTT TCTCTGACTT

270751  CAATTATGTT TGAAGGTCCT GAGGATCTTT TGATGGAAAC AGTACATAGT

270801  CAGCTAGCTA TTTATCTTCA TAGCATGGCT GTGGTAAAGG TTCTATCTCA

270851  GCGTTCTTCT ATTCAGCCTT CTTTAGTCTC TGGATTAAGT TTAGGGGAGT

270901  ATACTGCTTT AGTTGCTTCC GATAGAATCT CCGTGCTCGA CGGCCTTGAG

270951  CTTGTTAGAA AGCGTGGTCA GTTAATGAAT GAAGCTTGTA ATCAGAGCCC

271001  AGGGGCTATG GCGGCTTTAT TAGGGCTTCC CTCTGAAGTT ATAGAGGAAA

271051  ATATAACAAG TCTTGGTCAA GGAATTTGGA TTGCTAATTA TAATGCACCC

271101  AAACAGCTTG TAGTGGCTGG AATAGCAGAA AAAGTAGACC AAGCGATTGA

271151  GTTATTTCGT GATTTAGGAT GTAAAAAGC AGTTCGTTTA AAGGTGTCTG

271201  GAGCATTTCA TACTCCTTTA ATGCAAGTTG CTCAAGATGG CTTAGCTCCA

271251  GACATTTATG CTTTATGCAT GAAAGATTCT AGCCTTCCCT TAGTGTCACA
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271301  CGTGGTAGGA AAATCTTTAG TAAATACTGA AGAAATGCGA GAGTGTTTAG

271351  CTCGGCAAAT GACATCACCT ACGTTATGGT ATCAGAGTTG TTACCATATC

271401  GAATCAGAGG TGGATGAGTT TTTAGAATTA GGTCCAGGAA AAGTTTTGGC

271451  TGGTTTAAAT CGCTCTATAG GGATTTCTAA ACCGATTACA AGTCTTGGTA

271501  CTTTTGCTCA GATTGAAAAA TTCCTATCAG AGGTATGATT TGTATGGATA

271551  TAACATTAGT AGGCAAAAAA GTTATAGTAA CTGGAGGATC TCGAGGAATT

271601  GGACTCGGGA TAGTTAAGCT TTTTCTTGAG AACGGAGCAG ATGTAGAAAT

271651  TTGGGGATTG AATGAGGAGC GAGGTCAGGC TGTTATAGAA AGTTTAACAG

271701  GCTTGGGTGG CGAAGTTTCT TTTGCTCGTG TGGATGTGAG TCATAATGGT

271751  GGAGTGAAAG ATTGCGTGCA GAAATTTTTA GATAAGCACA ACAAAATAGA

271801  TATTTTGGTA AATAATGCAG GCATTACCAG GGATAATTTG TTGATGCGTA

271851  TGTCTGAGGA CGACTGGCAA TCGGTGATTA GCACCAACTT GACTTCCTTG

271901  TATTATACAT GTTCCTCAGT GATTCGCCAT ATGATTAAGG CGCGTTCAGG

271951  ATCTATTATA AATGTGGCTT CTATTGTTGC TAAGATCGGT AGTGCGGGCC

272001  AGACCAACTA TGCTGCTGCT AAAGCTGGGA TTATTGCTTT CACAAAATCT

272051  TTAGCTAAGG AAGTAGCTGC AAGAAATATT CGTGTCAACT GCCTTGCTCC

272101  AGGCTTTATT GAAACAGACA TGACAAGCGT GTTGAATGAC AATTTAAAAG

272151  CTGAGTGGCT TAAGTCGATC CCTTTAGGTA GGGCTGGCAC TCCAGAAGAT

272201  GTTGCTCGTG TGGCGTTGTT TTTAGCCTCG CAGTTATCGA GCTATATGAC

272251  CGCGCAGACA CTGGTTGTTG ATGGGGGATT GACTTACTAA GACAATAGAA

272301  GAAAGGGATT TGAAAATTTC TCTTCGAGAA CTAATTAAGT AACCGTCGAA

272351  TAAAAAATGA TTTTTTGCGA TACTAATTCT CTTTCTCTTT GTCCCTAGGG

272401  AATAGTGAAG TATTGTATAG TTTAAATAGT AAAAGGATAT AAGCAATGAG

272451  TTTAGAAGAT GATGTAATAG CAATTATTGT TGAGCAGTTA GGAGTGGATC

272501  CAAAAGAAGT TAATGAGAAC TCTTCTTTTA TTGAAGACTT GAATGCTGAT

272551  AGTTTAGATT TAACAGAATT GATTATGACT TTAGAAGAAA AATTTGCTTT

272601  TGAAATTTCA GAAGAAGATG CTGAGAAGCT TCGTACTGTC GGGGATGTAT
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272651   TTACTTATAT  TAAGAAACGT  CAAGCTGAAC  AATAAACTTT  CTTATATTCT

272701   GGGTGCGTCG  TAATCTTTTT  TAAAGCTATT  GTTTTTCAAT  AGTGATTACG

272751   GCGTGCCTTT  TTTTCTATAG  AGTAGCTCAT  CTAGAAAGAT  TTATTTTGTC

272801   TTTTTAAGGT  TCTCTGAACT  TGATTTGTTT  AGCATAGAGC  TCTAAAAAAG

272851   ATAAAGCTAC  GGATGGGCAC  TCTTCCACAA  TGTTTAGAAT  TTGTCCTTTG

272901   CTAAGAACTA  GCATGCGGAC  TTGTGTATTT  GCAGAAGCAT  TGTATTCCCT

272951   GGGCTTATTA  TTGAATAAGC  TTTCCTCTCC  AAAACAATCT  AAAGGTTTTA

273001   AATTTAGAGG  AGACTCTAGT  TTTTCTTTAG  AGATCGTAAT  GTATCCTTCT

273051   ACAATGATAT  AAAAGCTGAA  TCCAGGTTGT  CCTATAGAGA  ATACATTGCT

273101   GCCAGGCTTA  AATATTATCG  TTTCAGTTTT  ATCGGCAATT  GTTAAAAGAA

273151   GGTCCATGTC  TAAAGATTGG  AATATAATCG  TTTTTTTTAG  TAGAAAGGCG

273201   CGATCGATCA  AATTCATAAA  AAAGTTCCTT  ATTCACACCA  TAGTTTTAGT

273251   TTTT
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